Jena School for Microbial Communication
Graduate School of Excellence

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Research Profile

Microbiologist and bioinformatician with 10+ years of experience in microbial genomics, antimicrobial resistance, infectious disease research, metagenomics, microbiome and virome analysis, and functional omics. Experienced in short- and long-read sequencing, comparative genomics, phylogenetics, pathogen evolution, complete bacterial genome assembly, reproducible workflow development, and integrating genomic, microbiological, susceptibility, and project metadata. Combines computational expertise with a strong wet-lab background and experience in interdisciplinary collaboration, supervision, scientific publication and conference dissemination. Author of more than 50 peer-reviewed publications, h-index 26.

Main Research Interests

- Bacteriophage and prophage genomics, including the mobilisation of antibiotic resistance genes
- Microbial genomics, pathogen evolution and genome-based epidemiology
- Antimicrobial resistance genomics and identification of novel resistance determinants
- Metagenomics, microbiome and virome analysis across clinical and environmental samples
- Pathogen detection, functional omics and clinically relevant interpretation of sequencing data

Methodological Expertise

Bioinformatics and Research Computing	Microbiology and Molecular Methods
Illumina, Oxford Nanopore and PacBio analysis; genome assembly and annotation; comparative genomics; phylogenomics; metagenomics; microbiome and virome analysis; AMR genomics; transcriptomics; statistical analysis; Bash, Python, R, Snakemake, Git, Linux, HPC and SLURM; database management; machine learning and explainable AI.	Clinical and environmental sampling; microbial cultivation; DNA and RNA extraction; PCR and qPCR; molecular cloning; library preparation; high-throughput sequencing; antimicrobial susceptibility testing; validation of novel genetic determinants.

Professional Experience

01/2023 - Present: Bioinformatics Lab Manager

Friedrich Schiller University, Viral Ecology and Omics, Jena, Germany

- Investigates bacteriophage-mediated mobilisation of antibiotic resistance genes and conducts large-scale comparative genomics of Rhizobium species.
- Analyzes short- and long-read data from environmental and clinical samples for microbiome, metagenomic, virome and microbial-genomic studies.
- Develops, optimizes and documents reproducible Linux/HPC workflows using Snakemake, Bash, Python, R and Git, with quality assurance procedures.
- Maintains and optimizes SLURM-based computational infrastructure, software, databases and analysis environments for multi-user workflows.
- Integrates genomic, microbiological, antimicrobial resistance and project metadata and supports interdisciplinary collaborations and data exchange.

Professional Experience Continued

01/2022 - 06/2023: Project In-Charge, Deep-iAMR

Justus-Liebig University, Institute of Medical Microbiology, DZIF Center, Giessen, Germany

Deep-iAMR: Identification of novel antimicrobial resistance determinants using deep learning.

- Led project planning, execution, supervision and reporting and supervised a postdoctoral researcher and technicians.
- Applied machine learning, genome-wide association and comparative genomics to identify resistance determinants from large-scale sequencing and antimicrobial susceptibility datasets.
- Generated complete closed bacterial genomes using hybrid Illumina and Oxford Nanopore assemblies.
- Conducted cloning and validation experiments and developed a method for detecting colistin heteroresistance to reduce false-negative susceptibility results.

10/2014 - 12/2022: Research Associate

Justus-Liebig University, Institute of Medical Microbiology, DZIF Center, Giessen, Germany

Projects: TARGET-SPREAD and RESET, focused on high-risk bacterial pathogenic clones and genome-based epidemiology of multidrug-resistant Enterobacterales.

- Performed large-scale comparative genomics, phylogenetics and population genomics of multidrug-resistant Enterobacter, Serratia, Escherichia coli, Elizabethkingia and Listeria.
- Developed workflows for genome assembly, annotation, taxonomic classification, pathogen detection and genome-based epidemiology.
- Analyzed microbiome and transcriptomic data to study bacterial evolution, virulence, antimicrobial resistance and host-associated communities.
- Integrated genomic, transcriptomic, microbiome and associated metadata using statistical and computational methods.
- Collaborated with clinicians, microbiologists and international partners and contributed to publications, reports and collaborative projects.

Education

07/2010 - 10/2014: PhD in Microbiology, A Grade - Goa University, Goa, India

06/2006 - 04/2008: MSc in Microbiology, A Grade - Goa University, Goa, India

06/2003 - 04/2006: BSc in Microbiology, A Grade - Shivaji University, Kolhapur, India

Research Leadership Funding and Awards

- Project In-Charge, Deep-iAMR, BMBF-funded project on identification of novel antimicrobial resistance targets using deep learning, Giessen, Germany, 2022-2023.
- Co-Project Investigator, TranCeLis - Translation Center for Molecular Epidemiology of Listeria monocytogenes, funded by the Department of Biotechnology, Government of India, Goa, India, 2012-2015.
- Fulbright-Nehru Scholarship for Doctoral and Professional Research, United States-India Educational Foundation, Pennsylvania State University, USA, 2012-2013.

Selected Research Projects

Bacteriophages and antimicrobial resistance: Large-scale investigation of bacteriophages and prophages as potential vehicles for antibiotic resistance gene mobilisation.

Comparative genomics of Rhizobium: Large-scale comparative genomic analysis of Rhizobium species.

Deep-iAMR: Deep-learning, genome-wide association and comparative-genomic approaches to identify novel antimicrobial resistance determinants.

TARGET-SPREAD: Characterization of high-risk pathogenic bacterial clones.

RESET: Genome-based epidemiology of multidrug-resistant Enterobacterales.

Selected Research Contributions

- Reproducible analysis of clinical and environmental short- and long-read sequencing datasets across microbial genomics, metagenomics, microbiome and virome studies.
- Complete bacterial genome reconstruction using hybrid Illumina and Oxford Nanopore sequencing and downstream comparative analysis.
- Application of machine learning and explainable AI approaches to antimicrobial resistance discovery and interpretation.
- Development and optimization of Linux/HPC bioinformatics workflows and computational environments for interdisciplinary research teams.
- Integration of genomic, antimicrobial susceptibility, microbiological and contextual metadata for clinically and biologically relevant interpretation.

Training

Diploma in Information Technology: C-DAC Advanced Computing Training School, Pune, India

Prokaryote Genome Analysis Workshop: German Center for Infection Research, Giessen, Germany

Summer School on Microbial Community Data Analysis: German Network for Bioinformatics Infrastructure, Germany

Scientific Output and Profiles

More than 50 peer-reviewed publications; h-index 25. Complete and current publication records: Google Scholar and ORCID 0000-0002-0932-8542.

Core Competencies

- Research leadership, project planning, supervision and interdisciplinary collaboration
- Scientific writing, publication, reporting, presentation and external data exchange
- Bioinformatics pipeline development, benchmarking, optimization, documentation and quality assurance
- Data visualization, statistical analysis, biological interpretation and database management