

Vishal Bharti

Computational Biologist — CRISPR/Cas · RNA Structural Biology · Single-Cell Genomics

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RESEARCH PROFILE

I build computational and statistical methods for genome engineering and RNA biology, currently in the RNA Biology Group at **CSIR-IGIB**. The question I keep returning to is whether a biological conclusion actually follows from the data that produced it, and it runs through most of what I have done: a co-first-author method for predicting intramolecular RNA triple helices (*Biochemistry*, ACS), a three-layer inference pipeline contrasting repair-factor requirements at staggered versus blunt DNA double-strand breaks, and StickForStats, an open-source platform that validates the assumptions behind a statistical test before running it. I came to biology from electronics engineering, taught myself the field over two years, and entered through an M.Tech at IIT Guwahati (GATE-BT **All-India Rank 127, top ~1%**).

EDUCATION

M.Tech, Biotechnology — Indian Institute of Technology (IIT) Guwahati · 2020–2022 · CGPA 8.75/10
Master's thesis: NMD-susceptible transcripts in UPF3B-knockout cells (RNA-seq).

B.Tech, Electronics & Communication Engineering — Institute of Engineering & Management (IEM), Kolkata · 2014–2018 · CGPA 8.19/10

RESEARCH EXPERIENCE

Project Associate-II, RNA Biology Group (Dr. Debojyoti Chakraborty) — CSIR-Institute of Genomics and Integrative Biology (IGIB), New Delhi · Feb 2023 – Present (3+ years)

- **RNA intramolecular triple-helix prediction (TRIPinRNA)**. Co-developed (**co-first author**) a Python method to identify and characterize intramolecular RNA triple helices, with biophysical validation, applied to X-chromosome-inactivation and gene-regulation contexts. *Published in Biochemistry (ACS)*. Co-supervised with Dr. Souvik Maiti.
- **DNA double-strand-break repair from single-cell transcriptomes**. Designed a three-layer statistical-inference pipeline to contrast repair-factor requirements at staggered versus blunt-ended breaks from scRNA-seq, with a stringent QC/integration workflow, and identified pathway-specific gene sets validated across layers.
- **Interneuron-migration disorders in human forebrain assembloids**. Led RNA-seq, protein-protein-interaction-network, and pan-tissue analyses linking engineered forebrain assembloids on polymeric nanofiber scaffolds to interneuron-migration phenotypes. (*Preprint; under revision, Stem Cell Reports*.)
- **MLC leukodystrophy — disease modeling and diagnostics**. Led RNA-seq analysis and a computational approach to detect the 132dupC *MLC1* mutation, supporting iPSC disease-model work on the astrocyte-vacuolation phenotype. (*Published in Orphanet Journal of Rare Diseases, 2026*.)
- **G-quadruplex regulation of CCN1**. Computational and proteomics analysis of IGF2BP1-G-quadruplex regulation of *CCN1* expression. *Published in Biochemistry (ACS)*. Co-supervised with Dr. Mary K. Ekka.

Junior Research Fellow (Dr. Vibin Ramakrishnan) — IIT Guwahati · Jun – Sep 2022

- Hybrid proteomics-cheminformatics-network-medicine analysis of Ashwagandha and Yograj Guggulu for osteoarthritis: protein-protein-interaction analysis and computational drug repurposing.

M.Tech Thesis (Dr. Kusum K. Singh) — IIT Guwahati · 2021–2022

- RNA-seq identification and functional-enrichment analysis of nonsense-mediated-decay-susceptible transcripts in UPF3B-knockout HEK293 cells.

PUBLICATIONS

Name in bold; * equal contribution.

Peer-reviewed

1. Rakheja I.*, **Bharti V.***, et al. (2024) "Development of an *in silico* platform (TRIPinRNA) for the identification of novel RNA intramolecular triple helices and their validation using biophysical techniques." *Biochemistry* (ACS) 64(1):250–265. <https://doi.org/10.1021/acs.biochem.4c00334> (*Equal contribution.)
2. Sharma S., **Bharti V.**, et al. (2026) "MLC1 alteration in human iPSCs give rise to disease-like cellular vacuolation phenotype in the astrocyte lineage." *Orphanet Journal of Rare Diseases* 21:176. <https://doi.org/10.1186/s13023-026-04316-3> (Open access.)
3. Rakheja I., **Bharti V.**, Singh V., Maiti S. (2026) "Quercetin affects carcinogenic phenotype of breast and lung cancer cells differentially through sterol regulation mediated by MALAT1 perturbation." *Chemistry – An Asian Journal* 21(11):e70821. <https://doi.org/10.1002/asia.70821> (Open access.)
4. Das P.K., Aich M., Adu P., **Bharti V.**, Maiti S., Chakraborty D. (2025) "CRISPR–Cas diagnostics (CRISPR–Dx) of viral pathogens in low- and limited-resource areas: current state and future directions." *TrAC Trends in Analytical Chemistry* 118590. <https://doi.org/10.1016/j.trac.2025.118590>
5. Rana P., Ujjainiya R., **Bharti V.**, Maiti S., Ekka M.K. (2024) "IGF2BP1-mediated regulation of CCN1 expression by specific binding to a G-quadruplex structure in its 3' UTR." *Biochemistry* (ACS) 63(17):2166–2182. <https://doi.org/10.1021/acs.biochem.4c00172>

Preprints and manuscripts under review

6. **Bharti V.**, Chakraborty D. (2026) "StickForStats: automated statistical assumption validation for reproducible computational biology." *bioRxiv*. <https://doi.org/10.64898/2026.06.15.732278> (First author and corresponding; under review, BMC Bioinformatics.)
7. Rauthan R., **Bharti V.**, et al. "An interface of genetically engineered human forebrain assembloids and polymeric nanofiber scaffolds for multiscale profiling of interneuron-migration disorders." *Research Square* preprint. <https://doi.org/10.21203/rs.3.rs-3831019/v1> (Under revision, Stem Cell Reports.)
8. Kochar M., Rao S., Bhattacharjee S., Goel P., Timsina H., Azhar M.K., **Bharti V.**, et al. "Folding on the way in: vectorial substrate recognition by human Hsp60." (Submitted to Cell, 2026.)
9. Azam T., Kumar A., Singh P., **Bharti V.**, Ekka M.K. "Structural and functional analysis of the Chast–NUCB1 interaction in cardiac hypertrophy." (Submitted to Journal of Biological Chemistry, 2026.)

RESEARCH SOFTWARE & COMPUTATIONAL METHODS

StickForStats — statistical-analysis platform with automatic assumption validation. First-author, open-source platform whose *Guardian* engine validates the assumptions behind every test (normality, variance homogeneity, independence, outliers) before it runs, then either reports with full confidence or cascades to the correct nonparametric alternative — with a companion module that re-checks the statistical claims in uploaded manuscripts. Built to counter the assumption violations that drive irreproducible results. *Best Poster Award, EMBO Conference 2025; first-author preprint on bioRxiv, under review at BMC Bioinformatics; public beta live at stickforstats.com.*

RNA Lab Navigator — retrieval-augmented research assistant. A retrieval-augmented LLM system over internal lab documents and the primary literature for fast, grounded literature triage in a wet–dry lab; in routine use by ~21 researchers.

SELECTED TALKS & POSTERS

- **Best Poster Award** — "StickForStats: Publish Research with Confidence," **EMBO Conference 2025**, CCMB Hyderabad.
- Poster — "Boundary Without Fence," *Frontiers in Genome Engineering 2023*, BITS Pilani (Goa).

AWARDS & HONORS

- **Best Poster Award**, EMBO Conference 2025 (CCMB Hyderabad).
- **GATE Biotechnology — All-India Rank 127 (top ~1%)**, 2020.
- Graduate Assistantship, Ministry of Education, Government of India (2020–2022).
- **GATE Electronics & Communication — top ~3 percentile**, 2018.

TECHNICAL SKILLS

- **Languages & statistics**: Python, R, C, MATLAB; statistical modeling, experimental design, and test-selection methodology.
- **Genomics & bioinformatics**: scRNA-seq, RNA-seq, ChIP-seq; molecular docking, PyMOL; network analysis (Cytoscape, STRING, Gene Ontology).
- **ML & computational methods**: deep learning; retrieval-augmented LLM systems, vector databases, knowledge graphs; biomedical NLP (scispaCy, BioBERT).
- **Workflow**: Git, reproducible pipelines, Streamlit; scientific writing.

SELECTED COMPUTATIONAL PROJECTS

- **Deep learning for genome annotation**. Predicted DNA N6-methyladenine (6mA) sites in the rice genome with CNN and LSTM architectures; benchmarked predictive accuracy across models.
- **Sequence classification with RNNs**. Built an LSTM classifier to label DNA sequences by intronic, exonic, and exon–intron-boundary context, improving over a CNN baseline.
- **Computational-biology collaboration (UC Berkeley)**. Worked with a postdoctoral researcher at UC Berkeley to automate biological data-analysis pipelines in R and Python.

SELECTED COURSEWORK & CERTIFICATIONS

- Deep Learning Specialization (A. Ng, Coursera); Genomic Technologies (Johns Hopkins, Coursera); Principles of Biochemistry (Harvard, edX).

TEACHING & SERVICE

- **Teaching Assistant**, IIT Guwahati (2020–2022) — supported a class of 300+ students.
- **Core Organizing Team (IT lead)**, *Frontiers in Genome Engineering 2023*, BITS Pilani (Goa).
- **Mentor**, “One Week One Lab” outreach programme, CSIR–IGIB (2023).
- **Chairperson**, IEEE Circuits & Systems Society Student Branch Chapter, IEM Kolkata (2016–2018).