

# Derrin Bright

Bioinformatics | Biotechnology | ML in Biology

📞 +91 95666 35920

✉️ derrinbright@gmail.com

🌐 Portfolio

🔗 GitHub

👤 LinkedIn

## Education

### Vellore Institute of Technology (VIT)

Bachelor of Technology in Biotechnology

CGPA: 8.69 Vellore, India

2022-Present

## Technical Skills

Computational Biology Tools	BLAST   AlphaFold   AutoDocK Vina   GROMACS   MGLTools   Bioconductor   OpenBabel   Cytoscape   Seurat   GSEA   FIMO
Data Analysis Tools	Neo4J   KNIME   NetworkAnalyst
Programming Tools	R   Python   Bash
Machine Learning Tools	TensorFlow   Keras   NumPy   Pandas   Matplotlib

## Research Experiences

### Project Intern at Nanyang Technological University, Singapore

Jan 2026 - Present

- Performing computational analysis of ER stress responses through transcriptomic profiling, differential expression analysis, Weighted Gene Co-expression Network Analysis (WGCNA), and gene regulatory network construction.
- Supervised by Dr. Guillaume Thibault | Guillaume Thibault Lab

### Research Intern at Boston University, USA

Sept 2025 - Present

- Developed an automated bioinformatics pipeline for regulatory sequence analysis across 200+ Human Papillomavirus genomes.
- Performed large-scale transcription factor motif analysis and comparative regulatory profiling between high-risk and low-risk HPV types.
- Integrated motif-based approaches with deep learning-based sequence models to assess regulatory activity.

### Research Intern at University of Liverpool, UK

Sept 2025 - Present

- Analyzing single-cell RNA-seq data from Chronic Lymphocytic Leukemia (CLL) and Richter's Transformation (RT) patients.
- Developing multiple machine learning models including XGBoost, Logistic Regression, SVM, and Random Forest, applying feature importance analysis to differentiate CLL from RT at the transcriptomic level.

### Research Intern at IIT Bombay, India

May 2025 - Oct 2025

- Conducted differential expression analysis and WGCNA to identify key gene modules associated with autoimmune disease progression, followed by Gene Set Enrichment Analysis (GSEA) and Protein-Protein Interaction (PPI) network construction to uncover dysregulated pathways and functional gene relationships.
- Implemented predictive models to classify disease vs healthy states based on gene expression, enhancing biological interpretability through integrated network and machine learning approaches.

### Research Intern at Ashoka University, India

Jan 2025 - Mar 2025

- Analyzed five assembled *E. coli* genomes for carbapenem and beta-lactam resistance using BLAST and RGI-CARD to identify mutations, and correlated genotype-phenotype relationships through AST report analysis.
- Performed Multiple Sequence Alignment (MSA) of Penicillin-Binding Proteins (PBPs) from the five *E. coli* genomes against a reference wild-type sequence to detect conserved mutations, and conducted genomic analysis that led to the identification of a 12-base pair insertion in the PBP3 gene, contributing to antibiotic resistance mechanisms.

### Biotech Team Lead at NovaLinks, India

Feb 2025 - April 2025

- Led a project integrating miRNA analysis and histopathological imaging with machine learning to enhance lung cancer subtype classification and improve diagnostic precision.
- Conducted research on miRNA biomarkers specific to lung cancer and provided biological insights to support the development of an accurate classification model for distinguishing adenocarcinoma from squamous cell carcinoma.

## Publications

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**Comparative Analysis of HPV-Positive Cervical and Head and Neck Cancers Using WGCNA and Machine Learning Identifies Shared Biomarkers** | Under review at *Cellular Oncology (Springer)*  
B. Kiruba, S.B. Niranjan †, D. Bright †, N. Patel, C.A. Biju, V. Sundararajan\*, S.S. Lulu\*  
†Equal contribution \*Corresponding author

## Technical Projects

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### Transcriptomic Comparison of HPV-Associated Cancers Using Co-Expression Networks

- Conducted a comparative analysis of HPV-positive cervical and head and neck cancers using TCGA data. Performed DESeq2 and WGCNA to identify shared genes between both cancers.
- Applied machine learning models to filter features, identifying 16 HPV signature genes, and validated findings using single-cell RNA-seq analysis.
- Constructed PPI networks and performed functional enrichment analyses to identify shared molecular mechanisms underlying HPV-driven tumorigenesis.

### Computational Identification of Antimalarial Leads through Fingerprint Similarity Analysis

[GitHub Link](#)

- Screened a library of antimalarial molecules against a query (chloroquine drug) by generating molecular fingerprints and computing Tanimoto similarity coefficients using KNIME and RDKit nodes.
- Extracted molecular data from the Protein Data Bank (PDB) and visualized pairwise similarity scores as a heatmap to identify high-similarity candidates for antimalarial drug development.

### In Silico Analysis of 3DTC/CEP-6331 Complex using Molecular Docking

[GitHub Link](#)

- Implemented a molecular docking simulation using AutoDock Vina to model the interaction between the 3DTC kinase and the CEP-6331 inhibitor, achieving a predicted binding affinity of -12.23 kcal/mol.
- Analyzed the top binding pose to identify the specific amino acids responsible for the stable interaction, including key hydrophobic (ILE180, LEU274) and polar (LYS228, ASP284) residues.

### Single-Cell Transcriptomic Profiling of the B16 Melanoma's Microenvironment

[GitHub Link](#)

- Processed raw single-cell transcriptomic data from a B16 melanoma model using R (Seurat), applying quality control, normalization, and clustering to map the tumor's cellular heterogeneity.
- Characterized the resulting cell clusters by annotating fourteen distinct cell types within the tumor microenvironment and performed differential expression analysis to identify their unique gene signatures.

### Asthma Risk Prediction using Machine Learning

[GitHub Link](#)

- Optimized asthma risk prediction by developing multiple machine learning models, including Random Forest, SVM, and Gradient Boosting, and finetuning hyperparameters using Grid Search Cross-Validation to maximize accuracy.
- Enhanced model accuracy and reduced data dimensionality by applying Recursive Feature Elimination (RFE) to identify the most predictive features.

## Honors and Leadership

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**First runner-up in the Biomimicry Innovation Challenge and Showcase**, Vellore Institute of Technology, 2024

**Top 10 Winner of Bio-Inspired Design Fest (BIDFEST) Ideathon**, Vellore Institute of Technology, 2024

**Vice Chairperson at Alpha Bio Cell, VIT University, India**

January 2024 - December 2024

- Led several biotechnology and bioinformatics-related events, including hackathons, workshops, and quizzes, enhancing the club's engagement.
- Mentored junior core members and applied leadership, technical, and project management skills to ensure successful event planning and execution.

## Extra-Curricular

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### Volunteer | National Service Scheme, NGO

Conducted sessions in government schools on career opportunities and the importance of joining the armed forces.

### Volunteer | Becoming I Foundation, NGO

Taught science, math, and english in government schools, supporting underprivileged communities.

### Event Coordinator | BioSummit, School of Biosciences and Technology

Organized a flagship event connecting academia and food industries, managing food distribution and ensuring smooth execution.