

# MONISHA MITTAL

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## EDUCATION

<b>College of Science</b> Master of Science in Bioinformatics	<b>Northeastern University, Boston, MA</b>	<b>Expected Jul 2023</b> (GPA - 3.9/4)
<b>Carver College of Medicine</b> Master of Science in Pathology, <i>Thesis-based</i>	<b>The University of Iowa, Iowa City, IA</b>	<b>Aug 2018 - May 2021</b> (GPA - 3.2/4)
<b>Gargi College</b> Bachelor of Science in Microbiology	<b>The University of Delhi, New Delhi, India</b>	<b>Aug 2015 - May 2018</b> (GPA - 3.6/4)
<b>Relevant Coursework:</b> 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.
- 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
- Databases: MySQL
- Laboratory Techniques: Mammalian Cell Culture, Gel electrophoresis, PCR, DNA and RNA purification, western blotting, ELISA.
- Operating Systems: Linux, Windows, Mac.

## WORK EXPERIENCE

<b>FogPharma</b> <i>Data Science Co-op</i>	<b>Cambridge, MA, USA</b> <b>Jan 2023 - Present</b>
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### *"Structure-Activity Relationship of Helicon™ polypeptides"*

- Developing SAR (Structure-Activity Relationship) tools to better understand Helicon™ 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™ behavior.
- Demonstrated proficiency in R programming, data analysis, and problem-solving skills.

### **The University of Iowa**

#### *Graduate Research Assistant*

**Iowa City, IA, USA**

**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.
- Recipient of the American Association of Immunologists Trainee Abstract Award (2020).

## ACADEMIC PROJECTS

<b>Introduction to Machine Learning and Data Mining, Northeastern University</b>	<b>Sept 2022 - Dec 2022</b>
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### *"Predicting cervical cancer diagnosis from risk factor data"*

- 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.

### **Database Design, Access, Modeling and Security, Northeastern University**

**May 2022 - Aug 2022**

### *"Design and Implementation of a Hospital-Acquired Infection Tracking Database"*

- 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.

### **Bioinformatics Methods, Northeastern University**

**Aug 2021 - Dec 2021**

### *"RNA-Seq analysis of Aiptasia pallida transcriptome"*

- 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.

### **Practical Data Science and Bioinformatics, The University of Iowa**

**Jan 2020 - May 2020**

### *"Transcriptional activity in Lymph Node during initiation and progression of Experimental Autoimmune Encephalomyelitis"*

- 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.

## CERTIFICATIONS AND AWARDS

- HavardX: Statistical Inference and Modeling, Dimensional Data Analysis, Linear Models and Matrix Algebra.
- Recipient of The Indian Academy of Sciences-INSANA Summer Research Fellowship (2017).