

Aziz Khan

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EDUCATION	<p>Tsinghua University, Beijing, China</p> <p>Ph.D. in Computational Biology 2012 – 2016 Dissertation: Prediction, analysis and annotation of super-enhancers in the human and mouse genomes Adviser: Prof. Xuegong Zhang</p> <p>National University of Computer & Emerging Sciences, Islamabad, Pakistan</p> <p>MS in Computer Science 2008 – 2010</p> <p>Quaid-I-Azam University, Islamabad, Pakistan</p> <p>MSc in Information Technology 2006 – 2008</p> <p>Forman Christian College, Lahore, Pakistan</p> <p>BSc in Mathematics and Physics 2003 – 2005</p>
RESEARCH INTERESTS	<p>Bioinformatics, computational biology, machine learning, biocuration, regulatory genomics and epigenomics, integrative analysis of high throughput sequencing data</p>
RESEARCH EXPERIENCE	<p>Postdoctoral Research Fellow, Mathelier Lab, NCMM, University of Oslo 2016 - present</p> <p>PhD Research Student, Zhang Lab, Bioinformatic Division, Tsinghua University, 2012 – 2016 Projects: Enhancer prediction, dbSUPER, imPROSE</p> <p>Rotation Student, Jingren Lab, School of Medicine, Tsinghua University, 2012 Project: hands-on experience with molecular cloning</p> <p>Rotation Student, Tao Jiang, Tsinghua University & University of California - Riverside, 2013 Project: Operon prediction and pathway analysis using metagenomic data</p>
PROFESSIONAL EXPERIENCE	<p>Summer Intern, Merck, Beijing, China Jul 2014 – Jan 2015 Developed a medical expert ranking & network system using Python MVC framework Django.</p> <p>Consultant, Microfinance Opportunities, Washington, D.C. USA, 2011 – 2016 (Freelance) Developed various web apps, including Financial Capability Index Portal & Financial Education Library.</p> <p>Founder and CEO, ASN tECH, Islamabad, Pakistan 2012 - 2013 Founded ASN tECH with an aim to develop creative solutions that exemplify modern web standards.</p> <p>Web Developer, Pearl Communications, Islamabad, Pakistan 2011 – 2012 Designed and developed an online news publishing system and implemented HRMS using SugarHRM.</p> <p>Software Engineer, Value Technologies, Islamabad, Pakistan 2010 – 2011 Involved in all aspects of software life-cycle from analysis, design, develop, deploy and management.</p> <p>Intern, a joint project by Harvard Univ & FMFB, AKDN, Islamabad, Pakistan 2009 – 2010 Developed an automated data entry & report generation system for participatory wealth ranking research.</p>
AWARDS AND FELLOWSHIPS	<p>Postdoctoral Fellowship, NCMM, University of Oslo, 2016 – 2019</p> <p>Fully-funded Chinese Govt. Scholarship, for PhD program at Tsinghua University, 2012 – 2016</p> <p>Biocuration Travel Grant, Biocuration Conference 2018, Shanghai, China. 2018</p> <p>HEC Research Travel Grant, Higher Education Commission, Pakistan, 2016</p> <p>TWAS BIOVISION.Next Fellowship, to participate in BIOVISION conference, France. 2014</p> <p>TWAS BIOVISION.Next Fellowship, to participate in BIOVISION conference, France. 2013</p> <p>HEC Research Travel Grant, Higher Education Commission, Pakistan, 2012</p> <p>1st position in article writing competition, Benade Physics Society, FC College, Lahore, 2004</p>
SUPERVISION OF GRADUATE STUDENTS	<p>NCMM, University of Oslo, Norway</p> <p>Kübra Altınel (Master student) 2018 – 2019 Project: Characterization of driver cis-regulatory regions associated with microRNAs in cancer</p>

PUBLICATIONS AND PREPRINTS

- 1) **A. Khan**, and X. Zhang, “Making genome browsers portable and personal,” *Genome Biology* 2018; 19:93, doi: 10.1186/s13059-018-1470-9.
- 2) **A. Khan**+, A. Montenegro-Montero and A. Mathelier+, “Put science first and formatting later,” *EMBO reports* 2018; 19(5):e45731, doi: 10.15252/embr.201845731.
- 3) **A. Khan**+ and A. Mathelier+, “JASPAR RESTful API: accessing JASPAR data from any programming language,” *Bioinformatics* 2017; 34(9):1612-1614.
- 4) **A. Khan*** et al., “JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework,” *Nucleic Acids Res*, 2017; 46(D1):D260-D26.
- 5) The Bioconda Team et al., “Bioconda: sustainable and comprehensive software distribution for the life sciences,” *Nature Methods* 2018, 15:475–476.
- 6) **A. Khan**+ and A. Mathelier+, “Intervene: a tool for intersection and visualization of multiple gene or genomic region sets,” *BMC Bioinformatics* 2017;18:287.
- 7) **A. Khan** and X. Zhang, “dbSUPER: a database of super-enhancers in mouse and human genome,” *Nucleic Acids Res* 2016, 44(D1):D164–D171.
- 8) **A. Khan**+ and X. Zhang, “Integrative modelling reveals key chromatin and sequence signatures predicting super-enhancers,” *bioRxiv* 2017; doi:10.1101/105262. (In review)
- 9) **A. Khan**+, A. Mathelier and X. Zhang, “Super-enhancers are transcriptionally more active and cell-type-specific than stretch enhancers,” *bioRxiv* 2018; doi: 10.1101/310839. (In review)
- 10) M. Ishtiaq, **A. Khan**, M.A. Jaffar, “A hybrid feature selection approach by combining miD and miQ,” in *Proceeding of the ITFE Summer Conference* 2011, South Korea, (1), 367-373.
- 11) M. Ishtiaq, B. Sikandar, M.A. Jaffar, **A. Khan** “Adaptive Watermark Strength Selection using Particle Swarm Optimization,” *ICIC Express Letters*, 2010 , 4 (5), 1-6.

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POSTER PRESENTATIONS

- 1) **A. Khan** et al., “JASPAR: a comprehensive database of transcription factor binding profiles,” *11th International Biocuration Conference*, Shanghai Apr 2018.
- 2) **A. Khan** and A. Mathelier, “Intervene: a tool for intersection and visualization of multiple gene or genomic region sets,” *ISMB/ECCB 2017*, Prague, Czech Republic. Jul 2017.
- 3) **A. Khan** and X. Zhang, “Integrative analysis reveals significant differences between super and stretch enhancers,” *Gene Expression Data Analysis* , Mainz, Germany, Nov 2016.
- 4) **A. Khan** and X. Zhang, “Computational prediction, characterization and annotation of super-enhancers and analysis of their key features,” *CSH Asia meeting on Chromatin, Epigenetics and Transcription*, Suzhou, China, May 2016.
- 5) **A. Khan** and X. Zhang, “dbSUPER - an extensive and interactive database of super-enhancers,” *CSHA/AACR Meeting - Big Data, Comp. & Sys. Bio. in Cancer*, Suzhou, China, Dec 2015.
- 6) **A. Khan** and X. Zhang, “Super-enhancer prediction from epigenetic signatures and sequence motif data,” *ISMB/ECCB 2015*, Dublin, Ireland, Jul 2015.
- 7) **A. Khan** and X. Zhang, “An extensive and interactive database of super-enhancers – dbSUPER,” *ISCB Student Council Symposium 2015*, Dublin, Ireland, Jul 2015.
- 8) **A. Khan** and X. Zhang, “An extensive and interactive database of super-enhancers – dbSUPER,” *8th International Biocuration Conference (IBC)*, Beijing Apr 2015.

TALKS

JASPAR: a comprehensive database of transcription factor binding profiles, *11th International Biocuration Conference*, Shanghai, China, Apr 2018.

Intervene: a tool for intersection and visualization of multiple gene or genomic region sets, *ISCB Student Council Symposium 2017*, Prague, Czech Republic. Jul 2017.

Comprehensive analysis, prediction, and annotation of super-enhancers, *Sven Furberg Seminar in Bioinformatics and Statistical Genomics*, Oslo, Norway, Apr 2017.

Integrative analysis reveals significant differences between super and stretch enhancers, *Student Symposium on Computational Genomics*, Mainz, Germany, Nov 2016.

Integration of ChIP-seq and machine learning reveals super-enhancers and features of biological significance, *Synthetic Biology Workshops*, Tsinghua University, May 2014.

ORGANISATION OF SCIENTIFIC MEETINGS	Organizer , Young Investigator Meeting (YIM), University of Helsinki, Finland, 2017 Organizer , Young Investigator Meeting (YIM), University of Oslo, Norway, 2018
PROFESSIONAL AFFILIATIONS & ACTIVITIES	Ambassador , eLife, 2018 – Present Member , International Society for Computational Biology (ISCB), 2015 – Present Member , NORBIS, Norway, 2017 – Present Member , Centre for Digital Life Norway, 2017 – Present Member , International Society for Biocuration (ISB), 2015 – Present Curator , OMICtools, transcription factors and regulatory elements, 2014 – Present Chair , Web Committee, ISCB Student Council, 2016 – Present Reviewer , Bioinformatics, BMC Bioinformatics, OUP Database and PLOS ONE Reviewer , ISCB Student Council Symposium, 2015, 2016, 2017, 2018
SOCIAL ACTIVITIES	Volunteer , RECOMB 2013, Beijing, Apr 2013 Volunteer , ISMB/ECCB 2015, Dublin, and ISMB/ECCB 2017, Prague Volunteer , ICML (International Conference on Machine Learning), Jun 2014 Volunteer , Migrant Children's Foundation (MCF), China, 2013 – present Founder , Gilgit-Baltistan Academia, an academic portal, 2011 Participant , 3-Day Startup, Peking University, Beijing, China, 2012 Participant , Beijing TechHive, Microsoft Research Asia, Beijing, Mar 2015 Volunteer , to develop & maintain Tsinghua ENCODE Journal Club website, 2013
SKILLS	Programing languages : Python, R/Bioconductor, Shell scripting, PHP, SQL, C++ Bioinformatic tools : Bowtie, BWA, STAR, MACS, Tophat, Cufflinks, BEDTools, samtools, IGVTools, Galaxy, MEME, HOMER, deepTools, Snakemake, Genome Browsers etc. Machine learning tools : scikit-learn, Weka Web development : MVC, Django, Laravel, WordPress, R Shiny, jQuery/Ajax, HTML5, REST Databases : MySQL, SQLite Operating systems : Unix/Linux/Ubuntu, Mac OS, Windows Other tools : LATEX, MATLAB, Cytoscape, D3.js, Adobe Photoshop, Adobe Illustrator. Other skills : Integrative analysis of NGS data, development of pipelines
SOFTWARE & DATABASES	Intervene , Intersection & visualization of multiple sets - intervene.rtfid.io dbSUPER , a database of super-enhancers - bioinfo.au.tsinghua.edu.cn/dbsuper JASPAR , redesign and redevelopment of JASPAR database - jaspar.genereg.net JASPAR REST API , programmatic access to TF binding profile data - jaspar.genereg.net/api UniBind , a uniformly processed database of transcription factor binding sites ECRCentral , a central platform for early career researchers and postdocs - ecrcentral.org imPROSE , Integrated methods to predict super-enhancers - asntech.github.io/improse/
LANGUAGES	English: Fluent (speaking, reading, writing) Urdu: Native language Shinah: Mother tongue German: Basic Norwegian: Basic
HOBBIES	Volunteering, social work, swimming, marathon runner, traveling, football, cooking.
REFERENCES	References are available upon request.