Aziz Khan

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EDUCATION	**Tsinghua University**, Beijing, China
	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
	National University of Computer & Emerging Sciences, Islamabad, Pakistan
	MS in Computer Science · 2008 – 2010
	Quaid-I-Azam University, Islamabad, Pakistan
	MSc in Information Technology · 2006 – 2008
	Forman Christian College, Lahore, Pakistan
	BSc in Mathematics and Physics · 2003 – 2005

RESEARCH INTERESTS

Bioinformatics, computational biology, machine learning, biocuration, regulatory genomics and epigenomics, integrative analysis of high throughput sequencing data

RESEARCH EXPERIENCE

Postdoctoral Research Fellow, Mathelier Lab, NCMM, University of Oslo 2016 - present

PhD Research Student, Zhang Lab, Bioinformatic Division, Tsinghua University, 2012 – 2016
Projects: Enhancer prediction, dbSUPER, imPROSE

Rotation Student, Jingren Lab, School of Medicine, Tsinghua University, 2012
Project: hands-on experience with molecular cloning

Rotation Student, Tao Jiang, Tsinghua University & University of California - Riverside, 2013
Project: Operon prediction and pathway analysis using metagenomic data

PROFESSIONAL EXPERIENCE

Summer Intern, Merck, Beijing, China Jul 2014 – Jan 2015
Developed a medical expert ranking & network system using Python MVC framework Django.

Consultant, Microfinance Opportunities, Washington, D.C. USA, 2011 – 2016 (Freelance)
Developed various web apps, including Financial Capability Index Portal & Financial Education Library.

Founder and CEO, ASN tECH, Islamabad, Pakistan 2012 - 2013
Founded ASN tECH with an aim to develop creative solutions that exemplify modern web standards.

Web Developer, Pearl Communications, Islamabad, Pakistan 2011 – 2012
Designed and developed an online news publishing system and implemented HRMS using SugarHRM.

Software Engineer, Value Technologies, Islamabad, Pakistan 2010 – 2011
Involved in all aspects of software life-cycle from analysis, design, develop, deploy and management.

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.

AWARDS AND FELLOWSHIPS

Postdoctoral Fellowship, NCMM, University of Oslo, 2016 – 2019

Fully-funded Chinese Govt. Scholarship, for PhD program at Tsinghua University, 2012 – 2016

Biocuration Travel Grant, Biocuration Conference 2018, Shanghai, China. 2018

HEC Research Travel Grant, Higher Education Commission, Pakistan, 2016

TWAS BIOVISION.Next Fellowship, to participate in BIOVISION conference, France. 2014

TWAS BIOVISION.Next Fellowship, to participate in BIOVISION conference, France. 2013

HEC Research Travel Grant, Higher Education Commission, Pakistan, 2012

1st position in article writing competition, Benade Physics Society, FC College, Lahore, 2004

SUPERVISION OF GRADUATE STUDENTS

NCMM, University of Oslo, Norway

Kübra Altınel (Master student) · 2018 – 2019
Project: Characterization of driver cis-regulatory regions associated with microRNAs in cancer

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.

* co-first authors, +co-corresponding authors

TALKS AND POSTER PRESENTATIONS

1) Towards a format-free submission policy: Let's put science first, *2nd annual conference of Digital Life Norway Research School*, Stiklestad, Norway. Jun 2018. - [**Talk**]

2) JASPAR: a comprehensive database of transcription factor binding profiles, *11th International Biocuration Conference*, Shanghai Apr 2018. - [**Poster and Talk**]

3) A novel web framework and RESTful API for the JASPAR database of transcription factor binding profiles, *3rd annual conference of NORBIS*, Tromsø, Norway. Nov 2017. - [**Poster**]

4) JASPAR RESTful API: accessing JASPAR data from any programming languages, *GREEKC Training on Knowledge Commons and Tools interoperability*, Lisbon, Portugal Oct 2017. - [**Talk**]

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

6) Intervene: a tool for intersection and visualization of multiple gene or genomic region sets, *ISMB/ECCB 2017*, Prague, Czech Republic. Jul 2017. - [**Poster**]

7) Integrative analysis reveals significant differences between super and stretch enhancers, *Gene Expression Data Analysis"* , Mainz, Germany, Nov 2016. - [**Poster and Talk**]

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

9) Computational prediction, characterization & annotation of super-enhancers & analysis of their key features, *CSHA - Chromatin, Epig. & Trans.*, Suzhou, China, May 2016. - [**Poster**]

10) dbSUPER - an extensive and interactive database of super-enhancers, *CSHA/AACR Meeting - Big Data, Comp. & Sys. Bio. in Cancer*, Suzhou, China, Dec 2015. - [**Poster**]

11) Super-enhancer prediction from epigenetic signatures and sequence motif data, *ISMB/ECCB 2015*, Dublin, Ireland, Jul 2015. - [**Poster**]

12) An extensive and interactive database of super-enhancers – dbSUPER, *ISCB Student Council Symposium 2015*, Dublin, Ireland, Jul 2015. - [**Poster**]

13) An extensive and interactive database of super-enhancers – dbSUPER, *8th International Biocuration Conference (IBC)*, Beijing Apr 2015. - [**Poster**]

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

ORGANISATION OF SCIENTIFIC MEETINGS	**Organizer**, Young Investigator Meeting (YIM), University of Oslo, Norway, Sep 2018
	Chair Web Committee, ISCB African Student Symposium 2017, Entebbe, Uganda., Oct 2017
	Organizer, Young Investigator Meeting (YIM), University of Helsinki, Finland, Sep 2017
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, MongoDB
	Operating systems: Unix/Linux/Ubuntu, Mac OS, Windows
	Other tools: Git, TravisCI, LaTeX, MATLAB, Cytoscape, D3.js, Adobe Suite.
	Other skills: Integrative analysis of NGS data, development of pipelines
SOFTWARE & DATABASES	**Intervene**, Intersection & visualization of multiple sets - intervene.rtfd.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.**