

BHAVYA DHAKA

Dublin, Ireland | bhavya.dhaka@ucdconnect.ie | linkedin.com/in/bhavyadhaka | github.com/bhavya1929 |

PROFESSIONAL SUMMARY

I am a computational biologist and machine learning researcher with seven years of experience in cancer genomics, perturbation biology, deep learning, and multi-omics analysis. My work has focused on modeling how genes, drugs, and tumours behave across biological contexts, including perturbation-response transfer, mutation-driven tumour biology, and immunotherapy response. I have designed and built computational models end to end, led projects from conception through publication, and developed analyses that translate complex biological data into testable hypotheses. Across India, Ireland, and the United States, I have worked with multidisciplinary research groups and large-scale consortia, with first-author publications in peer-reviewed journals.

CORE SKILLS

AI / ML: PyTorch, deep learning, meta-learning, graph neural networks, perturbation modelling, autoencoder, VAE, transformers, representation learning, transfer learning, foundation model benchmarking, model architecture design and optimisation, SHAP interpretability, Random Forest, Linear modeling, mixed effects.

Genomics & Single-Cell: scRNA-seq, Perturb-seq, CRISPR screens, ATAC-seq, RNA-seq, multi-omics integration, functional genomics, regulatory genomics, large-scale cancer and regulatory genomics datasets including TCGA, PCAWG, and FANTOM, Scanpy, Seurat.

Tools & Infrastructure: Python, R, Bash, Nextflow, Docker, SLURM/HPC, Git, GitHub, reproducible pipeline development, scalable workflow design, benchmarking protocols, technical documentation.

Domain Knowledge: Perturbation biology, cancer genomics, drug response prediction, therapeutic target prioritisation, precision oncology, biomarker discovery, lncRNA target discovery, biological signal interpretation.

PROFESSIONAL EXPERIENCE

Researcher | Ideker Lab, UC San Diego, USA

2024 – 2026

- Developed **HyperMAP**, a PyTorch-based **deep learning framework for transferring gene and drug perturbation responses across biological contexts**, achieving approximately 70% higher Pearson correlation and 20x faster inference than leading baseline models.
- Benchmarked HyperMAP against GEARS and scGPT** using biologically meaningful evaluation metrics, including Pearson correlation, differentially expressed gene recovery, ranking-based metrics, and top-20 gene evaluation.

- Applied HyperMAP to transfer drug-response signals from cell-line models to public triple-negative breast cancer patient dataset, identifying predicted response patterns consistent with mutation-based patient stratification.
- Led the project end to end, from research design, model architecture development, benchmarking, biological interpretation, and analysis through to manuscript preparation and submission.

MSCA Doctoral Fellow | GoldLab, University College Dublin

2022 – Present

Marie Skłodowska-Curie Actions Fellowship - competitive EU-wide award

- Developed TransCistor, a cis-regulatory lncRNA discovery framework, characterising 268 human and 134 mouse regulatory targets and supporting the systematic inclusion of non-coding elements in CRISPR study design and perturbation atlases. Published in Nucleic Acids Research.
- Developed a prime-editing-based perturbation screening protocol to improve confidence in target discovery, reduce technical noise, and support more reliable prioritisation of regulatory candidates.
- Contributed multi-omics analytical expertise to the FANTOM6 consortium, involving 50+ institutions globally, profiling RNA–DNA interactions across cell types as part of a large-scale regulatory genomics study.

Bioinformatician | National Centre for Biological Sciences, India

2019 – 2022

- Led two independent cancer genomics projects: chromatin accessibility profiling in p53 gain-of-function mutants and pan-cancer immunoproteasome activity analysis, identifying regulatory mechanisms relevant to immunotherapy response and tumour stratification.
- Developed random forest models to evaluate immunoproteasome activity as a predictor of immunotherapy response and compare its performance against established response markers.
- Built reproducible Nextflow pipelines for ATAC-seq and RNA-seq workflows across 500+ tumour samples, achieving approximately 40% runtime reduction and enabling scalable, version-controlled pan-cancer regulatory analysis.
- Collaborated with the NIH on single-cell RNA-seq analysis of small-cell lung cancer patient cohorts, modelling tumour evolution and transcriptional heterogeneity to support translational clinical research.

PUBLICATIONS

1. Dhaka B et al. HyperMap: An Efficient Meta-Learning Framework for Transferring Perturbation Responses Across Diverse Biological Contexts. Preprint, 2026.
2. Dhaka B et al. Functional identification of cis-regulatory long noncoding RNAs at controlled false-discovery rates. Nucleic Acids Research, 2024.
3. Kumar R*, Dhaka B* et al. Prognostic association of immunoproteasome expression in solid tumours. Molecular Oncology, 2023. Co-first author.
4. Dhaka B and Sabarinathan R. Differential chromatin accessibility landscape of gain-of-function mutant p53 tumours. BMC Cancer, 2021.
5. Lambolez A, ..., Dhaka B, ..., Carninci P et al. The human RNA-DNA interactome is cell type-specific and dynamic. Under review, 2026.

LEADERSHIP & SCIENTIFIC ENGAGEMENT

- **Mentored MSc and PhD students** across computational genomics and machine learning projects, supporting study design, data analysis, model development, and project completion.
- **Organised a 150-person national genomics symposium**, secured industry sponsorship, and chaired a monthly international scientific speaker series.
- **Presented at international conferences**, including Perturb2026 and EMBL Cancer Genomics.

AWARDS & FELLOWSHIPS

- 2022 Marie Skłodowska-Curie Actions (MSCA) PhD Fellowship: Competitive EU-wide doctoral fellowship awarded to outstanding early-stage researchers
- 2021 Indian Council of Medical Research (ICMR) Senior Research Fellowship
- 2019 Bangalore Life Science Cluster (BLiSC) Fellowship

EDUCATION

PhD, Genomics Data Science | University College Dublin, Ireland

Expected August 2026

Thesis: "From Predictive Models to Mechanistic Insight in Perturbation Biology"

MSc, Bioinformatics & Applied Biotechnology | IBAB, India