

Osama A. Arshad

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EDUCATION & TRAINING

Wellcome Sanger Institute, Hinxton, England, UK

Postdoctoral Research Fellow, Computational Genomics

Feb 2020 - Present

Pacific Northwest National Laboratory, Richland, WA, USA

Postdoctoral Research Associate, Computational Cancer Biology

May 2017 - Jan 2020

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

Ph.D., Electrical Engineering

May 2017

- 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, Optimization

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

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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1074/mcp.RA119.001540)
- [7] Vasaiakar, 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](https://doi.org/10.1016/j.cell.2019.03.030)
- [8] Ghaffari[†], N., O.A. Arshad[†], 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](https://doi.org/10.1109/TCBB.2015.2446478) [†]co-first authors
- [9] Arshad, O.A., 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](https://doi.org/10.1186/s12859-017-1522-2)
- [10] Arshad, O.A., 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](https://doi.org/10.1109/JBHI.2014.2368391)

CONFERENCE
PRESENTATIONS &
PUBLICATIONS

- [1] Van Dongen, H., B. Koritala, K. Porter, O. Arshad, R. Gajula, H. Mitchell, T. Arman, M. Manjanatha, J. Teeguarden, J. McDermott and S. Gaddameedhi Night shift work and elevated cancer risk: circadian dysregulation of DNA repair genes and increased sensitivity to endogenous and exogenous sources of DNA damage. *Journal of Sleep Research*, 2020
- [2] McDermott, J., O. Arshad, V. Petyuk, Y. Fu, M. Gritsenko, C. Chai, S. Payne, M. Thiagarajan, C. Kinsinger, A. Robles *et al.* Proteogenomic characterization reveals mitotic kinase and replication stress implicated in ovarian high-grade serous cancer. *Cancer Research*, 2020
- [3] Arshad, O.A., J.E. McDermott, V.A. Petyuk, S.H. Payne, M.A. Gritsenko, T.R. Clauss, R.J. Moore, M.E. Monroe, M. Thiagarajan, C.R. Kinsinger *et al.* Multiomic characterization of pathway abnormalities in high grade serous ovarian cancer. *Human Proteomics Organization World Congress (HUPO 2018)*, Orlando, September 30 - October 3, 2018.
- [4] Arshad, O.A., and A. Datta. Towards targeted combinatorial therapy design for the treatment of castration-resistant prostate cancer. *Proceedings of the 7th ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB 2016)*, Seattle, October 2-5 2016.
- [5] Ghaffari, N., O.A. Arshad, H. Jeong, J. Thiltges, M.F. Criscitello, B.J. Yoon, A. Datta and C.D. Johnson. De novo transcriptome assemblies for Pacific whiteleg shrimp. *Proceedings of the 2014 IEEE Global Conference on Signal and Information Processing (GlobalSIP 2014)*, Atlanta, December 3-5, 2014.
- [6] Arshad, O.A., P.S. Venkatasubramani, A. Datta, and J. Venkatraj. Exploiting the cancer and diabetes metabolic connection for therapeutic purposes. *Proceedings of the 2013 IEEE Workshop on Genomic Signal Processing and Statistics (GENSIPS 2013)*, Houston, November 17-19 2013.
- [7] Venkatasubramani, P.S., O.A. Arshad, A. Datta, and J. Venkatraj. On exploiting links between cancer and metabolism for therapeutic purposes. *Proceedings of the 16th Yale Workshop on Adaptive and Learning Systems*, New Haven, June 2013.

TECHNICAL
SKILLS

- Analysis of high-throughput sequencing data.
- Programming in R, Python and MATLAB.
- Proficiency in Linux and knowledge of bash scripting.
- Experience with high performance computing clusters.
- Machine learning, statistics, cancer genomics.

PROFESSIONAL
EXPERIENCE

Wellcome Sanger Institute, Hinxton, England, UK

Postdoctoral Research Fellow

February 2020 to present

- Lead large scale computational analyses of RNA-Seq datasets from cellular models for neurodevelopmental and psychiatric diseases.
- Conduct integrative analyses of high-throughput transcriptomic data from iPSC models for tens of neurodevelopmental diseases in concert with gene expression data from drug response profiles of hundreds of pharmacological and genetic perturbations in order to discover candidate therapeutic targets that might reverse the disease phenotypes.

Pacific Northwest National Laboratory, Richland, WA, USA

Postdoctoral Research Associate

May 2017 to January 2020

- Computational analysis and modeling of cancer multi-omics data.
- Development of methods for integrating disparate types of data, network inference and predictive modeling of outcomes.
- Application of machine learning, statistics and bioinformatics techniques to high throughput and multi-modal datasets.

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

Research Assistant

August 2013 to April 2017

- Modeling of gene regulatory networks.
- Explored combination therapy design for cancer by Boolean modeling of growth factor signaling pathways.
- Developed a pipeline for quality assessment of de novo transcriptome assemblies from RNA-Sequencing data.

**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.
- Developed Capex annual plan in close coordination with relevant stakeholders.
- Administered the online Capital Proposal system.

Valtech Technologies, College Station, TX, USA

Consultant I

January 2008 to July 2008

- As a consultant in a global IT consultancy specializing in agile software development, worked with a team of consultants in building and delivering enterprise applications using Microsoft's ASP.NET application development framework.
- Wrote code to develop features and documented software solutions.

PROFESSIONAL
ACTIVITIES

Reviewer for the IEEE Transactions on Biomedical Engineering, IEEE Journal of Biomedical and Health Informatics, ACM/IEEE Transactions on Computational Biology and Bioinformatics and IEEE Access.