Osama A. Arshad

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RESEARCH
EXPERIENCE

Wellcome Sanger Institute, Cambridge, UK

Postdoctoral Research Fellow, Computational Genomics   Feb 2020 - Present

- Conducting large scale computational analyses of RNA-Seq datasets from iPSC derived neural cells with CRISPR engineered mutations modelling chromatin-related neurodevelopmental disorders (NDDs).
- Lead analyst on a multi-million pound collaborative project between several academic groups funded through Open Targets, a Sanger/EBI/Pharma consortium.
- Wrote several thousand lines of code in R orchestrated through Snakemake.
- This analysis of the largest NDD cohort to date will inform our understanding of molecular underpinnings of such diseases.
- First author and second author manuscripts in preparation.

Pacific Northwest National Laboratory, Richland, WA, USA

Postdoctoral Research Associate, Computational Cancer Biology   May 2017 - Jan 2020

- Several projects applying statistical and bioinformatics techniques to interrogate complex multi-omic cancer datasets.
- In my main project, carried out comprehensive proteogenomic analysis from a large prospectively collected cohort of clinical samples from high-grade serous ovarian cancer.
- In another project, carried out integrative analysis of proteomic and phosphoproteomic profiles from over 150 tumours in order to characterise the landscape of kinase-substrate phosphorylation interactions.
- Developed statistical analyses from gene expression profiles of volunteers on simulated day and night shift schedules offering insights as to how shift work may elevate cancer risk.
- Multiple co-first author papers with dozens of independent citations each.

Center for Bioinformatics and Genomics Systems Engineering,
Texas A&M University, College Station, TX, USA

Research Assistant   August 2013 to April 2017

- Modeling and inference of gene regulatory networks.
- Explored combination therapy design for cancer by Boolean modeling of growth factor signaling pathways.
- Three first author publications.

EDUCATION

Texas A&M University, College Station, TX, USA

Ph.D., Electrical Engineering   May 2017

- Area: Genomic Signal Processing
- Dissertation: On Boolean Modeling of Gene Regulatory Networks for Improved Cancer Combinatorial Therapy Design
- GPA: 3.89
- Selected Coursework: Data Mining and Analysis, Pattern Recognition, Statistical Analysis, Bayesian Statistics, R for Genomics Systems Engineering, Large Scale Biological Data Analysis, Engineering Genomics, Optimisation

Texas A&M University, College Station, TX, USA

M.S., Electrical Engineering   December 2007

Ghulam Ishaq Khan Institute of Engineering Sciences and Technology, Topi, Pakistan

B.S., Electronics Engineering   May 2005

TECHNICAL
SKILLS

- Programming: R | MATLAB | bash

- Software Development: git | conda | Linux

- Workflow Managers: Snakemake

- High Performance Computing: LSF

- Scientific writing: LaTeX

JOURNAL
PUBLICATIONS

[1] Levitin, M.O., L.E. Rawlins, G. Sanchez-Andrade, O.A. Arshad, S.C. Collins, S.J. Sawiak, P.H. Iffland, M.H. Andersson, C. Bupp, E.L. Cambridge *et al.* Models of KPTN related disorder implicate mTOR signalling in cognitive and overgrowth phenotypes, *Brain*, vol. 146, no. 11, pp. 4766-4783, 2023. doi:10.1093/brain/awad231

[2] Neaverson, A., M.H. Andersson, O.A. Arshad, L. Foulser, M. Goodwin-Trotman, A. Hunter, B. Newman, M. Patel, C. Roth, T. Thwaites *et al.* Differentiation of human induced pluripotent stem cells into cortical neural stem cells, *Frontiers in Cell and Developmental Biology*, 2023. doi:10.3389/fcell.2022.1023340

[3] Joshi, S.K., T. Nechiporuk, D. Bottomly, P.D. Piehowski, J. Pittsenbarger, A. Kaempf, S.J. Gosline, Y.T. Wang, J.R. Hansen, M.A. Gritsenko *et al.* The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance, *Cancer Cell*, vol. 39, no. 7, pp. 999-1014, 2021. doi:10.1016/j.ccell.2021.06.003

[4] Koritala[†], B.S., K.I. Porter[†], O.A. Arshad[†], R.P. Gajula, H.D. Mitchell, T. Arman, M.G. Manjanatha, J. Teeguarden, H.P. Van Dongen, J.E. McDermott and S. Gaddameedhi. Night shift schedule causes circadian dysregulation of DNA repair genes and elevated DNA damage in humans, *Journal of Pineal Research*, vol. 70, no. 3, 2021. doi:10.1111/jpi.12726 †*co-first authors*

[5] McDermott[†], J.E., O.A. Arshad[†], V.A. Petyuk, Y. Fu, M.A. Gritsenko, T.R. Clauss, R.J. Moore, R. Zhao, M.E. Monroe, M. Schnaubelt *et al.* Proteogenomic characterization of ovarian HGSC implicates mitotic kinases, replication stress in observed chromosomal instability, *Cell Reports Medicine*, vol. 1, no. 1, 2020. doi:10.1016/j.xcrm.2020.100004 †*co-first authors*

[6] Arshad, O.A., V. Danna, V.A. Petyuk, P.D. Piehowski, T. Liu, K.D. Rodland and J.E. McDermott. An integrative analysis of tumor proteomic and phosphoproteomic profiles to examine the relationships between kinase activity and phosphorylation, *Molecular & Cellular Proteomics*, 18 (8 suppl 1):S26-S36, 2019. doi:10.1074/mcp.RA119.001540

[7] Vasaikar, S., C. Huang, X. Wang, V.A. Petyuk, S.R. Savage, B. Wen, Y. Dou, Y. Zhang, Z. Shi, O.A. Arshad *et al.* Proteogenomic analysis of human colon cancer reveals new therapeutic opportunities, *Cell*, vol. 177, no. 4, pp. 1035-1049, 2019. doi:10.1016/j.cell.2019.03.030

[8] Ghaffari[†], N., <u>O.A. Arshad</u>[†], H. Jeong[†], J. Thiltges, M.F. Criscitello, B.J. Yoon, A. Datta and C.D. Johnson. Examining de novo transcriptome assemblies via a quality assessment pipeline. *ACM/IEEE Transactions on Computational Biology and Bioinformatics*, vol. 15, no. 2, pp. 494-505, 2018. doi:10.1109/TCBB.2015.2446478 †*co-first authors*

[9] <u>Arshad, O.A.</u>, and A. Datta. Towards targeted combinatorial therapy design for the treatment of castration-resistant prostate cancer, *BMC Bioinformatics*, 18 (Suppl. 4):134, 2017. doi:10.1186/s12859-017-1522-2

[10] <u>Arshad, O.A.</u>, P.S. Venkatasubramani, A. Datta, and J. Venkatraj. Using Boolean logic modeling of gene regulatory networks to exploit the links between cancer and metabolism for therapeutic purposes, *IEEE Journal of Biomedical and Health Informatics*, vol. 20, no. 1, pp. 399-407, 2016. doi:10.1109/JBHI.2014.2368391

OTHER
EXPERIENCE

School of Electrical Engineering and Computer Science,
National University of Sciences and Technology, Islamabad, Pakistan

Lecturer September 2011 to June 2012

- As a lecturer in the department of electrical engineering, responsible for teaching undergraduates courses in the Bachelors in Electrical Engineering program.
- Instructor for undergraduate courses in Signals and Systems and Power Electronics.
- Average student feedback of 87% (excellent).

Unilever, Karachi, Pakistan

Project Engineer October 2009 to September 2011

- Responsible for all aspects of Capital Expenditure (Capex) management including budgeting, authorizations and spend.

Valtech Technologies, College Station, TX, USA

Consultant I January 2008 to July 2008

- Worked in a team of software developers building and delivering enterprise applications using Microsoft's ASP.NET application development framework.

REFERENCES

Dr. Sebastian G. Gerety (e-mail: sg13@sanger.ac.uk; phone: +44 (0)1223 834244)
- Principal Staff Scientist, Wellcome Sanger Institute
- ⋄ Wellcome Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
- ⋆ *Dr. Gerety is my current postdoctoral supervisor.*

Dr. Jason E. McDermott (e-mail: Jason.McDermott@pnnl.gov; phone: +1-509-372-4360)
- Team Lead, Systems Biology, Pacific Northwest National Laboratory
- ⋄ 902 Battelle Boulevard, PO Box 999, Richland, WA, USA 85287-6106
- ⋆ *Dr. McDermott is my former postdoctoral supervisor.*

Professor. Aniruddha Datta (e-mail: a-datta@tamu.edu; phone: +1-979-845-5917)
- J.W. Runyon Jr. '35 Professor II, Department of Electrical and Computer Engineering, Texas A&M University
- ⋄ 301 Wisenbaker Engineering Building, College Station, TX 77843-3128, USA
- ⋆ *Professor Datta is my doctoral supervisor.*