

Clabe Wekesa, PhD

Computational Biologist & Molecular Microbiologist

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Computational biologist and molecular microbiologist with extensive experience in bioinformatics, transcriptomics, genomics, metagenomics, multi-omics integration, and reproducible computational workflow development. Experienced in analysing large-scale sequencing datasets and integrating transcriptomic, metabolomic, microbiome, phenotypic, and environmental data to investigate complex biological processes. Strong programming and data-analysis experience in Python and R, with extensive use of Linux, shell scripting, high-performance computing, and scientific software development.

CORE EXPERTISE

Bioinformatics • Microbial Genomics • RNA-seq • Transcriptomics • Metagenomics • Multi-omics Integration • Microbial Ecology • Plant-Microbe Interactions • Python • R • HPC • Scientific Software

PROFESSIONAL EXPERIENCE

Postdoctoral Researcher

2023-2025

Max Planck Institute for Chemical Ecology, Jena, Germany

- Developed and implemented computational workflows for transcriptomic, metagenomic, metabolomic, and integrative biological data analyses.
- Analysed RNA-seq datasets and performed differential gene-expression and functional analyses using R- and Linux-based workflows.
- Integrated transcriptomic, metabolomic, microbiome, phenotypic, and environmental datasets across multiple molecular and organismal levels.
- Developed reproducible Python, R, and Bash workflows for processing, analysing, and visualizing large biological datasets.
- Managed large sequencing datasets and computational analyses in high-performance computing environments.
- Applied statistical and machine-learning approaches to identify biologically meaningful patterns in complex datasets.
- Worked closely with experimental scientists to connect computational results with biological hypotheses and experimental observations.
- Coordinated collaborative research activities between scientists in Germany and Norway, contributed to manuscripts and proposals, and supported student research.

Lecturer and Researcher

Masinde Muliro University of Science and Technology (MMUST), Kenya

- Conducted research in molecular biology, microbiology, genomics, biotechnology, and bioinformatics.
- Taught undergraduate and postgraduate courses in molecular biology, microbiology, biotechnology, and bioinformatics.
- Supervised undergraduate, MSc, and PhD research projects and guided students in experimental design, biological data analysis, interpretation, and scientific writing.
- Contributed to collaborative research projects, proposal development, scientific workshops, seminars, and practical bioinformatics training.

EDUCATION

PhD in Molecular Biology / Microbiology

Friedrich Schiller University Jena, Germany

Research focused on plant-microbe interactions, microbial molecular biology, genomics, transcriptomics, stress responses, and biological nitrogen fixation.

MSc in Biotechnology

Masinde Muliro University of Science and Technology, Kenya

BSc in Biochemistry

Masinde Muliro University of Science and Technology, Kenya

SELECTED RESEARCH & SOFTWARE PROJECTS

BOTAS - Bacterial Operon and Transcriptome Analysis Suite

Open-source bacterial RNA-seq analysis framework

Developed an end-to-end framework for bacterial RNA-seq analysis covering reference indexing, read alignment, gene-level quantification, operon inference, and reproducible downstream analysis. Benchmarked with experimental RNA-seq data, with emphasis on reproducibility, transparent evaluation, computational performance, usability, and circular bacterial genomes.

[GitHub](#) | [PyPI](#)

Multi-omics Integration of Plant Defence Responses

Integrated transcriptomic, metabolomic, microbiome, phenotypic, and environmental datasets; developed cross-dataset analysis, statistical evaluation, visualization, and interpretation workflows.

Comparative and Evolutionary Genomics

Performed comparative genomic and phylogenomic analyses using sequence retrieval, multiple-sequence alignment, phylogenetic inference, genome annotation, and comparative analysis.

Metagenomics and Microbiome Analysis

Developed workflows for sequence preprocessing, assembly, taxonomic classification, functional annotation, comparative analysis, and biological interpretation of complex microbial communities.

Scientific Software Development

Developed MLDockKit and additional Python-based utilities for molecular docking, biological sequence analysis, quantitative data processing, visualization, and reproducible research.

TECHNICAL EXPERTISE

Programming & data science	Python, R, Bash, pandas, NumPy, scikit-learn, statistical modelling, machine learning, data visualization.
RNA-seq & transcriptomics	DESeq2, edgeR, featureCounts, Salmon, Kallisto, HISAT2, Bowtie2, Trinity; differential expression and functional analysis.
Genomics & metagenomics	SPAdes, Kraken2/Bracken, BLAST/DIAMOND, genome annotation, comparative genomics, microbial community analysis.
Phylogenomics & pangenomics	MAFFT, IQ-TREE, Prokka, Panaroo; sequence analysis, phylogenetic inference, comparative analysis.
Computing & reproducibility	Linux, HPC (SGE/Slurm), Git/GitHub, Conda, Docker, large-scale sequencing-data processing, workflow documentation.

RESEARCH COORDINATION, SUPERVISION & COMMUNICATION

- Coordinated research implementation and communication between collaborating scientists in Germany and Norway.
- Supervised and supported undergraduate, MSc, and PhD research; guided experimental design, data analysis, interpretation, and scientific writing.
- Contributed to international collaborative proposals, manuscripts, technical documentation, and research presentations.
- Organized workshops, seminars, and practical bioinformatics training and communicated findings to multidisciplinary audiences.

SCIENTIFIC INTERESTS

Computational Biology · Gene Regulation · Single-cell Genomics · Multi-omics Integration · Regulatory Network Inference · Transcriptomics · Functional Genomics · Systems Biology · Reproducible Bioinformatics

Interested in integrating multiple molecular layers to resolve regulatory relationships and in extending transcriptomics and multi-omics expertise toward single-cell transcriptomics, chromatin-accessibility analysis, and gene regulatory network reconstruction.

PUBLICATIONS, PROFILES & PROFESSIONAL DEVELOPMENT

Google Scholar Publications & citations	ORCID 0000-0002-1815-9357	GitHub Software & research code
Certification Google Project Management Professional Certificate	Languages English - Fluent · German - Intermediate · Swahili - Native	References Available on request

Website: clabe-wekesa.github.io