Derrin Bright

Bioinformatics | Biotechnology | AI in Healthcare

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Education

Vellore Institute of Technology (VIT) — CGPA: 8.69 — Vellore, India
Bachelor of Technology in Biotechnology — 2022-Present

Chettinad Vidyashram — 12th - 94.8% — Chennai, India
CBSE Biology-Mathematics — 2008-2021

- **Relevant Courses:** Bioinformatics, Genomics and Proteomics, Molecular Biology, Cell Biology, Genetic Engineering, Biochemistry, Immunology, Biology, Probability and Statistics, Linear Algebra, Calculus
- **Relevant Certifications:** ML A-Z, Python for Data Science, AI & Development, Bioinformatic; Bulk RNA-Seq Data Analysis, Advanced Bioinformatics, Bioinformatics; Learn Docking & Molecular Dynamics Simulation, Single-Cell RNA-Seq Data Analysis using R & Python, Oracle Cloud Infrastructure Generative AI Professional Certificate

Technical Skills

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

Technical Experiences

Research Intern at Boston University, USA — *September 2025 - Present*

* Developing an automated bioinformatics pipeline to parse and extract regulatory regions from a large-scale genomic dataset of over 200 viral genomes.
* Conducting a comparative sequence analysis to identify genomic signatures significantly enriched in specific disease-associated subtypes.

Research Intern at University of Liverpool, UK — *September 2025 - Present*

* Analyzing bulk RNA-seq data to identify the key molecular drivers and biological pathways involved in the progression of Chronic Lymphocytic Leukemia.
* Building and evaluating multiple classifiers to distinguish between Chronic Lymphocytic Leukemia (CLL) and Richter's Syndrome (RS) cells, identifying Logistic Regression as the top-performing model with a high AUC of 0.94 on unseen patient data.

Research Intern at IIT Bombay, India — *May 2025 - June 2025*

* Conducted differential expression analysis and Weighted Gene Co-expression Network Analysis (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 using NetworkAnalyst 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 — *January 2025 - March 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 — *February 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.

Technical Projects

Transcriptomic Comparison of HPV-Associated Cancers Using Co-Expression Networks
- Extracting and analyzing transcriptomic data from TCGA for HPV-associated cancers to perform both differential expression analysis and WGCNA, identifying key genes and co-expression modules.
- Constructing a PPI network in Cytoscape from a core gene set, and further analyzing these genes with functional enrichment in R to determine their shared biological roles.

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.

Computational Analysis of Transcriptional Regulation by the MOV10 Protein   *GitHub Link*
- Investigated the transcriptomic impact of MOV10's knockdown and overexpression by analyzing a public RNA-seq dataset, identifying hundreds of differentially expressed genes under knockdown and overexpression conditions.
- Uncovered a dual regulatory mechanism for MOV10, where its knockdown and overexpression induce two distinct and often inverse transcriptional responses.

Honors and Leadership

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

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.

Green Ambassador | Eco Club, Chettinad Vidyashram
Led tree plantations, recycling drives, and plastic waste collection, promoting sustainability and environmental awareness.

Event Coordinator | BioSummit, School of Biosciences and Technology
Organized a flagship event connecting academia and food industries, managing food distribution and ensuring smooth execution.