

Rezwanuzzaman Laskar, PhD

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Objective

Computational biologist specializing in translational bioinformatics within a dynamic 'lab in a loop' environment. Proficient in developing and integrating advanced bioinformatics pipelines, including multi-omics signature prediction (DNA/RNA), single-cell RNA sequencing (scRNA-seq), and spatial transcriptomics, to address complex biological questions. Experienced in genomic surveillance and rare disease research, with a current focus on studying congenital melanocytic nevus (CMN) patients with melanoma. Passionate about integrating multi-omics data to identify genetic drivers, biomarkers of treatment response, and pathways of resistance, contributing to precision oncology and the development of innovative therapies.

GitHub: github.com/r1askar

Visa Status

United Kingdom Skilled Worker Visa, valid until 14 March 2025.

Skills

Programming & Scripting Languages: Python | Bash | R

High-Performance Computing (HPC) & Cloud: HPC (Slurm) | AWS

Package & Workflow Management: Conda | Mamba | Snakemake | Nextflow

Containerization & Package Installation: Docker | Singularity | GitHub

Data Science & Machine Learning Libraries: Pandas | Numpy | Sklearn | Matplotlib | Seaborn

Data Visualization: Tableau | PowerBI

Next-Generation Sequencing (NGS) & Bioinformatics Data: Illumina | ONT

Genomic Databases: Genomics England | TCGA | UK-BioBank | GISAID | NCBI | RCSB | IEDB

Pipeline Development:

Human Genomics: DNA and RNA | Somatic and Germline | Gene fusion | Variant calling (SNV, CNV, SV, Alternative Splicing, Mosaic variant) | bulk RNA-seq |

scRNA-seq (Seurat, Scanpy) | Spatial Transcriptomics (Xenium) | Hyperplex ICC

Microbial Genomics: Metagenomics | Recombination Detection | Intra-Host Single Nucleotide Variation

Machine Learning: Sklearn, PyTorch, TensorFlow

Image Analysis: Fiji

Experience

Post Doctoral Experience

Research Fellow – Bioinformatics

Feb 2024 – Present

The Francis Crick Institute and University College London

Mosaicism and Precision Medicine Laboratory, The Francis Crick Institute, Seconded from UCL Great Ormond Street Institute of Child Health (ICH), Genetics and Genomic Medicine (GGM) Department

- **Directed** bioinformatics analysis and processing of genomic data for multiple high-impact lab projects, including large-scale datasets from **Genomics England** and **UK Biobank**, focusing on pediatric skin disorders and cancer predispositions.
- **Collaborated** with clinicians and wet-lab scientists to identify novel genes, gene fusions, and variants, providing key insights into disease pathways and mechanisms.

- **Designed, developed, and optimized** data processing pipelines for mosaic variant detection, including SNVs, CNVs, and transcript expression analysis across various NGS platforms, enhancing the lab's genomic interpretation capabilities.
- **Implemented machine learning techniques** to analyze multi-omics data, aiming to identify causal variants for precision medicine.

Research Experience

Senior Project Associate (Bioinformatics)

Dec 2022 – Feb 2024

National Institute of Bio-Medical Genomics (NIBMG), Kalyani, West Bengal, India

International Research Consortia: SARS-CoV-2 network For Genomic Surveillance in **Brazil, Russia, India, China, and South Africa (NGS-BRICS)**

- **Key contributor** to the NGS-BRICS consortium, translating genomic data into actionable insights for COVID-19 surveillance and improving public health outcomes.
- **Streamlined data pipelines** using Bash scripts, enabling efficient lineage assignment and mutation identification with CLI tools.
- **Created data visualizations** in Tableau and PowerBI, improving the monitoring of key findings and communication with stakeholders.
- **Performed in-depth genomic analysis** (FASTQ level) to track intrahost transmission and assess the pathogenicity of specific mutations.

Project Associate II (Bioinformatic Analysis)

2021 - 2022

NIBMG, Kalyani, West Bengal, India

National Research Consortia: Indian SARS-CoV-2 Genomic Consortia (**INSACOG**)

- Led genomic surveillance of SARS-CoV-2 variants, **analyzing over 35 million sequences** to inform pandemic response strategies.
- Developed pipelines for recombinant variant identification and assisted in setting up NGS pipelines in new labs.
- Conducted comprehensive NGS data analysis (Illumina, ONT), converting raw BCL/FAST5 files into consensus FASTA, and generated reports for public health authorities.
- Published first-author research, advancing the scientific understanding of SARS-CoV-2 genomics.

Teaching Experience

Hands-on Training Workshop Instructor

Nov 21-25, 2022

NIBMG, Kalyani, West Bengal, India

- Led a comprehensive training workshop on "Hands-on Training Workshop on SARS-CoV-2 Genome Sequencing and Surveillance," imparting in-depth knowledge on data handling and surveillance methodologies using High-Performance Computing systems.
- Fostered an interactive learning environment that led to effective skills transfer and received high praise from attendees.

Research Scholar

Oct 2018 – 2023

Department of Biological Sciences, Aliah University, Kolkata, India

- Supervised Master's students and taught undergraduate courses.
- Conducting practical classes and demonstrations.
- Participating in conferences and workshops to enhance knowledge.

Guest Lecturer

Sep 2013 - Sep 2018

Department of Botany, Uluberia College, University of Calcutta, India

- Delivered undergraduate lectures and practical classes across a diverse range of subjects, including Phycology, Mycology, Microbiology, Physiology, and Molecular Biology.
- Actively participated in field trips as a guide, enriching students' practical understanding of the subject.

Research Assistant

Research Assistant

2011 - 2013

Department of Botany, Uluberia College, University of Calcutta, India

- Contributed to a major project on the characterization of Indigenous Cyanobacterial Diversity in West Bengal.
- Demonstrated proficiency in species identification, strain characterization, culturing and maintaining cultures, underpinning robust laboratory skills.

Research Fields

Core Domain

- **Next-Generation Sequencing (NGS) Data Analysis** — Over 5 years of experience in analyzing and interpreting NGS data (Illumina and Oxford Nanopore) for human genomics, oncology, and infectious diseases. Developed custom pipelines for whole genome and transcriptome sequencing, with a focus on variant calling (SNV, CNV, SV) and mosaicism analysis.
- **Genomics and Metagenomics** — Proficient in analyzing human whole genome and metagenomic datasets. Built high-throughput pipelines using Kaiju, Kraken, and QIIME for metagenomic analysis, contributing to large-scale pathogen surveillance.
- **Pipeline Development** — Expert in developing automated pipelines using Nextflow and bash scripting, integrating tools for variant calling, quality control, and visualization. Successfully processed thousands of patient samples, delivering data-driven insights for both research and clinical applications.
- **Machine Learning for Genomic Analysis** — Applied machine learning models to multi-omics datasets to predict causal variants and therapeutic targets. Leveraged Python libraries like Sklearn and TensorFlow to develop classification and regression models for precision medicine.
- **Virus Evolution and Phylogenetics** — Specialized in tracking virus evolution using phylogenetic trees and network-based approaches (Nextstrain, MEGA). Played a key role in identifying new SARS-CoV-2 lineages (e.g., BA.2.10.1), offering critical insights into epidemiological trends.

Extended Domain

- **Protein Structure Prediction** — Utilized advanced tools like AlphaFold and RoseTTAFold to predict the impact of mutations on protein structure and function, contributing to research on drug resistance and viral evolution.
- **Drug Discovery and Molecular Dynamics** — Performed in-silico drug discovery using AutoDock and PyRx, coupled with molecular dynamics simulations (GROMACS), to study biomolecular interactions and screen potential therapeutic compounds.
- **Vaccine Design** — Developed comprehensive pipelines for in-silico vaccine design, focusing on target identification and epitope prediction, with applications in emerging infectious diseases.
- **Cyanobacteria Culture** — Proficient in the culture and maintenance of cyanobacteria (BGA), with expertise in morphological identification using microscopy techniques.

Publications

1. **Rezwanuzzaman Laskar**, M. Hoque, and Safdar Ali. (2024), Phylogeogenomic analysis of the earliest reported sequences of SARS-CoV-2 from 161 countries. APMIS. <https://doi.org/10.1111/apm.13499> **IF: 2.2**
2. Animesh K Singh*, **Rezwanuzzaman Laskar*** et al. Contrasting Distribution of SARS-CoV-2 Lineages across Multiple Rounds of Pandemic Waves in West Bengal, the Gateway of East and North-East States of India. Microbiol Spectr. 2022;10(4):e0091422. doi:10.1128/spectrum.00914-22; PMID: PMC9430150. **IF: 9.043** *Equally contributed.
3. **Rezwanuzzaman Laskar**, Md Gulam Jilani, Taslima Nasrin, Safdar Ali. Microsatellite Signature of Reference Genome Sequence of SARS-CoV-2 and 32 Species of Coronaviridae Family. Int J Infect. 2022;9(2):e122019. <https://doi.org/10.5812/iji-122019>.
4. **Rezwanuzzaman Laskar** and Safdar Ali . Differential mutation profile of SARS-CoV-2 proteins across deceased and asymptomatic patients. Chem Biol Interact. 2021 Sep 25; 347: 109598. Published online 2021 Jul 23. doi: 10.1016/j.cbi.2021.109598; PMID: PMC8299203. **IF: 5.168**

5. **Rezwanuzzaman Laskar** and Safdar Ali . Phylo-geo-network and haplogroup analysis of 611 novel coronavirus (SARS-CoV-2) genomes from India. Life Sci Alliance. 2021 Mar 16;4(5):e202000925. doi: 10.26508/lsa.202000925. PMID: 33727249; PMCID: PMC7994317. **IF: 5.781**
6. **Rezwanuzzaman Laskar** and Safdar Ali . Mutational analysis and assessment of its impact on proteins of SARS-CoV-2 genomes from India. Gene. 2021 Apr 30;778:145470. doi: 10.1016/j.gene.2021.145470. Epub 2021 Feb 4. PMID: 33549714; PMCID: PMC7860943. **IF: 3.913**
7. **Rezwanuzzaman Laskar**, Md Gulam Jilani, Safdar Ali. Implications of genome simple sequence repeats signature in 98 Polyomaviridae species. 3 Biotech. 2021 Jan;11(1):35. doi: 10.1007/s13205-020-02583-w. Epub 2021 Jan 6. PMID: 33432281; PMCID: PMC7787124. **IF:2.893**

Conference Paper

1. Md Gulam Jilani, **Rezwanuzzaman Laskar** and Safdar Ali (2020): Genome- wide scans for analysis of simple and imperfect microsatellites in diverse Lyssavirus. Abstract published in the Proceedings of International Conference on Innovations in Biotechnology and Life Sciences. AB-088. PP:128. ISBN: 978-93-88647-33-5; DOI: 10.6084/m9.figshare.13947833
2. **Rezwanuzzaman Laskar**, Md Gulam Gilani and Safdar Ali (2020): Microsatellite Mining and Protein Dynamics of 43 Species of Alphapolyomavirus. Abstract published online in the International Conference on Drug Discovery organised by Schrodinger, USA and BITS Pilani, Hyderabad, 29th Feb – 2nd March 2020. <https://papers.ssrn.com/sol3/papers.cfm?abstractid=3535344>
3. **Rezwanuzzaman Laskar**, Md Gulam Gilani and Safdar Ali (2019): Microsatellite elicitation and investigation of 30 Betapolyomavirus: In-silico approach. Abstract published online in the Young Scientists' Conference as a part of India International Science Festival – 2019 organised by DST, Gol and Vijnana Bharati, 5th – 8th November, 2019.
4. **Rezwanuzzaman Laskar** and Safdar Ali (2018): In-silico Extraction and Analysis of Imperfect microsatellites Across 37 Species of Polyomaviridae. Abstract published in the abstract volume of 3rd Regional Science and Technology Congress, Southern region 18th and 19th December, 2018.
5. N.C. Halder and **Rezwanuzzaman Laskar** (2017): Studies on Production of Nitrogen Fixing Cyanoprokaryota (BGA) starter Culture of Nostoc sp. In open and Laboratory Culture Condition. Full paper published in the proceeding of sequel to UGC-Sponsored National Seminar on Mission Sustainability: Through Environmental Education, 1st - 2nd March in Dept. of B.Ed., Uluberia College, Uluberia, Howrah. ISBN: 978-81-928627-5-0.
6. **Rezwanuzzaman Laskar** and N.C. Halder (2016): Biodiversity of Nitrogen fixing unicellular and filamentous Cyanobacteria in different rice fields of Howrah district in West Bengal, India. Abstract published in the abstract volume of the International Conference on 'The Green Planet: past, present and future', 21st – 23rd December, 2016 in Dept. of Botany, University of Calcutta, Kolkata.

Education

PhD in Biological Sciences

2018–2023

Specialization in **Bioinformatics, Microbiology and Virology**

Aliah University, Kolkata, West Bengal, India

Thesis Title: Studying the Viral Genome Evolution and its Impact on Viral Proteins of SARS-CoV-2

- Analyzed SARS-CoV-2 genome sequences to understand viral evolution across time and demographics.
- Identified prevalent mutations and nucleotide diversity, and their associations with clinical outcomes.
- Constructed phylogeonetworks, revealing insights into viral evolution and dominant haplogroups in the Indian population.

- Discovered deleterious mutations in viral proteins linked to increased fatality rates.
- Demonstrated protein stability loss caused by mutations, influencing disease progression.

Master of Science in Botany <i>Vidyasagar University, West Bengal, India</i>	2009–2011
Post Graduate Diploma in Information Technology <i>SITD, Kolkata, West Bengal, India</i>	2008–2009
Bachelor of Science in Botany (Honours) <i>University of Calcutta, Kolkata, West Bengal, India</i>	2005–2008

Certifications

Genomics England Research Summit 2024 <i>London, United Kingdom</i>	9 Jul 2024
High-End Equipment for Clinical Applications – Flow Cytometry <i>CSIR-IICB, Kolkata, West Bengal, India</i>	11 Sep – 25 Sep, 2019

Awards and Honors

Best Poster Award International Conference on Drug Discovery Organised by Schrodinger, USA and BITS Pilani, Hyderabad	29 Feb – 2 March 2020.
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Professional Memberships

American Chemical Society	2020-2021
World Society for Virology	2020

Journal Service

Journal Reviewer- Scientific Reports	2023
Journal Reviewer- Infection, Genetics and Evolution	2023

References

Available upon request