Aziz Khan

Centre for Molecular Medicine Norway (NCMM), Forskningsparken Gaustadalléen 21 0349, Oslo, Norway aziz.khan@ncmm.uio.no ● +47 -46379301 ● asntech.github.io ● github.com/asntech ● publons.com/a/382123

EDUCATION 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) <u>A. Khan</u> and A. Mathelier, "JASPAR RESTful API: accessing JASPAR data from any programming language," *Bioinformatics 2017*, *btx804*, doi: 10.1093/bioinformatics/btx804
- 2) <u>A. Khan</u> 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) <u>A. Khan</u>, A. Montenegro-Montero and A. Mathelier, "Put science first and formatting later," *EMBO reports 2018*; *doi:* 10.15252/embr.201845731.
- 4) The Bioconda Team et al., "Bioconda: A sustainable and comprehensive software distribution for the life sciences," *Nature Methods 2018 (In press); Preprint: 10.1101/207092.*
- 5) <u>A. Khan</u> and A. Mathelier, "Intervene: a tool for intersection and visualization of multiple gene or genomic region sets," *BMC Bioinformatics 2017;18:287*.
- 6) <u>A. Khan</u> and X. Zhang, "Integrative modelling reveals key chromatin and sequence signatures predicting super-enhancers," *bioRxiv* 2017; *doi:* 10.1101/105262.
- 7) <u>A. Khan</u> and X. Zhang, "dbSUPER: a database of super-enhancers in mouse and human genome," *Nucleic Acids Res* 2016, 44(D1):D164–D171.
- 8) <u>A. Khan</u>, A. Mathelier and X. Zhang, "Integrative analyses reveal significant differences between superand stretch enhancers in ten human cell-types," *In submission*.
- 9) M. Ishtiaq, <u>A. Khan</u>, 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, <u>A. Khan</u> "Adaptive Watermark Strength Selection using Particle Swarm Optimization," *ICIC Express Letters*, 2010, 4 (5), 1-6.

POSTER PRESENTATIONS

- 1) <u>A. Khan</u> et al., "JASPAR: a comprehensive database of transcription factor binding profiles," *11th International Biocuration Conference*, Shanghai Apr 2018.
- 2) <u>A. Khan</u> and X. Zhang, "Integrative analysis reveals significant differences between super and stretch enhancers," *Gene Expression Data Analysis*", Mainz, Germany, Nov 2016.
- 3) <u>A. Khan</u> 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.
- 4) <u>A. Khan</u> 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.
- 5) <u>A. Khan</u> and X. Zhang, "Super-enhancer prediction from epigenetic signatures and sequence motif data," *ISMB/ECCB 2015*, Dublin, Ireland, Jul 2015.
- 6) <u>A. Khan</u> and X. Zhang, "An extensive and interactive database of super-enhancers dbSUPER," *ISCB Student Council Symposium 2015*, Dublin, Ireland, Jul 2015.
- 7) <u>A. Khan</u> 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.

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

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

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

 $\textbf{Programing languages:} \ \ \text{Python, R/Bioconductor, Shell scripting, PHP, SQL, C++} \\$

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

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

English: Fluent (speaking, reading, writing) | Urdu: Native language Shinah: Mother tongue | German: Basic | Norwegian: Basic LANGUAGES

HOBBIES Volunteering, social work, swimming, marathon runner, traveling, football, cooking.

REFERENCES References are available upon request.