

# Aziz Khan

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

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## 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) 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]
- 5) Intervene: a tool for intersection and visualization of multiple gene or genomic region sets, *ISMB/ECCB 2017*, Prague, Czech Republic. Jul 2017. - [Poster]
- 6) Integrative analysis reveals significant differences between super and stretch enhancers, *Gene Expression Data Analysis* , Mainz, Germany, Nov 2016. - [Poster and Talk]
- 7) Comprehensive analysis, prediction, and annotation of super-enhancers, *Sven Furberg Seminar in Bioinformatics and Statistical Genomics*, Oslo, Norway, Apr 2017. - [Talk]
- 8) Computational prediction, characterization & annotation of super-enhancers & analysis of their key features, *CSHA - Chromatin, Epig. & Trans.*, Suzhou, China, May 2016. - [Poster]
- 9) dbSUPER - an extensive and interactive database of super-enhancers, *CSHA/AACR Meeting - Big Data, Comp. & Sys. Bio. in Cancer*, Suzhou, China, Dec 2015. - [Poster]
- 10) Super-enhancer prediction from epigenetic signatures and sequence motif data, *ISMB/ECCB 2015*, Dublin, Ireland, Jul 2015. - [Poster]
- 11) An extensive and interactive database of super-enhancers – dbSUPER, *ISCB Student Council Symposium 2015*, Dublin, Ireland, Jul 2015. - [Poster]
- 12) An extensive and interactive database of super-enhancers – dbSUPER, *8th International Biocuration Conference (IBC)*, Beijing Apr 2015. - [Poster]
- 13) Integration of ChIP-seq and machine learning reveals super-enhancers and features of biological significance, *Synthetic Biology Workshops*, Tsinghua University, May 2014. - [Talk]

<b>ORGANISATION OF SCIENTIFIC MEETINGS</b>	<p><b>Organizer</b>, Young Investigator Meeting (YIM), University of Oslo, Norway, Sep 2018</p> <p><b>Chair Web Committee</b>, ISCB African Student Symposium 2017, Entebbe, Uganda., Oct 2017</p> <p><b>Organizer</b>, Young Investigator Meeting (YIM), University of Helsinki, Finland, Sep 2017</p>
<b>PROFESSIONAL AFFILIATIONS &amp; ACTIVITIES</b>	<p><b>Ambassador</b>, eLife, 2018 – Present</p> <p><b>Member</b>, International Society for Computational Biology (ISCB), 2015 – Present</p> <p><b>Member</b>, NORBIS, Norway, 2017 – Present</p> <p><b>Member</b>, Centre for Digital Life Norway, 2017 – Present</p> <p><b>Member</b>, International Society for Biocuration (ISB), 2015 – Present</p> <p><b>Curator</b>, OMICtools, transcription factors and regulatory elements, 2014 – Present</p> <p><b>Chair</b>, Web Committee, ISCB Student Council, 2016 – Present</p> <p><b>Reviewer</b>, Bioinformatics, BMC Bioinformatics, OUP Database and PLOS ONE</p> <p><b>Reviewer</b>, ISCB Student Council Symposium, 2015, 2016, 2017, 2018</p>
<b>SOCIAL ACTIVITIES</b>	<p><b>Volunteer</b>, RECOMB 2013, Beijing, Apr 2013</p> <p><b>Volunteer</b>, ISMB/ECCB 2015, Dublin, and ISMB/ECCB 2017, Prague</p> <p><b>Volunteer</b>, ICML (International Conference on Machine Learning), Jun 2014</p> <p><b>Volunteer</b>, Migrant Children's Foundation (MCF), China, 2013 – present</p> <p><b>Founder</b>, Gilgit-Baltistan Academia, an academic portal, 2011</p> <p><b>Participant</b>, 3-Day Startup, Peking University, Beijing, China, 2012</p> <p><b>Participant</b>, Beijing TechHive, Microsoft Research Asia, Beijing, Mar 2015</p> <p><b>Volunteer</b>, to develop &amp; maintain Tsinghua ENCODE Journal Club website, 2013</p>
<b>SKILLS</b>	<p><b>Programing languages</b>: Python, R/Bioconductor, Shell scripting, PHP, SQL, C++</p> <p><b>Bioinformatic tools</b>: Bowtie, BWA, STAR, MACS, Tophat, Cufflinks, BEDTools, samtools, IGVTools, Galaxy, MEME, HOMER, deepTools, Snakemake, Genome Browsers etc.</p> <p><b>Machine learning tools</b>: scikit-learn, Weka</p> <p><b>Web development</b>: MVC, Django, Laravel, WordPress, R Shiny, jQuery/Ajax, HTML5, REST</p> <p><b>Databases</b>: MySQL, SQLite, MongoDB</p> <p><b>Operating systems</b>: Unix/Linux/Ubuntu, Mac OS, Windows</p> <p><b>Other tools</b>: Git, TravisCI, L<sup>A</sup>T<sub>E</sub>X, MATLAB, Cytoscape, D3.js, Adobe Suite.</p> <p><b>Other skills</b>: Integrative analysis of NGS data, development of pipelines</p>
<b>SOFTWARE &amp; DATABASES</b>	<p><b>Intervene</b>, Intersection &amp; visualization of multiple sets - <a href="http://intervene.rtfid.io">intervene.rtfid.io</a></p> <p><b>dbSUPER</b>, a database of super-enhancers - <a href="http://bioinfo.au.tsinghua.edu.cn/dbsuper">bioinfo.au.tsinghua.edu.cn/dbsuper</a></p> <p><b>JASPAR</b>, redesign and redevelopment of JASPAR database - <a href="http://jaspar.genereg.net">jaspar.genereg.net</a></p> <p><b>JASPAR REST API</b>, programmatic access to TF binding profile data - <a href="http://jaspar.genereg.net/api">jaspar.genereg.net/api</a></p> <p><b>UniBind</b>, a uniformly processed database of transcription factor binding sites</p> <p><b>ECRCentral</b>, a central platform for early career researchers and postdocs - <a href="http://ecrcentral.org">ecrcentral.org</a></p> <p><b>imPROSE</b>, Integrated methods to predict super-enhancers - <a href="http://asntech.github.io/improse/">asntech.github.io/improse/</a></p>
<b>LANGUAGES</b>	<p>English: Fluent (speaking, reading, writing)   Urdu: Native language</p> <p>Shinah: Mother tongue   German: Basic   Norwegian: Basic</p>
<b>HOBBIES</b>	Volunteering, social work, swimming, marathon runner, traveling, football, cooking.
<b>REFERENCES</b>	<b>References are available upon request.</b>