

# 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**+, A. Montenegro-Montero and A. Mathelier+, “Put science first and formatting later,” *EMBO reports* 2018; 19(5):e45731, doi: 10.15252/embr.201845731.
  - 2) **A. Khan** and A. Mathelier+, “JASPAR RESTful API: accessing JASPAR data from any programming language,” *Bioinformatics* 2017; 34(9):1612-1614.
  - 3) **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.
  - 4) The Bioconda Team et al., “Bioconda: sustainable and comprehensive software distribution for the life sciences,” *Nature Methods* 2018, 15:475–476.
  - 5) **A. Khan** and A. Mathelier+, “Intervene: a tool for intersection and visualization of multiple gene or genomic region sets,” *BMC Bioinformatics* 2017;18:287.
  - 6) **A. Khan** and X. Zhang, “dbSUPER: a database of super-enhancers in mouse and human genome,” *Nucleic Acids Res* 2016, 44(D1):D164–D171.
  - 7) **A. Khan** and X. Zhang, “Integrative modelling reveals key chromatin and sequence signatures predicting super-enhancers,” *bioRxiv* 2017; doi:10.1101/105262. (In review PLOS CompBio)
  - 8) **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 Epigenetics)
  - 9) M. Gheorghe, GK Sandve, **A. Khan** et al., “An integrative approach maps direct TF-DNA interactions in the human genome,” 2018 (In submission)
  - 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

## 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.

<b>ORGANISATION OF SCIENTIFIC MEETINGS</b>	<b>Organizer</b> , Young Investigator Meeting (YIM), University of Helsinki, Finland, 2017 <b>Organizer</b> , Young Investigator Meeting (YIM), University of Oslo, Norway, 2018
<b>PROFESSIONAL AFFILIATIONS &amp; ACTIVITIES</b>	<b>Ambassador</b> , eLife, 2018 – Present <b>Member</b> , International Society for Computational Biology (ISCB), 2015 – Present <b>Member</b> , NORBIS, Norway, 2017 – Present <b>Member</b> , Centre for Digital Life Norway, 2017 – Present <b>Member</b> , International Society for Biocuration (ISB), 2015 – Present <b>Curator</b> , OMICtools, transcription factors and regulatory elements, 2014 – Present <b>Chair</b> , Web Committee, ISCB Student Council, 2016 – Present <b>Reviewer</b> , Bioinformatics, BMC Bioinformatics, OUP Database and PLOS ONE <b>Reviewer</b> , ISCB Student Council Symposium, 2015, 2016, 2017, 2018
<b>SOCIAL ACTIVITIES</b>	<b>Volunteer</b> , RECOMB 2013, Beijing, Apr 2013 <b>Volunteer</b> , ISMB/ECCB 2015, Dublin, and ISMB/ECCB 2017, Prague <b>Volunteer</b> , ICML (International Conference on Machine Learning), Jun 2014 <b>Volunteer</b> , Migrant Children's Foundation (MCF), China, 2013 – present <b>Founder</b> , Gilgit-Baltistan Academia, an academic portal, 2011 <b>Participant</b> , 3-Day Startup, Peking University, Beijing, China, 2012 <b>Participant</b> , Beijing TechHive, Microsoft Research Asia, Beijing, Mar 2015 <b>Volunteer</b> , to develop & maintain Tsinghua ENCODE Journal Club website, 2013
<b>SKILLS</b>	<b>Programing languages</b> : Python, R/Bioconductor, Shell scripting, PHP, SQL, C++ <b>Bioinformatic tools</b> : Bowtie, BWA, STAR, MACS, Tophat, Cufflinks, BEDTools, samtools, IGVTools, Galaxy, MEME, HOMER, deepTools, Snakemake, Genome Browsers etc. <b>Machine learning tools</b> : scikit-learn, Weka <b>Web development</b> : MVC, Django, Laravel, WordPress, R Shiny, jQuery/Ajax, HTML5, REST <b>Databases</b> : MySQL, SQLite <b>Operating systems</b> : Unix/Linux/Ubuntu, Mac OS, Windows <b>Other tools</b> : LATEX, MATLAB, Cytoscape, D3.js, Adobe Photoshop, Adobe Illustrator. <b>Other skills</b> : Integrative analysis of NGS data, development of pipelines
<b>SOFTWARE &amp; DATABASES</b>	<b>Intervene</b> , Intersection & visualization of multiple sets - <a href="http://intervene.rtfid.io">intervene.rtfid.io</a> <b>dbSUPER</b> , a database of super-enhancers - <a href="http://bioinfo.au.tsinghua.edu.cn/dbsuper">bioinfo.au.tsinghua.edu.cn/dbsuper</a> <b>JASPAR</b> , redesign and redevelopment of JASPAR database - <a href="http://jaspar.genereg.net">jaspar.genereg.net</a> <b>JASPAR REST API</b> , programmatic access to TF binding profile data - <a href="http://jaspar.genereg.net/api">jaspar.genereg.net/api</a> <b>UniBind</b> , a uniformly processed database of transcription factor binding sites <b>ECRCentral</b> , a central platform for early career researchers and postdocs - <a href="http://ecrcentral.org">ecrcentral.org</a> <b>imPROSE</b> , Integrated methods to predict super-enhancers - <a href="http://asntech.github.io/improse/">asntech.github.io/improse/</a>
<b>LANGUAGES</b>	English: Fluent (speaking, reading, writing)   Urdu: Native language Shinah: Mother tongue   German: Basic   Norwegian: Basic
<b>HOBBIES</b>	Volunteering, social work, swimming, marathon runner, traveling, football, cooking.
<b>REFERENCES</b>	<b>Anthony Mathelier, PhD</b> Group Leader, Centre for Molecular Medicine Norway (NCMM), University of Oslo, Norway <a href="mailto:anthony.mathelier@ncmm.uio.no">anthony.mathelier@ncmm.uio.no</a> • (+47) 228-40-561  <b>Xuegong Zhang, PhD</b> Professor, Department of Automation and Director, Bioinformatics Division, Tsinghua University, China <a href="mailto:zhangxg@tsinghua.edu.cn">zhangxg@tsinghua.edu.cn</a> • +86 (10)-6279-4919  <b>Guy Stuart, PhD</b> Executive Director, Microfinance Opportunities, Washington, D.C. Fellow, Ash Center, Harvard University <a href="mailto:guystuart@mfopps.org">guystuart@mfopps.org</a> • <a href="mailto:guy_stuart@harvard.edu">guy_stuart@harvard.edu</a>