Aziz Khan

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EDUCATION	**University of Oslo**, Oslo, Norway
	Postdoctoral fellow at Centre for Molecular Medicine Norway (NCMM)　　　2016 – present
	Tsinghua University, Beijing, China
	Ph.D. in Bioinformatics　　　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, phpDAVIDws

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, 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
Developed various web apps, including Financial Capability Index Portal & Financial Education Library.

Founder and CEO, ASN tECH, http://asntech.org, 2012
Founded ASN tECH with an aim to develop creative solutions that exemplify modern web standards.

Web Developer, Pearl Communications (Pvt.) Limited, 2011 – 2012
Designed and developed an online news publishing system and implemented HRMS using SugarHRM.

Software Engineer, Value Technologies, Islamabad, 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, Aga Khan Development Network 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

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

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

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

PUBLICATIONS

1) A. Khan and A. Mathelier, "JASPAR RESTful API: accessing JASPAR data from any programming language," *Bioinformatics 2017, btx804*, doi: 10.1093/bioinformatics/btx804

2) 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, doi:10.1093/nar/gkx1126

3) A. Khan et al., "Bioconda: A sustainable and comprehensive software distribution for the life sciences," *Nature Methods 2018 (In revision); Preprint: 10.1101/207092*.

4) A. Khan et al., "Towards a format-free submission policy to put science first and formatting later," *EMBO reports 2018 (In press)*.

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, "Analysis and prediction of super-enhancers using sequence and chromatin signatures," *bioRxiv 2017; doi: 10.1101/105262*.

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, "Comparative analysis of super and stretch enhancers by integrating epigenomic and transcriptomic data in ten human cell-types," *In submission*.

9) 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.

10) 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.

POSTER PRESENTATIONS

1) A. Khan and X. Zhang, "Integrative analysis reveals significant differences between super and stretch enhancers," *Gene Expression Data Analysis"* , Mainz, Germany, Nov 2016.

2) 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.

3) 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.

4) A. Khan and X. Zhang, "Super-enhancer prediction from epigenetic signatures and sequence motif data," *ISMB/ECCB 2015*, Dublin, Ireland, Jul 2015.

5) A. Khan and X. Zhang, "An extensive and interactive database of super-enhancers – dbSUPER," *ISCB Student Council Symposium 2015*, Dublin, Ireland, Jul 2015.

6) A. Khan and X. Zhang, "An extensive and interactive database of super-enhancers – dbSUPER," *8th International Biocuration Conference (IBC)*, Beijing Apr 2015.

TALKS

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.

PROFESSIONAL ACTIVITIES

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, BMC Bioinformatics, OUP Database and PLOS ONE

Reviewer, ISCB Student Council Symposium, 2015, 2016, 2017

Member Editorial Committee, Clinical and Biomedical Research (CBR), 2013 – 2014

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, R Shiny, Shell scripting, PHP, SQL, C++
	Bioinformatic tools: Bowtie, BWA, STAR, MACS, Tophat, Cufflinks, BEDTools, samtools, IGVTools, Galaxy, MEME, HOMER, deepTools, Snakemake, Genome Browsers (UCSC, IGV, JBrowse)
	Machine learning tools: scikit-learn, Weka
	Web development: MVC, Django, Laravel, WordPress, Joomla, 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
MOOC CERTIFICATIONS	**Epigenetic Control of Gene Expression** by Marnie Blewitt, University of Melbourne – Coursera (**Verified certificate with distinction**)
	Machine Learning by Andrew Ng, Stanford University – Coursera
	Computing for Data Analysis by Roger Peng, Johns Hopkins University – Coursera
	Data Analysis by Jeff Leek, Johns Hopkins University - Coursera
	Critical Thinking in Global Challenges by University of Edinburgh – Coursera
	Genes and the Human Condition by University of Maryland on Coursera
	Interprofessional Healthcare Informatics by Karen A.M., University of Minnesota – Coursera
DIPLOMAS & CERTIFICATIONS	**Diploma in English Language**, National University of Modern Languages Islamabad, 2005
	A + Certification, Iman Institute of Information Technology, Abbottabad, 2003
	25 Computer Application Courses, Iman Institute of Information Technology, Abbottabad, 2003
	Web & Graphics Designing, Computer Center IoG, University of the Punjab, 2005
	Disaster & Risk Management Training, FOCUS Humanitarian Assistance Pakistan, 2004
	Banking and Accounting, Sidat Haider and Kushhali Bank Limited, 2011
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 of JASPAR database and it's RESTful API - jaspar.genereg.net
	imPROSE, Integrated methods to predict super-enhancers - asntech.github.io/improse/
	phpDAWIDws, a PHP framework for DAVID - http://asntech.github.io/phpDAVIDws
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.**