

Ashwani Devi

ashwanisiwach132003@gmail.com | +91-8307854345 | [Portfolio](#) | [GitHub](#) | [LinkedIn](#)

Research Interest

Computational Genomics; Non-coding RNA Analysis; Machine Learning for Genomic Data; Disease Genomics; Multi-omics Integration; Interpretable AI in Biology

Proposed PhD Research Topic

AI-driven Analysis of Non-coding RNA and Genomic Variants for Disease Mechanism Discovery

Research Summary

I aim to develop machine learning and deep learning frameworks for identifying disease-associated non-coding RNAs and genomic variants. My work focuses on integrating sequence features, expression profiles, predicted structure-based and mutation data to build interpretable and biologically meaningful predictive models for chronic diseases such as Type-2 Diabetes and cancer.

Education

Master of Technology (M.Tech) – Communication & Signal Processing

Indian Institute of Information Technology, Design & Manufacturing (IIITDM), Jabalpur, India
Expected Award: June 2026 *Expected Thesis submission: May 2026* **CPI: 8.9 / 10.0**
Thesis: Computational Identification of Non-coding RNA–Disease Association (Type-2 Diabetes)

Bachelor of Technology (B.Tech) – Computer Science & Engineering

Maharshi Dayanand University (MDU), Rohtak, India
Year of Award: June 2024 **CPI: 8.1 / 10.0**

Research Experience

Graduate Research Assistant Aug 2024 – Present, IIITDM Jabalpur, India

- Conducting master's thesis research on computational identification of disease-associated non-coding RNAs in Type-2 Diabetes.
- Developed end-to-end bioinformatics and ML pipelines integrating HISAT2, GATK, SAMtools for sequence alignment and variant calling.
- Performed SNP detection and genomic variation analysis and integrated mutation features into predictive ML models.
- Engineered sequence-based (k-mer, motif), structure-based (secondary structure, folding energy), and expression-based (TPM, Log2FC) features.
- Implemented ML/DL models including Random Forest, XGBoost, CNNs, and BiLSTM with class imbalance handling.

Additional Research Activities

- Mentored undergraduate students on projects in computational genomics (Parkinson's disease, Enhancer prediction, microexon discovery, splice-site prediction).
- Studying transformer-based foundation models for genomics, including DNABERT and

Nucleotide Transformer.

- Exploring attention-based sequence embeddings for biological representation learning.

Publications & Academic Outputs

Conference Poster

Feature Engineering for AI-Based Genomic Data Analysis. Inbix 2025.

Repository: [INBIX Conference certificate](#)

Manuscript

Manuscript in preparation based on thesis findings; expected submission in late Dec. 2025.

(LncRNAs associated with Type 2 Diabetes patients, specialized medicine)

Relevant Courses

Master's Courses (in English)

- 1) Genomics and Proteomics Signal Processing
- 2) Signal Processing

Bachelor's Courses

- 1) Machine Learning
- 2) Data Structures and Algorithms

Technical Skills

Computational Genomics: HISAT2, BLAST, GATK, SAMtools, VCFtools, GEO, Ensembl

Machine Learning & Deep Learning: Scikit-learn, PyTorch, XGBoost, CNNs, BiLSTM, HuggingFace Transformers, Shap

Programming: Python, MATLAB, Biopython, NumPy, Pandas, Plotly, AWS, MySQL, Streamlit, Flask, RestAPI, RAG/LLMs

Research Practices: Statistical analysis, reproducible pipelines, Git/GitHub, AWS, Docker, model validation and interpretation

Research Outputs & Reproducibility

- Built an end-to-end computational pipeline that starts from RNA-seq data, extracts sample-specific lncRNA (or gene) sequences, derives sequence, structural, and expression features, and applies machine-learning models for interpretable, sample-level disease diagnosis.
- Designed the workflow to be modular and reproducible, with clearly defined steps for preprocessing, feature extraction, model training, and evaluation, allowing results to be easily reproduced and fairly compared across datasets.
- Enables population-specific biomarker discovery and supports personalized diagnosis by identifying molecular contributors at the individual-sample level.

Referees

Prof. S.N. Sharma

Department of ECE, IIITDM
Jabalpur, India

Email: snsharma@iiitdmj.ac.in

Dr. Sunil Kumar

Department of ECE, Central University
of Jammu, India

Email: sunil.ece@cuammu.ac.in

Statement of Career Goal

To pursue a research-intensive PhD in Computational Genomics, focusing on AI-driven analysis of non-coding RNA and genomic variants to advance precision medicine for chronic diseases.

Last updated: December 2025