Shreya Sharma

Email: sharma.119@iitj.ac.in
LinkedIn: https://www.linkedin.com/in/shreya-sharma-a2526881/
Mobile: +91-9997063438
Github: https://shreya-droid.github.io

EDUCATION

Indian Institute of Technology Roorkee (IIT-R) — Uttarakhand, India
PhD. in Computational Biology — *July 2023 - Present*

Indian Institute of Technology Jodhpur (IIT-J) — Rajasthan, India
M.Tech. in Biosciences and Bioengineering; CGPA: 9.00/10.00 — *Aug 2021 - June 2023*
Important Courses: Algorithms in Biology, Systems Biology, Biophysics, Bioimage Computing, Statistics, and Data Science.

Banaras Hindu University (BHU), Varanasi — Uttar Pradesh, India
Master of Science in Bioinformatics.; Finished in Top Quintile; CGPA: 7.78/10.00 — *June 2016 - May 2018*
Important Courses: Molecular Genetics, Cell Biology, Bioinformatics, Genomics and Proteomics.

Choudhary Charan Singh University (CCSU), Meerut — Uttar Pradesh, India
Bachelor of Science in Biotechnology; Among top 3 students in cohort class of 80 students

SKILLS SUMMARY

- **Languages**: Python, SQL, Unix scripting
- **Tools**: Rstudio, Galaxy, BedTools, SAMTools, FastQC, Cytoscape, PLINK
- **Packages**: Python (scikit-learn, seaborn, pandas), Bioconductor (DESeq, autotuner)
- **Wet Lab Skills**: Bacterial Cell Culture, PCR, DNA/RNA Isolation, Gel Electrophoresis

EXPERIENCE

Indian Institute of Technology Jodhpur (IITJ) — Rajasthan, India
Teaching Assistant; Course Name: Introduction to Bioengineering; Course Instructors: Prof. Mitali Mukerji Nov 2022 - Jan 2023
Teaching Assistant; Course Name: System Biology; Course Instructors: Dr. Dipanjan Roy and Dr. Pankaj Yadav Jan 2023 - May 2023

- **Provide support and oversight in the classroom alongside the primary teacher to help ensure quality learning for all students**:

Indian Institute of Science Education and Research (IISER), Thiruvananthapuram — Kerala, India
Project Assistant ; Supervision by: Dr. Sabari Sankar Thirupathy, Assistant Professor — *Sep 2020 - Aug 2021*

- **Bacterial genome analysis for gene strand-bias**: Preprocessing of bacterial genome sequence data and its analysis, writing programming scripts (using Python) to analyze sequence data, Preparation of appropriate documentation and generating analysis reports and summary dashboards, Leverage on the HPC servers for data transfer, management, and storage
- **Developed web-based database for lab**: using SQL server, HTML, JavaScript and PHP scripts

National Institue of Immunology (NII), New Delhi — New Delhi, India
Research Trainee ; Supervision by Dr. Anil Kumar, Staff Scientist-IV — *Sep 2018 - May 2019*

- **Oxford Nanopore 16S rRNA sequencing and its analysis** : using EPI2ME for real-time nanopore sequencing reads to enable rapid species identification and quantification from metagenomic samples

ACADEMIC PROJECTS

- **M.Tech. Project: "Alu-map: a natural language processing-based Alu feature annotation on the human genome"**: The project is aimed at developing a database entitled "ALU-map" that structures information related to various functions of Alu's using natural language processing (NLP) approach via text mining of abstracts available in PubMed. The database provide information on the involvement of Alu's at different functional hierarchies e.g. Genetic, Transcriptomic, Proteomics, Pathways, and Cellular where biological functions of Alus have been well reported. A fine-tuned BERT model generated that classify Alu abstracts into 10 label categories. The merit in this approach is that the identification of semantic relations uses only linguistic information present in abstracts and does not depend on other existing hard-coded scripts or tools.

  - **Duration**: 6 months
  - **Key Technologies**: Machine Learning, Natural Language Processing (NLP), BERT, Bio-BERT.

- **Post M.Sc. Project: "Bacterial genome analysis of GC skew in order to find compositional biasness of genes on leading/lagging strand"**:
  Background: The DNA replication and transcription machinery share a common DNA template and therefore can collide with each other co-directionally or head-on. Replication-transcription collisions can cause replication fork arrest, premature transcription termination, DNA breaks, and recombination intermediates threatening genome integrity. Collisions may also trigger mutations, which are major contributors to genetic disease and evolution. However, the nature and mechanisms of collision-induced mutagenesis remain poorly understood.
  Aim: Analysis of inversion and percentage distribution of genes on leading vs. lagging strands across the bacterial domain and classes. Comparative results were achieved when compared with the doriC database. Further visual validation of such Inversions with IGV and genome annotation using Prokka.
    - **Duration**: 6 months
    - **Key Technologies**: GC skew biasness, Inversion analysis.
- **M.Sc. Project: "Prediction of miRNAs within the long non-coding RNAs and search for their targets"**: MEG3 gene which encodes for a non-coding RNA, a total of 168 mature miRNAs were predicted using miRbase from six MEG3 transcripts, which include five splice variants and MEG3 primary assembly. Gene Ontology enrichment analysis of target genes was performed using Gorilla and DAVID which advocates pathway and disease association with MEG3. MEG3 found to be associated with pathways in cancer, tobacco use disorder, bone development, type II diabetes, and in Alzheimer's.
    - **Duration**: 6 months
    - **Key Technologies**: mRNA silencing, Gene Ontology (GO) enrichment analysis.

HONORS AND AWARDS

- Institute MTech fellowship 2021-2023 at IIT Jodhpur funded by Ministry of Education (MoE), Government of India

- Qualified GATE (Biotechnology) in 2021

- Qualified IIT-JAM (Life Sciences) with AIR-400 in 2016

- Obtained NCC (National Cadet Corps) 'B' and 'C' certificate by Ministry of Defense, Govt of India

- Twice selected for National Basketball Championship affiliated to School Games Federation of India (SGFI), India

CONFERENCES

- Participated in "Next-gen AI: Inspiration from Brain Science (NAiBS)" at IIT Jodhpur. from January 26 to 28, 2023.

VOLUNTEER WORK

- Contributed as an organising team member in a CME Workshop on "Drug designing, drug delivery and theranostic tools and approaches" under the Centre of Excellence in Ayurtech at IIT Jodhpur. from January 09 to 13, 2023.

REFERENCES

[1] Malhar Atre, Bharat Joshi, Shabduli Sawant, Shreya Sharma, Jebin Babu and T. Sabari Sankar. *"Replication-driven selection fine-tunes the evolution of inverted repeats to maintain bacterial genome organization and stability"*.
**(manuscript in preparation)

REFERENCES (MENTORS)

- Dr. Devesh Bhimsaria, Assistant Professor, Indian Institute of Technology Roorkee (IIT-R), Uttarakhand, India. Email: devesh.bhimsaria@bt.iitr.ac.in; Tel: +91-1332-285011.

- Dr. Mitali Mukerjee, Head of the Department, Indian Institute of Technology Jodhpur (IIT-J), Rajasthan, India. Email: mitali@iitj.ac.in; Mob: +91 9811288052.

- Dr. Sabari Sankar Thirupathy, Assistant Professor, Indian Institute of Science Education and Research (IISER), Thiruvananthapuram, Kerala. Email: sabari@iisertvm.ac.in; Mob: +91 8870858750.

- Dr. Pankaj Yadav, Assistant Professor, Institute of Technology Jodhpur (IIT-J), Rajasthan, India. Email: pyadav@iitj.ac.in; Tel: +91 (0) 291280 1211.