CONTACTS and INFO

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carrusmeryam@gmail.com

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Caprarola (Vt)

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21/09/2000

PROFILE

Motivated, detail-oriented, and well-organized bioinformatician. Ambitious and enthusiastic about continuously growing and advancing in the field of bioinformatics, developing new skills and expanding scientific and technical expertise.

LANGUAGES

- Italian – Native
- English – B2
- Arabic – Basic
- Spanish – Basic
- French – Basic

MERYAM CARRUS

PhD Student in Ecology and Sustainable Management of Environmental Resources
MSc in Experimental Biology and Bioinformatics

EDUCATION

University of Tuscia

PhD in Ecology and Sustainable Management of Environmental Resources | Nov 2025 - present

University of Tuscia

Master's Degree in Experimental Biology and Bioinformatics (LM-6) (110/110 cum laude) | Oct 2022 - May 2025

University of Tuscia

Bachelor's Degree in Ecological and Biological Sciences (L-13) (108/110) | Oct 2019 - Feb 2023

Paolo Ruffini Scientific High School

Scientific High School Diploma – Applied Sciences (96/100) | Sep 2014 - Jun 2019

WORK AND TRAINING EXPERIENCE

Internship – CINECA Interuniversity Consortium, High Performance Computing Department. (January 2025 - February 2025)

- Implemented workflow management systems to develop bioinformatics pipelines using Snakemake
- Gained foundational skills in High-Performance Computing (HPC) for sequencing data analysis
- Applied Python tools for scientific research

Internship – Natural Reserve of Lake Vico (CRAS). (October 2022 - December 2022)

- Gained experience in on-site and office-based wildlife conservation activities
- Monitored species movements in their natural habitat and recorded/analyzed data using Microsoft Excel

School-Work Program – Stelliferi & Itavex S.r.l. (2017)

- Analyzed the supply chain of raw materials (hazelnuts), from procurement to processing and commercialization
- Performed logistical and administrative accounting tasks using digital tools
- Issued invoices and transport documents (DDTs)
- Managed product labeling
- Used search engines and Microsoft Office applications

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TECHNICAL SKILLS

- **Linux/Unix Environment**

Command-line proficiency for file management, pipeline execution, and bioinformatics data processing locally or on HPC servers.

- **Scripting & Automation**

Practical knowledge of Bash and Python for biological data manipulation (FASTQ, FASTA, GTF formats), output processing, and workflow management.

- **NGS Data Analysis**

Experience with amplicon-based and RNA-seq data, including:
Quality control (FastQC);
Trimming (Trimmomatic);
Alignment (HiSat2);
Transcript assembly (StringTie);
OTU clustering (VSEARCH);
Gene expression analysis (HTSeq, DESeq2).

- **Data Visualization**

Visualization and graphical representation of bioinformatics data using R (ggplot2), Excel, and specialized tools for interpreting clustering results, relative abundance, phylogenetic analyses, and gene expression patterns.

- **Molecular Docking & 3D Structures**

Use of AutoDock for molecular interaction simulations and PyMOL for 3D protein structure visualization.

- **Biological Databases & Data Management**

Familiarity with NCBI, SILVA, RefSeq, Ensembl, and KEGG databases.
Basic SQL knowledge for managing relational biological datasets.

RESEARCH PROJECTS

- **Comparative Genomics of Microalgae: Molecular Mechanisms Underlying Efficient CO_2 Assimilation**
  [Under review: Springer Nature]

This study investigates the molecular mechanisms enabling certain microalgae species to efficiently capture atmospheric CO_2, contributing to potential biological carbon sequestration strategies. The work presents a comparative genomic analysis of 29 microalgal species belonging to the clades Chlorophyta, Stramenopiles, and Alveolata.

PUBLICATIONS

- **Identification of Multiple *Blastocystis* Subtypes in Marine Turtles and Cetaceans from the Mediterranean Sea Using Amplicon-Based Next-Generation Sequencing**
  [Food and Waterborne Parasitology]

This study, forming the core of my Master’s thesis, explores the presence and genetic diversity of the enteric protist Blastocystis in marine turtles (Caretta caretta) and cetaceans from the Mediterranean Sea. It represents the first application of amplicon-based NGS to characterize subtype diversity in these marine hosts.
I developed and managed the entire bioinformatics pipeline, including:

- Raw data quality control using FastQC and adapter trimming with Trimmomatic
- Read assembly with VSEARCH and chimera removal
- OTU clustering at 99% identity threshold
- Subtype assignment using BLASTn against reference Blastocystis databases, with manual validation of results

CERTIFICATIONS

High Performance Bioinformatics
Cineca (Dec 2024)

Corso di formazione per lavoratori (rischio alto)
Università degli Studi della Tuscia (Feb/Mar 2023)

Excel Data Analytics
ELEVEL Academy (Jan 2023)

Cybersecurity
ELEVEL Academy (Jan 2023)

Python Programming
ELEVEL Academy (Feb 2023)

English - B2
Università degli Studi della Tuscia
(2023)