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PROFESSIONAL SUMMARY

Accomplished Bioinformatics Scientist with a strong background in developing innovative, scalable bioinformatics workflows and integrating complex multi-omics datasets to support cutting-edge research in **genomics, transcriptomics, and precision medicine**. Demonstrated expertise in both **somatic** and **germline variant analysis**, including **whole-exome (WES) and whole-genome sequencing (WGS)**, applied across oncology and rare disease contexts.

Skilled in bulk and single-cell transcriptomic analysis, cancer genomics, and multi-omics integration, with a proven track record of enhancing disease phenotype classification and contributing to high-impact discoveries in genetic disorders, target identification, and validation studies. Adept at solving complex biological questions through computational innovation and data-driven approaches.

EXPERIENCE

COMPUTATIONAL GENOMICS SPECIALIST , Clinical

National Institute of Allergy and Infectious Diseases (NIAID), February 2023-Present

Provided end-to-end bioinformatics support for a diverse portfolio of principal investigator (PI)-driven clinical genomics and transcriptomics research projects, encompassing:

Whole-Exome Sequencing (WES) & Whole-Genome Sequencing (WGS): Designed, optimized, and deployed robust pipelines for somatic and germline variant calling, with a focus on rare genetic disorders and oncogenic profiling. Collaborated closely with clinical teams to ensure analytical workflows met diagnostic and research needs.

Transcriptomics Analysis: Conducted in-depth single-cell RNA sequencing (scRNA-seq) and bulk RNA-seq analyses, including data preprocessing, normalization, clustering, differential expression, and pathway enrichment. Supported studies in cancer, neurodegeneration, and immunological disorders.

Multi-Omics Integration: Integrated genomics, transcriptomics, and epigenomics datasets using state-of-the-art statistical and machine learning methods to improve disease phenotype classification and uncover novel biomarkers.

Mitochondrial DNA Analysis: Developed a comprehensive mitochondrial DNA (mtDNA) variant calling and annotation workflow tailored for detecting pathogenic variants in mitochondrial diseases. This pipeline included quality control, heteroplasmy estimation, and clinical variant interpretation.

Workflow Development & Automation: Implemented scalable, reproducible workflows using workflow management systems (e.g., Snakemake) and cloud-based infrastructure, improving turnaround times and enabling high-throughput analysis.

BIOINFORMATICS SCIENTIST

Fate Therapeutics Inc., April 2022-February 2023

Led the development of advanced bioinformatics workflows to support innovative cellular immunotherapy programs, including CAR-T and Natural Killer (NK) cell therapies. Contributions spanned target discovery, platform evaluation, and translational research:

Target Identification & Vetting: Designed and implemented computational pipelines to systematically identify and validate novel therapeutic targets for CAR-T and NK cell platforms. Integrated bulk and single-cell transcriptomics, and public datasets to prioritize tumor-specific antigens.

Platform Vetting for Cell Therapies: Developed bioinformatics strategies to assess and compare engineered cell therapy platforms based on multi-dimensional data.

Disease Phenotype Classification: Created transcriptomics-based molecular signatures for robust classification of disease phenotypes using integrated single-cell, bulk RNA-seq, and epigenomic datasets. Employed machine learning techniques for feature selection, biomarker identification, and subtype delineation.

Single-Cell Analytics: Applied cutting-edge single-cell RNA-seq methods to dissect tumor heterogeneity, immune microenvironment, and treatment response. Conducted clustering, and cell-cell interaction mapping.

BIOINFORMATICS POSTDOCTORAL RESEARCHER/RESEARCH SCIENTIST

University of Illinois at Urbana-Champaign, June 2018-April 2022

Applied integrative bioinformatics approaches to investigate the molecular mechanisms underlying hypersensitivity and resistance to cisplatin in testicular germ cell tumors (TGCTs). Focused on multi-omics data analysis to uncover regulatory networks and therapeutic vulnerabilities:

Transcriptomic Profiling (RNA-seq): Performed differential gene expression and pathway enrichment analyses to identify transcriptional signatures associated with cisplatin response in TGCT models.

Epigenomic Analysis: Utilized ChIP-seq to profile chromatin state dynamics and DNA methylation EPIC array data to explore epigenetic modifications linked to drug sensitivity and resistance.

Public Data Mining: Leveraged TCGA, GEO, and other publicly available datasets to validate findings,

compare across cohorts, and identify clinically relevant biomarkers.

BIOINFORMATICS POSTDOCTORAL RESEARCHER

Stanford University, January 2017-January 2018

Computational Drug Discovery Researcher | Antimicrobial Resistance & Microgravity Studies

Conducted **high-throughput virtual screening** of approximately 2 million small molecules to identify novel inhibitors targeting **bacterial antioxidant defense systems**, with potential application in combating antimicrobial resistance.

Collaborated cross-functionally with **microbiology and bioinformatics teams** to support drug discovery initiatives, specifically within the unique context of **antibiotic sensitivity under microgravity conditions**—a critical aspect of infectious disease management in spaceflight environments.

EDUCATION

PHD IN ANIMAL SCIENCES (BIOINFORMATICS CONCENTRATION), IL

University of Illinois at Urbana-Champaign, January 2017

MS IN BIOINFORMATICS, IL

University of Illinois at Urbana-Champaign, January 2012

Awards & Honors

- NASA Group Achievement Award, 2018: Contributed to the CubeSat biological experiment studying microgravityinduced antibiotic resistance.
- Department of Animal Sciences Graduate Fellowship, 2017: Recognized for exemplary representation of the department at scientific meetings.
- Government of Pakistan Fellowship, 2010: Supported Master's degree at UIUC.
- Institute Bronze Medal (BS Bioinformatics), 2009.
- Associate Member, American Association for Cancer Research (AACR), 2019–Present.
- Member, National Postdoctoral Association, 2019–Present.

Publications (Selected)

1. Shokry, D., Khan, M.W., Powell, C., Johnson, S., Rennels, B.C., Boyd, R.I., Sun, Z., et al. "Refractory testicular germ cell tumors are highly sensitive to the targeting of polycomb pathway demethylases KDM6A and KDM6B." Cell Communication and Signaling, 22 (1), 528, 2024.
2. Boyd, R.I., Shokry, D., Fazal, Z., Rennels, B.C., Freemantle, S.J., La Frano, M.R., et al. "Perfluorooctanesulfonic Acid Alters Pro-Cancer Phenotypes and Metabolic and Transcriptional Signatures in Testicular Germ Cell Tumors." Toxics, 12 (4), 232, 2024.
3. Corbet, A.K., Bikorimana, E., Boyd, R.I., Shokry, D., Kries, K., Gupta, A., Paton, A., et al. "G0S2 promotes antiestrogenic and pro-migratory responses in ER+ and ER-breast cancer cells." Translational Oncology, 33, 101676, 2023.
4. Boyd, R.I., Ahmad, S., Singh, R., Fazal, Z., Prins, G.S., Madak Erdogan, Z., et al. "Toward a mechanistic understanding of poly-and perfluoroalkylated substances and cancer." Cancers, 14 (12), 2919, 2022.
5. Singh, R., Fazal, Z., Bikorimana, E., Boyd, R.I., Yerby, C., Tomlin, M., Baldwin, H., et al. "Reciprocal epigenetic remodeling controls testicular cancer hypersensitivity to hypomethylating agents and chemotherapy." Molecular Oncology, 16 (3), 683-698, 2022.
6. Wen, Y., Rashid, F., Fazal, Z., Singh, R., Spinella, M.J., Irudayaraj, J. "Nephrotoxicity of perfluorooctane sulfonate (PFOS)—effect on transcription and epigenetic factors." Environmental Epigenetics, 8 (1), dvac010, 2022.
7. Fazal, Z., Singh, R., Fang, F., Bikorimana, E., Baldwin, H., Corbet, A., Tomlin, M., et al. "Hypermethylation and global remodelling of DNA methylation is associated with acquired cisplatin resistance in testicular germ cell tumours." Epigenetics, 16 (10), 1071-1084, 2021.
8. Singh, R., Fazal, Z., Freemantle, S.J., Spinella, M.J. "Between a rock and a hard place: an epigenetic-centric view of testicular germ cell tumors." Cancers, 13 (7), 1506, 2021.
9. Albany, C., Fazal, Z., Singh, R., Bikorimana, E., Nasser, N.A., Hanna, H., et al. "A phase 1 study of combined guadecitabine and cisplatin in platinum refractory germ cell cancer." Cancer Medicine, 30, 2020.
10. Singh, MJS., Fazal, Z., Freemantle, S.J. "Mechanisms of cisplatin sensitivity and resistance in testicular germ cell tumors." Cancer Drug Resistance, 58, 2019.
11. Singh, R., Fazal, Z., Corbet, A.K., Bikorimana, E., Rodriguez, J.C., Khan, E.M., et al. "Epigenetic remodeling through downregulation of polycomb repressive complex 2 mediates chemotherapy resistance in testicular germ cell tumors." Cancers, 11 (6), 796, 2019.
12. Ge, W., Fazal, Z., Jakobsson, E. "Using Optimal F-Measure and Random Resampling in Gene Ontology Enrichment Calculations." Frontiers in Applied Mathematics and Statistics, 5, 16, 2019.
13. Jakobsson, E., Argüello-Miranda, O., Chiu, S.W., Fazal, Z., Kruczek, J., et al. "Towards a unified understanding of lithium action in basic biology and its significance for applied biology." The Journal of Membrane Biology, 250, 587-604, 2017.
14. Fazal, Z., Pelowitz, J., Johnson, P.E., Harper, J.C., Brinker, C.J., Jakobsson, E. "Three-Dimensional Encapsulation of Saccharomyces cerevisiae in Silicate Matrices Creates Distinct Metabolic States as Revealed by Gene Chip Analysis." ACS Nano, 11 (4), 3560-3575, 2017.
15. Fazal, Z., Southey, B.R., Sweedler, J.V., Rodriguez-Zas, S.L. "Multifactorial Understanding of Ion Abundance in Tandem Mass Spectrometry Experiments." Journal of Proteomics & Bioinformatics, 6 (2), 023, 2013.
16. Akhtar, M.N., Bukhari, S.A., Fazal, Z., Qamar, R., Shahmuradov, I.A. "POLYAR, a new computer program for prediction of poly (A) sites in human sequences." BMC Genomics, 11, 1-10, 2010.