

# Arafat Rahman

Bioinformatics Scientist

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## Summary

- Computational biologist with experience in microbiology, bioinformatics, and molecular biology with a track record of independent and collaborative research.
- Expert in analyzing diverse NGS data, including amplicon-seq, whole-genome, metagenomics, RNA-Seq, and pipeline development, with extensive experience in high-performance computing (HPC) environments and workflow automation (Snakemake and NextFlow).
- Adept at leading cross-functional research initiatives and effectively communicating complex scientific findings to diverse audiences, as evidenced by published journal articles, conference talks, and presentations.

## Professional Experiences

Research Associate | Oregon State University, Corvallis, OR | 08/2026-Current

- Transmission dynamics bio-surveillance analysis using plasmid-driven horizontal gene transfer and its influence on virulence, symbiosis, and host adaptation across hundreds of pathogenic and symbiotic bacteria strains, leveraging k-mer based containment sketch and pangenomic-graph.

Postdoctoral Researcher | Oregon State University, Corvallis, OR | 08/2023-08/2026

- Processed terabytes of NGS data (Illumina & Nanopore) to thoroughly analyze bacterial epidemiology, evolution, phylodynamics, plasmid and mobile genetic elements mediated host adaptation, leading 4 peer-reviewed journal articles and 5 conference presentations (3 talks, 2 posters).
- Combined historical records with population genomics for *Xanthomonas hortorum* pv. *carotae*, a seedborne pathogen of carrots, where I reconstruct how changes in agricultural practices influenced pathogen evolution over centuries. The study demonstrates that major transitions in crop production are associated with lineage turnover and reshaping of pathogen population structure
- Developed genome annotation pipeline (beav) and Snakemake workflows on HPC to analyze big genomic data, method development for variant calling from long-read data. Used NextFlow workflows for bacterial annotation.
- Mentoring REEU interns and undergraduate researchers, teaching as guest lecturer (BOT332), conducting Nanopore sequencing workshop, HPC workshop and science outreach in STEM-camp.

Graduate Researcher | University of California, Riverside, CA | 09/2017-06/2023

- Conducted dissertation research on competitive interaction of *Rhizobia* during symbiosis, as well as collaborative research on RNA-Seq based taxonomic profiling of toxicology-assay on lungs epithelial cell-line, leading to 4 peer-reviewed journal articles and 8 conference presentations (4 talks, 4 posters).
- Mentored and managed teams of 1-2 direct reports (6 mentees total), enhancing their technical skills and contributing to successful project outcome.

## Tool Development & Engineering

- Beav – Designed and maintained a Python-based annotation pipeline (Beav) currently available on Bioconda, optimizing bacterial genome annotation. Currently working on the beta version to be released on nf-core: <https://github.com/weisberglab/beav>, <https://github.com/weisberglab/nf-core-beav> <https://doi.org/10.1128/msphere.00209-24>
- PySyntenyViz – Developed a dockerized CLI tool for synteny visualization, automating manual plotting tasks for comparative genomics: <https://github.com/acarafat/PySyntenyViz>
- TangleR – R package for analyzing cophylogeny: <https://github.com/acarafat/tangler>

## Education

- Ph.D. in Genetics, Genomics, and Bioinformatics, University of California, Riverside, CA, USA (09/2017- 06/2023).
- M.S. in Microbiology, University of Dhaka, Dhaka, Bangladesh (2012-2013).
- B.S. in Microbiology, University of Dhaka, Dhaka, Bangladesh (2009-2012)

## Technical Skills

- |                               |                           |                          |
|-------------------------------|---------------------------|--------------------------|
| • Python, R, Unix             | • PCR, qPCR               | • Light and Transmission |
| • HPC, SLURM, AWS             | • Nanopore, Illumina      | Electron Microscopy      |
| • Conda, Pixi                 | • Amplicon Seq, RNA-Seq   | • Molecular Cloning      |
| • Pandas, NumPy               | • Whole Genome Sequencing | • Singularity   Docker   |
| • Sklearn, JAX, Flax          | • DADA2, Kraken2, DESeq2  | • Snakemake   Nextflow   |
| • Seaborn, ggplot, Matplotlib |                           |                          |

## Current Focus

- Skill-up by following the book: Deep Learning for Biology (Ravarani and Latysheva, 2025)

## Certification

Link to the certificates available at: <https://arfrhmn.net/certification/>

- Oxford Biodiscovery (2026): Machine Learning & Deep Learning for Biologists

## Selected Scientific Publications

- Total journal article publications 18, # first author publication 5.
- Complete list available in [https://scholar.google.com/citations?user=9H1HF\\_kAAAAJ](https://scholar.google.com/citations?user=9H1HF_kAAAAJ)
- **Rahman A**, Mancini M, Nadon C, Perez IA, Farsamin WF, Lampe MT, Le TH, Martínez LT, Weisberg AJ, Chang JH, Sachs JL. *Competitive interference among rhizobia reduces benefits to hosts*. Current Biology. 2023 Jul 24;33(14):2988-3001.
- Schiffer AM, **Rahman A\***, Sutton W, Putnam ML, Weisberg AJ. *A comparison of short-and long-read whole genome sequencing for microbial pathogen epidemiology*. Msystems 10 (12), e01426-25 \*Co-first author
- Jung JM, **Rahman A\***, Schiffer AM, Weisberg AJ. *Beav: a bacterial genome and mobile element annotation pipeline*. Msphere. 2024 Aug 28;9(8):e00209-24. \*Co-first author
- Weisberg AJ, **Rahman A**, Backus D, Tyavanagimatt P, Chang JH, Sachs JL. Pangenome evolution reconciles robustness and instability of rhizobial symbiosis. Mbio. 2022 Jun 28;13(3):e00074-22.