

KANISHKA MANNA

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ACADEMIC QUALIFICATIONS

Ph.D., Bioinformatics, University of Arkansas, Little Rock (UALR) &
University of Arkansas for Medical Sciences (UAMS), Little Rock, AR Aug. 2019 – Dec. 2023

- Dissertation: *“Techniques in Multi-Omics Data Integration to Develop a Novel Proteogenomics Framework for Identification of Proteoforms.”*

M.Sc., Microbiology, Vijaygarh Jyotish Ray College, Kolkata, India. 2015 – 2017

- Thesis: *“Glycated Hemoglobin for the Diagnosis of Diabetes Mellitus and to Determine Estimated Average Glucose Concentration.”*

B.Sc. (Honours), Microbiology, Vijaygarh Jyotish Ray College
(affiliated to University of Calcutta), Kolkata, India. 2012 – 2015

BIOINFORMATICS EXPERIENCE

Research Assistant, University of Arkansas for Medical Sciences (UAMS) Jul. 2020 – Dec. 2023

IDEA Proteomics & Bioinformatics Core &

Byrum Lab, Department of Biochemistry and Molecular Biology

Role Description:

- Developing scalable & reproducible proteogenomics pipeline for efficient identification of proteoforms originating from alternative splicing of genes for complex model systems (Patient-derived xenografts).
- Generating and annotating custom-curated database(s) for multi-omics samples (accurate annotation for newly identified peptides from proteoforms/protein isoforms).
- Analyzing bulk next-generation sequencing data (WGS, WXS, RNA-seq), proteomics (DIA, DDA) and epigenetics (PTM, DNA methylation), microbiome (shotgun, amplicon), transcriptomic (single-cell and spatial) datasets.
- Integrating and curating multi-omics data using algorithms in R and Python.
- Protein identification by peptide database searching and *de novo* peptide sequencing of proteomics data.
- Analyzing proteomics and post-translation modification data for pathway/network analysis, differential gene expression analysis.
- Analyzing microbiome dataset.
- Performing statistical and data science techniques like cleaning, normalization, mining and visualization.

- Applying machine learning algorithms (supervised and unsupervised) to analyze multi-omics data.
- Communicating research findings, created summaries and presented them to principal investigators to advocate further research, funding or recognition in scientific journals.

Research Assistant, University of Arkansas, Little Rock (UALR)

Sep. 2019 – Jun. 2020

Department of Information Science

Role Description:

- Performed comparative genomics analysis for bacterial genomes.
- Developed viral phylogenetic tree using alignment free methods like k-mer.
- Familiarity with public databases and repositories of bulk and single-cell DNA and RNA profiling data.
- Performed exploratory data analysis, cluster analysis to name a few.
- Performed cloud-based bioinformatics analysis using HPC, Amazon AWS.
- Presented findings to investigators to advocate further research.

LABORATORY RESEARCH EXPERIENCE

Research Assistant, University of Arkansas for Medical Sciences (UAMS)

Jul. 2020 – Dec. 2023

Byrum Lab, Department of Biochemistry and Molecular Biology

Role Description:

- Performing DNA extraction, PCR analysis, electrophoresis, western blotting using standard techniques.
- Performing cloning and assay experiments of plasmid DNA by following standardized protocols.
- Maintaining cell lines.
- Performing next-generation sequencing by extracting DNA/RNA, library prepping, sequencing and QC analysis.
- Working knowledge of mass-spectrometry based bottom-up proteomics and top-down proteomics techniques.
- Performing spatial transcriptomics analysis by following standardized protocols for quantifying mRNA expression of genes and proteins in conjunction with single-cell RNA seq using 10x genomics Visium platform.
- Communicating research findings, created summaries and presented them to supervisors to advocate further research, funding or recognition in scientific journals.
- Organizing laboratory and maintained lab inventory to promote laboratory efficiency.

Research Intern, R. G. Kar Medical College & Hospital, Kolkata, India

Jun. 2016 – Aug. 2016

Department of Biochemistry

Role Description:

- Demonstrated a relationship between Diabetes Mellitus and Glycated Hemoglobin
- Collected patient blood samples, labeled vials and prepared quality specimens (tissues, swab, urine, feces) for lab testing.

- Performed a variety of routine blood draws from patients including venipuncture, heel sticks and finger sticks using standard equipment.
- Estimated ischemia modified albumin, blood sugar, lipids, glucose-6-phosphate dehydrogenase (G6PD), glycated hemoglobin, sodium ions, potassium ions, assay procedures in blood plasma.
- Performed bacterial and fungal culture, staining and estimated colony count using standard protocols and equipment.
- Maintained laboratory equipment like spectrometers, centrifuge, ion
- Maintained records of patient information and reported diagnostic findings to physicians and other practitioners.
- Maintained sample data and performed statistical analysis using R and SPSS for master's thesis.

TEACHING EXPERIENCE

Teaching Assistant, “Microbiome Analysis Workshop.” Held on UAMS Campus for National Center for Toxicological Research (NCTR) staff. *Apr. 12th – 14th, 2023*

Instructor: Michael S. Robeson II, Ph.D.

Role Description:

- Assisted students/attendees with installation of bioinformatics software, coding and interpreting results.
- Assisted the instructor with workshop academic goal by working with small groups or individual student.

Teaching Assistant, “UALR & UAMS Spring Genomics Virtual Workshop”. *Mar. 21st – 23rd, 2022*

Instructor: David W. Ussery, Ph.D. & Elizabeth Pierce, Ph.D.

Role Description:

- Assisted learners with navigating the workshop academic goal, assignment, discussion, writing and other key areas to ensure learner success and workshop completion.
- Assisted instructors in managing the evaluation of assignments and development of feedback.

SKILLS

Computational

- Programming languages: R, Python, Bash, SQL, CSS, HTML, Quarto, La/Tex, RShiny, Markdown, Snakemake, Nextflow
- Bioinformatics software/tools: GATK, BWA, DeepVariant, MOGSA, MixOmics, Galaxy, Bowtie2, Samtools, Picard, Strelka2, Cutadapt, FastQC, Limma, MaxQuant, DIA-NN, Mascot, Salmon, DESeq2, ProteoDA, ProteoViz, PTM Viz, Seurat, QIIME 2,
- CMG-biotools, BiocManager, 10X Genomics cloud platform.
- Other: Jupyter notebook, Conda, Singularity, Docker, Slurm, Grid computing (HPC-Grace), Cloud platforms (GCP), TensorFlow, version control (Git), SPSS, SRA, TCGA, PRIDE, SRA, Microsoft office, TCGA, NCBI, ENSEMBL, PRIDE.

Instruments

- MinIon (Oxford Nanopore)
- Chromium (10X Genomics)
- Spectrophotometer, Colorimeter
- Cryo-centrifuge
- Confocal, Fluorescence and Phase-contrast microscopes
- Auto analyzer (EBRA)
- PCR/ RT PCR
- ELISA analyzer

Methods

- Proteogenomics analysis
- Next-generation sequencing data analysis
- Single-cell and spatial transcriptomics analysis

- Data mining, curation and integration
- Multi-omics data analysis
- Metaproteomics analysis
- Metagenomics analysis
- Proteomics analysis (Epigenetics and Post-translation modifications)
- Comparative genomics analysis
- Machine Learning algorithms (supervised, unsupervised, reinforcement and regression learning)
- Statistical analysis with R
- Advanced microbiology, molecular biology and biochemistry skills
- Venipuncture

Interpersonal

- Ability to understand and follow specific instructions and procedures
- Excellent communication skills (written and verbal)
- Problem solving and time management
- Highly organized

HONORS AND AWARDS

- **Awarded 2nd place in poster presentation^α** *Sep. 17, 2023*
Bioinformatics Division, SE-IDeA 2023 Conference, Columbia, SC
- **Arkansas INBRE Travel Award** *Aug. 01, 2023*
Supported by NIGMS, P20 GM103429 from the NIH
- **Outstanding Doctoral Student Award** *Apr. 28, 2023*
Joint UALR/UAMS Graduate Program in Bioinformatics
Certificate for outstanding academic achievements and commitment to excellence in research
- **Awarded 3rd place in poster presentation*** *Oct. 2015*
West Bengal State Student-Youth Science Fair, Kolkata, India.

PUBLICATIONS

- Robeson MS 2nd, **Manna K**, Randolph C, Byrum S, Hakkak R. Short-Term Metformin Treatment Enriches *Bacteroides dorei* in an Obese Liver Steatosis Zucker Rat Model. *Front Microbiol.* 2022; 13:834776. Published 2022 Mar 30. doi: 10.3389/fmicb.2022.834776 2022
- Chappell K, **Manna K**, Washam CL, et al. Multi-omics data integration reveals correlated regulatory features of triple negative breast cancer. *Mol Omics.* 2021;17(5):677-691. Published 2021 Oct 11. doi:10.1039/d1mo00117e 2021

Non-peer Reviewed Publications (e.g., Preprints)

- **Manna K.**, Dharanipragada P., Alkam D.H., Avaritt N.L., Washam C.L., Robeson M.S., Edmondson R.D., Mackintosh S.G., Yang Z., Wang Y., Lomeli S., Moriceau G., Byrum S., Lo R., Tackett A.J. (2023) Proteogenomics Analysis to Identify Acquired Resistance-Specific Alterations in Melanoma PDXs on MAPKi Therapy. *Original bioRxiv preprint* . doi: 10.1101/2022.02.15.480454. 2023

ABSTRACT AND PRESENTATIONS

Oral Presentations

Invited Talks

- “A novel proteogenomics workflow for proteoforms detection”. 9th Annual Meeting of the Arkansas Bioinformatics Consortium (AR-BIC). Mar. 13th – 14th, 2022

General Talks

- “A novel proteogenomics workflow for proteoforms detection”. Student Seminar. Department of Biochemistry and Molecular Biology, UAMS. Sep. 1st, 2022
- “Multi-omics data integration reveals correlated regulatory features of triple negative breast cancer”. Intelligent Systems for Molecular Biology (ISMB)/ European Conference on Computational Biology (ECCB) - International Society for Computational Biology (ISCB). (Virtual). Jul. 25th – 30th, 2021
- “ProteoClade: A taxonomic toolkit for multi-species and metaproteomic analysis”. Student Seminar. Department of Biochemistry and Molecular Biology, UAMS. Mar. 18th, 2021

Posters

National/International Meeting Posters

- **Manna K**, Robeson MS, Byrum SD. ‘A novel proteogenomics workflow for proteoforms detection’^a, Poster presentation, Southeast Regional IDeA Conference. Sep. 2023
- **Manna K**, Dharanipragada P, Alkam D, et al. ‘Proteogenomics analysis to identify acquired resistance-specific alterations in melanoma PDXs on MAPKi therapy’, Poster presentation, Intelligent Systems for Molecular Biology (ISMB) Conference. Jul. 2022
- **Manna K**, Dharanipragada P, Alkam D, et al. ‘Proteogenomics analysis to identify acquired resistance-specific alterations in melanoma PDXs on MAPKi therapy’, Poster presentation, DART Annual Conference. May 2022
- **Manna K**, Chappell K, Washam CL, et al. ‘Multi-omics data integration reveals correlated regulatory features of triple negative breast cancer’, Poster presentation, ISMB/ECCB 2021 Virtual Conference – International Society for Computational Biology (ISCB) Jul. 2021
- **Manna K.**, Adhikary A, Chakraborty S, ‘Treating Cancer Cell by Focusing on Protein Degradation’, Poster presentation, Science and Engineering Fair 2016, Kolkata, India Jan. 2016

- **Manna K.**, Adhikary A., ‘Early Detection of Cancer by Screening’*, Poster presentation, West Bengal State Student-Youth Science Fair 2015, Netaji Indoor Stadium, Kolkata. Oct. 2015

PROFESSIONAL MEMBERSHIPS AND ACTIVITIES

International Society for Computational Biology	Apr. 2022 – Present
American Association of Pharmaceutical Scientists	May 2020 – May 2021

OTHER CREATIVE PRODUCTS AND NEWS

- ‘UA Little Rock Researcher Studying How to Combat Diseases By Identifying Therapeutic Vulnerabilities’. By Angelita Faller, UALR News. Sep. 14, 2022
- ‘UA Little Rock Researcher Studying How to Combat Disease’. By Vasti Hernandez, The Forum (The University of Arkansas at Little Rock’s Student Newspaper) Oct/Nov. 2022

PROFESSIONAL REFERENCES

Stephanie D. Byrum, Ph.D.

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 Director of CTPR Proteogenomics Core,
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 Distinguished Professor of Biochemistry and Molecular Biology,
 Scharlau Family Endowed Chair in Cancer Research,
 Director, NIH IDeA National Resource for Quantitative Proteomics,
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(Ph.D. co-mentor, Graduate advisory committee member, co-author)

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