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 EXPERIENCE

Postdoctoral Research Fellow, Mathelier Lab, NCMM, University of Oslo   2016 - present
PhD Student, Xuegong Lab, Bioinformatic Division, Tsinghua University   2012 – 2016
Rotation Student, Jingren Lab, School of Medicine, Tsinghua University   2012
Rotation Student, Tao Jiang, Tsinghua University & University of California - Riverside   2013

RESEARCH INTERESTS

Computational biology, machine learning, transcriptional gene regulation, regulatory genomics and epigenomics, integrative analysis of bulk/single-cell omics data, and resource development

PUBLICATIONS & PREPRINTS

1. **A. Khan**[+], A. Mathelier and X. Zhang, Super-enhancers are transcriptionally more active and cell-type-specific than stretch enhancers, *Epigenetics 2018. doi: 10.1080/15592294.2018.1514231*.

2. **A. Khan** and X. Zhang, Making genome browsers portable and personal, *Genome Biology 2018;* 19:93, doi: 10.1186/s13059-018-1470-9.

3. **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.

4. **A. Khan**[*], O. Fornes[*], A. Stigliani[*] et al., JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework, *Nucleic Acids Res.* 2018; 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[+], JASPAR RESTful API: accessing JASPAR data from any programming language, *Bioinformatics 2018;* 34(9):1612-1614.

7. H. Feng, S. Bao, S.M. Weyn-Vanhentenryck, **A. Khan** et al. Modeling RNA-binding protein specificity in vivo by precisely registering protein-RNA crosslink sites, *bioRxiv 2018; doi: 10.1101/428615*

8. M. Gheorghe, GK Sandve, **A. Khan**, et al. A map of direct TF-DNA interactions in the human genome, *bioRxiv 2018;* doi: 10.1101/394205.

9. **A. Khan**[+] and A. Mathelier[+], Intervene: a tool for intersection and visualization of multiple gene or genomic region sets, *BMC Bioinformatics 2017;18:287*.

10. **A. Khan**[+] and X. Zhang[+], Integrative modelling reveals key chromatin and sequence signatures predicting super-enhancers, *bioRxiv 2017; doi:10.1101/105262*.

11. **A. Khan** and X. Zhang, dbSUPER: a database of super-enhancers in mouse and human genome, *Nucleic Acids Res* 2016, 44(D1):D164–D171.

12. M. Ishtiaq[*], **A. Khan**[*], M.A. Jaffar, H.J. Kim, A hybrid feature selection approach by combining miD and miQ, *ITFE Summer Conference* 2011, South Korea, (1), 367-373.

13. 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

AWARDS AND FELLOWSHIPS	**CSC fully-funded PhD Scholarship**, Tsinghua University, China	2012 – 2016
	Research Travel Grant, Higher Education Commission (HEC), Pakistan	2016
	TWAS BIOVISION.Next Fellowship, BioVision conference Lyon, France	2014
	TWAS BIOVISION.Next Fellowship, BioVision conference Lyon, France	2013
	Research Travel Grant, Higher Education Commission (HEC), Pakistan	2012
	1st position in article writing competition, Benade Physics Society, FC College, Lahore	2004
PROFESSIONAL EXPERIENCE	**Summer Intern**, Merck, Beijing, China	2014 – 2015
	Consultant, Microfinance Opportunities, Washington, D.C. USA (Freelance)	2011 – 2016
	Founder and CEO, ASN tECH, Islamabad, Pakistan	2012 - 2013
	Web Developer, Pearl Communications, Islamabad, Pakistan	2011 – 2012
	Software Engineer, Value Technologies, Islamabad, Pakistan	2010 – 2011
	Intern, a joint project by Harvard Univ & FMFB, AKDN, Islamabad, Pakistan	2009 – 2010
ADMINISTRATIVE EXPERIENCE	**Co-Chair**, Web Committee, ISCB Student Council	2016 – Present
	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
	Co-Chair, Tuesday Seminars, NCMM, University of Oslo	2017 – 2018
	Organizer, Tsinghua ENCODE Journal Club	2013 – 2014
PROFESSIONAL DEVELOPMENT ACTIVITIES	**Co-Supervisor**, Master student thesis (Kübra Altınel)	
	Reviewer, NAR, Genome Biology, Bioinformatics, BMC Bioinfo., Database, & PLOS ONE	
	Reviewer, ISCB Student Council Symposiums, 2015, 2016, 2017, 2018	
PROFESSIONAL AFFILIATIONS	**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

PROGRAMMING & OTHER SKILLS	**Languages**: Python, R/Bioconductor, Shell scripting, PHP, SQL, C++
	Tools/Resources: Bowtie, BWA, STAR, MACS, Tophat, Cufflinks, BEDTools, samtools, DEGseq, Salmon, Galaxy, MEME, HOMER, deepTools, Snakemake, Genome Browsers etc.
	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, scikit-learn, Weka, LaTeX, MATLAB, Cytoscape, D3.js, Adobe Suite.

SOFTWARE & RESOURCES DEVELOPED	**JASPAR**, an open and widely used database of transcription factor binding profiles - jaspar.genereg.net
	Intervene, a Python tool for intersection & visualization of multiple sets - intervene.rtfd.io
	dbSUPER, a database of super-enhancers - bioinfo.au.tsinghua.edu.cn/dbsuper
	JASPAR REST API, programmatic access to TF binding profile data - jaspar.genereg.net/api
	Intervene Shiny App, an app for intersection & visualization of sets - asntech.shinyapps.io/intervene
	UniBind, a uniformly processed database of transcription factor binding sites - unibind.uio.no
	mCrossBase, a database of RBP binding motifs and crosslink sites
	ECRCentral, a central platform for early career researchers and postdocs - ecrcentral.org
	imPROSE, Integrated methods to predict super-enhancers - asntech.github.io/improse/

VOLUNTEER & **SOCIAL WORK**	**Volunteer**, ISMB/ECCB 2017, Prague	Jul 2017
	Volunteer, ISMB/ECCB 2015, Dublin	Jul 2015
	Volunteer, ICML (International Conference on Machine Learning), Beijing	Jun 2014
	Web administrator, Migrant Children's Foundation (MCF), China	2013 – 2018
	Volunteer, RECOMB 2013, Beijing	Apr 2013
	Founder, Gilgit-Baltistan Academia, an academic portal	2011

TALKS AND POSTER PRESENTATIONS

1. A dynamic landscape of enhancer clusters during mouse development, *CSHL meeting on Epigenetics and Chromatin*, New York, USA. Sep 2018. - [**Poster**]

2. 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**]

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

4. 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**]

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

6. 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**]

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

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

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

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

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

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

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

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

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

LANGUAGES	English: Fluent (speaking, reading, writing)	Urdu: Native language
	Shinah: Mother tongue	Chinese: Basic	Norwegian: Basic
INTERESTS	Volunteering, sports (football and badminton), gardening, photography, and cooking.
REFERENCES	**References are available upon request.**