NICOLÒ CINTI

NGS Specialist | Bioinformatics | Metagenomics

Email: nicolo.cinti2@unibo.it | ncinti94@gmail.com | nicolo.cinti@outlook.com
Phone: +39 3898477436 | **LinkedIn**: www.linkedin.com/in/ncinti

PERSONAL PROFILE

NGS specialist with extensive hands-on experience in complete sequencing workflows. Over 10,000 samples sequenced (16S, ITS, shotgun metagenomics). Strong expertise in Illumina library preparation, quality control, troubleshooting, and bioinformatic analysis on HPC systems.

Languages: Italian (native), English (C1)
Skills: Team worker, excellent communication, problem-solving, lab instrumentation proficiency

EXPERIENCE

PHD STUDENT IN ENVIRONMENTAL MICROBIOLOGY AND METAGENOMICS | 11/2023 - Present
Alma Mater Studiorum University of Bologna, Italy

- 10,000+ samples sequenced (16S rRNA, ITS, shotgun metagenomics)
- Complete NGS workflow: DNA extraction, Illumina library prep, QC, sequencing coordination
- Advanced bioinformatics on HPC: assembly, binning, MAG reconstruction, functional annotation

RESEARCH FELLOW IN ENVIRONMENTAL MICROBIOLOGY | 06/2022 - 11/2023
University of Bologna, Italy - Microbiology, metagenomics, microbial community analysis

INTERNSHIP IN PROTEIN ENGINEERING | 09/2020 - 05/2021
Copenhagen Biocenter, Denmark - Protein expression, bioinformatics, artificial design

TECHNICIAN FOR EDUCATIONAL LABORATORIES | 09/2019 - 02/2020
University of Bologna, Italy - Lab management and routine methods

INTERNSHIP IN ANALYTICAL BIOCHEMISTRY | 04/2018 - 09/2018
University of Bologna, Italy - Bioluminescence assays, protein-ligand interactions

EDUCATION

Master's Degree in Industrial and Molecular Biotechnology | University of Bologna
Bachelor's Degree in Biotechnology | University of Bologn

TECHNICAL SKILLS

MICROBIOLOGICAL TECHNIQUES

Microbial isolation and culturomics • Functional enzymatic screening • DNA extraction and QC (NanoDrop, Qubit) • NGS library preparation (Illumina) • Batch fermentation (Applikon bioreactors) • Microbial biobanking

MOLECULAR BIOLOGY & SEQUENCING

16S rRNA and ITS amplification • Shotgun metagenomics • PCR optimization • Quality control (FastQC, MultiQC, FastP Q20 filtering, KneadData)

BIOINFORMATICS & COMPUTATIONAL ANALYSIS (HPC)

- **Taxonomic profiling**: Kraken2/Bracken, MetaPhlAn4, PhyloFlash, CAT/BAT/RAT, MEGAN, Tiara
- **Assembly & binning**: MEGAHIT, metaSPAdes, MetaWRAP (MetaBAT2, MaxBin2, CONCOCT)
- **MAG quality & reconstruction**: CheckM, BUSCO, GUNC, QUAST, GTDB-Tk, dRep
- **Functional annotation**: Prokka, Bakta, eggNOG-mapper, dbCAN, DIAMOND, METABOLIC, antiSMASH
- **Phylogenetics**: SINA, TrimAl, FastTreeMP, IQ-TREE
- **Comparative genomics**: ANI, OrthoFinder
- **Custom databases**: UniProt-derived enzyme databases

STATISTICAL & ECOLOGICAL ANALYSIS (R, Python)

- **Diversity**: Shannon, Chao1, Faith's PD, UniFrac, Bray-Curtis, Aitchison
- **Statistics**: PERMANOVA, betadisper, envfit, Mantel, Procrustes, MFA
- **Ordination**: PCoA, NMDS, RDA
- **Differential abundance**: Random Forest, Kruskal-Wallis, LEfSe, ALDEx2, ANCOM-BC, MaAsLin2
- **Machine learning**: Random Forest, PLSR for multi-omics integration
- **Visualization**: ggplot2, ComplexHeatmap, custom heatmaps
- **R packages**: vegan, phyloseq, ggplot2, gplots, tidyverse, DESeq2, FactoMineR, mixOmics

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SELECTED PUBLICATIONS

1. **Zonation of the Vitis vinifera microbiome in Vino Nobile di Montepulciano PDO**
   Communications Biology, 2024. DOI: 10.1038/s42003-024-07261-8
2. **Composition and biodiversity of soil and root-associated microbiome in Vitis vinifera cultivar Lambrusco**
   Frontiers in Microbiology, 2024. PMID: 36910169
3. **Microbiome variation at the clam-sediment interface explains productivity changes of Chamelea gallina**
   BMC Microbiology, 2023. DOI: 10.1186/s12866-023-03146-8
4. **A 15-day pilot biodiversity intervention leads to gut microbiome rewilding in urban children**
   One Health, 2024. DOI: 10.1016/j.onehlt.2024.100902
5. **Physiological Plasticity of Chamelea Gallina During a Marine Heatwave**
   Environmental Research, 2024. DOI: 10.1016/j.envres.2024.120287

Availability: September 2026