MONISHA MITTAL

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EDUCATION

College of Science	**Northeastern University,** *Boston, MA*	**Expected Jul 2023**
Master of Science in Bioinformatics		**(GPA - 3.9/4)**
Carver College of Medicine	**The University of Iowa,** *Iowa City, IA*	**Aug 2018 - May 2021**
Master of Science in Pathology, *Thesis-based*		**(GPA - 3.2/4)**
Gargi College	**The University of Delhi,** *New Delhi, India*	**Aug 2015 - May 2018**
Bachelor of Science in Microbiology		**(GPA - 3.6/4)**

Relevant Coursework: Bioinformatics Computational Methods, Bioinformatics Programming, Intro to Data Mining and Machine Learning, Biostatistics, Graduate Immunology, Microbial and Animal Biotechnology

TECHNICAL SKILLS

- **Programming Languages:** R, Python, Bash Shell, SQL
- **Operating Systems:** Linux, Windows, Mac.
- **Bioinformatics Tools:** BLAST, GSNAP, Trimmomatic, SAMtools, Transcriptome Assembly (Trinity, de-novo), DESeq2, Seurat, Salmon, QIIME2, PLINK(GWAS), Bioconductor, TransDecoder, hmmscan, SPAdes, QUAST, InterProScan, BEAST, Nextflow
- **Laboratory Techniques:** PCR and Molecular Cloning, Cell Culture and maintenance, Protein purification and Western Blotting, Enzyme Assays, Flow Cytometry, Mouse model handling (EAE)

WORK EXPERIENCE

FogPharma	**Cambridge, MA, USA**
Data Science Co-op	**Jan 2023 - Present**

"Structure-Activity Relationship of Helicon^{TM} polypeptides"
- Developing SAR (Structure-Activity Relationship) tools to better understand Helicon^{TM} polypeptide using R and other relevant programming languages, under the guidance of senior team members.
- Conducted extensive data analysis and visualization to evaluate the effectiveness of the SAR tool in predicting Helicon^{TM} behavior.
- Demonstrated proficiency in R programming, data analysis, and problem-solving skills.

The University of Iowa	**Iowa City, IA, USA**
Graduate Research Assistant	**May 2019 - May 2021**

"Role of cGAS in Experimental Autoimmune Encephalomyelitis"
- Implemented techniques including EAE mouse model, genotyping, protein extraction, ELISA, nuclear transfection, CD4+ and CD8+ T cell purification, flow cytometric analysis of surface and intracellular markers, western blotting, BMDC harvesting, in vitro BMDC stimulation assay and in vitro T cell priming assay.

ACADEMIC PROJECTS

"Predicting cervical cancer diagnosis from risk factor data" — **Sept 2022 - Dec 2022**
- Developed Cervical cancer classifier using ensemble of Naive Bayes, Decision Trees and Logistic Regression algorithms.
- Evaluated model performance using accuracy, specificity, recall, and AUC, and enhanced model accuracy through parameter tuning and meta-learning techniques.
- Deployed the classifier for practical use in the medical field, facilitating early detection and prevention of cervical cancer through data-driven insights.

"Design and Implementation of a Hospital-Acquired Infection Tracking Database" — **May 2022 - Aug 2022**
- Designed and implemented a relational database for a hospital to track patient visits and Hospital Acquired Infections (HAIs).
- Analyzed the entities involved, created a comprehensive database model, and inserted sample data into the model, which was forward engineered the model to the server for efficient data management and retrieval.
- Developed custom queries to produce insightful reports that helped identify the distribution and risk factors of HAIs in the hospital, utilizing SQL and database management tools to efficiently manage and manipulate large datasets.

"RNA-Seq analysis of Aiptasia pallida transcriptome". — **Aug 2021 - Dec 2021**
- Achieved high-quality transcriptome data by trimming and aligning paired-end reads of *Aiptasia pallida* using GSNAP aligner.
- Identified key genes and pathways by estimating relative abundance and detecting differentially expressed genes using DESeq2.
- Annotated the transcriptome from Trinity de-novo assembly with KEGG pathways and GO terms, providing insights into gene function and regulation.

"Transcriptional activity in Lymph Node during initiation and progression of EAE " — **Jan 2020 - May 2020**
- Developed microarray data analysis pipeline of expression profiling data obtained from NCBI GEO.
- Performed pre-processing (quality assessment and normalization) of data, identified differentially expressed genes, classified genes based on expression patterns and annotated the genes using Gene Ontology.

AWARDS

- Recipient of the American Association of Immunologists Trainee Abstract Award (2020).
- Recipient of The Indian Academy of Sciences-INSA-NASI Summer Research Fellowship (2017).