

Pyaree Mohan Dash

Email: pyareemohandash@gmail.com • Phone: [+4915170867686](tel:+4915170867686) • GitHub: [pyareedash](https://github.com/pyareedash) • LinkedIn: [pmdash](https://www.linkedin.com/in/pmdash)

Summary

Bioinformatics professional specializing in AI for genomic medicine. Proven track record of developing scalable computational frameworks for gene-regulation analysis, variant-effect prediction, and therapeutic candidate prioritization. Work recognized through international consortium research, publications (Nature, IEEE) and international conferences (ISMB).

Research Experience

Research Assistant at University Hospital Heidelberg, Germany (Part-time)

June 2025 – Present

Precision cardiac gene delivery

- Developed a multimodal framework to identify heart-targeting gene-delivery candidates with strong translational potential, with leading candidates successfully validated in mice and pigs.
- Elucidated candidate biological drivers providing a reusable strategy to prioritize next-generation delivery vectors.

Bioinformatics Scientist at Berlin Institute of Health at Charité, Berlin, Germany

Dec 2021 – Feb 2025

Decoding variation in human genome

- Designed a scalable framework for variant-effect prediction spanning linear, ensemble, and large DNA foundation models; fine-tuned a task-specific CNN that improved Pearson correlation by 60% over the larger models, demonstrating that focused model design could outperform scale.
- Developed interpretation algorithms that connected model predictions to biologically meaningful regulatory signals, strengthening candidate selection and focusing downstream experimental validation.

High-Throughput Genomics

- Co-built MPRAsnakeflow, a reproducible analysis framework for high-throughput regulatory assays, converting raw Illumina sequencing data into quality-controlled measurements, reports, and visualizations for 240,000 variants.
- Led pilot studies that established an AI-guided framework for disease-relevant variant design and analysis, laying the groundwork for consortium-wide adoption within [NHGRI-IGVF](#).
- Developed an end-to-end, model-guided framework that ranked enhancers and variants by predicted effect size and delivered experiment-ready candidates for targeted gene-delivery studies.

Graduate Research Assistant at CIPMM Homburg (HS-KL), Saarland, Germany

Mar 2018 – Oct 2021

Immune Receptor Evolution and Function

- Reconstructed the evolutionary landscape of bacterial FPR immune receptor families across 19 species; traced how receptor diversification shaped distinct roles in immune signaling.
- Performed high-throughput cellular screening and bio-imaging data analysis of mammalian cells that identified novel receptor-specific peptide binders.

Graduate Research Assistant at HIPS, Saarbrücken, Germany

Aug 2019 – Jan 2020

- Built an integrated GPCR structure-drug-ligand knowledge base, creating the foundation for graph-based analysis of receptor-ligand relationships and drug-target discovery.
- Identified key amino acid residues governing GPCR ligand binding through integrative structural analysis.

Research Intern at School of Biotechnology, Amrita University, India

Aug 2015 – Dec 2015

- Contributed to a *Bill and Melinda Gates Foundation*-funded project on developing biocontrol-based disinfection technologies for regions with poor sanitation and wastewater challenges.

Honors and Awards

- Invited Poster presentation with honorable mentions at ISCB RSG conference with DREAM challenges – [2022](#)
- Master thesis featured at the Upper-Rhine Artificial Intelligence Symposium - [2021](#)
- Indian Academy of Science, Research Fellowship – 2016, 2017 (≈ 250 students selected across India)

Tools and Technologies

Programming	Python, Bash, R, C++, SQL
Machine learning	scikit-learn, Keras, TensorFlow, PyTorch, Hugging Face, SHAP, LangChain
Web & Workflows	AWS, Google Cloud, Docker, Snakemake, Nextflow, FastAPI, Flask
Bioinformatics	BWA-MEM, bcftools, VEP, bedtools, FastQC, pysam, Biopython

Education

Master of Science in Bioinformatics

Saarland University, Saarbrücken, Germany

Advisor: Prof. Dr. Volkhart Helms

2017 – 2021

GPA: 1.7

Bachelor of Science in Biotechnology

Amrita University – School of Biotechnology, Kerala, India

Advisors: Prof. Dr. Nandita Mishra, Prof. Dr. Sanjay Pal

2014 – 2017

GPA: 9.2/10.0 (German equivalent: 1.3)

Language Skills

English	Full professional proficiency (C1)
German	Limited working proficiency (A2)

Academic Projects

Master's thesis: Saarland University, Saarbrücken, Germany

Jan 2021 – July 2021

Machine Learning-Guided Peptide Design

- Proposed an ensemble-learning method that accelerated prioritization of peptide binders for bacterial-sensing FPR immune receptors. This method achieved 75% precision while reducing the screening burden by over 90%.
- Defined distinct functional features across FPR receptors, clarifying within-family specialization and guiding receptor-specific peptide design.

Bachelor thesis: Amrita University – School of Biotechnology, Kerala, India

Jan 2017 – May 2017

Biochemical Systems Theory in Parkinson's disease

- Designed an integrated mathematical model of Parkinson's disease by linking core cell-death pathways with secondary regulatory processes, enabling system-level analysis of disease progression.
- Analyzed time-series simulations to identify candidate biomarkers associated with early disease progression.

Selected Talks

- Dash P. M.**, Deng C., Shendure J., Ahituv N., Schubach M., & Kircher M. Accelerating high-throughput characterization of regulatory variants with deep learning. RSG Chair - ISMB RSGDREAM [2024](#)
- Agarwal, V., Inoue, F., Schubach, M., Penzar, D., Martin, B. K., **Dash, P. M.**, ... & Ahituv, N. Massively parallel characterization of transcriptional regulatory elements. MLCSB Chair - ISMB/ECCB [2023](#)

Publications

- Salomon, K., Deng, C., **Dash, P. M.**, Chalkiadakis, T., Li, Q., Chen, Z., ... & Kircher, M. (2026). Massively parallel characterization and predictive modelling of neuronal regulatory variation. [bioRxiv](#), 2026-07.
- Rosen, J. D., V., A. D., Salomon, K., de Lange, N., **Dash, P. M.**, Keukeleire, P., ... & Schubach, M. (2026). Uniform processing and analysis of IGVF massively parallel reporter assay data with MPRAsnakeflow. [Genome Research](#)
- Agarwal, V., Inoue, F., Schubach, M., Penzar, D., Martin, B. K., **Dash, P. M.**, ... & Ahituv, N. (2025). Massively parallel characterization of transcriptional regulatory elements. [Nature](#), 1-10.
- Sasidharakurup, H., **Dash, P.M.**, ... and Diwakar, S., 2017, September. Computational modelling of apoptosis in Parkinson's disease using biochemical systems theory. (ICACCI). [IEEE](#)

Professional Services

Peer review	Reviewer for Bioinformatics and Bioinformatics Advances. (Oxford University Press) (2023-2024)
Activities	Co-organized an IGVF international workshop on MPRA design for AI applications. (2024)
Mentorship	Co-supervised 2 bachelor's and 1 master student at CIPMM. (2018-2021)