

# ENVIRONMENTAL METAGENOMICS

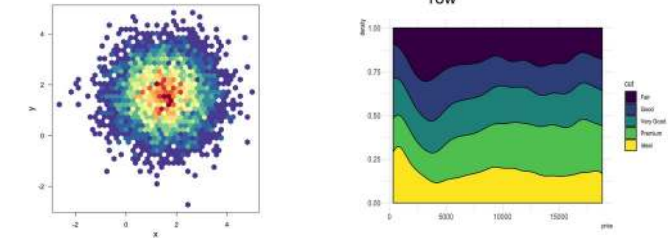
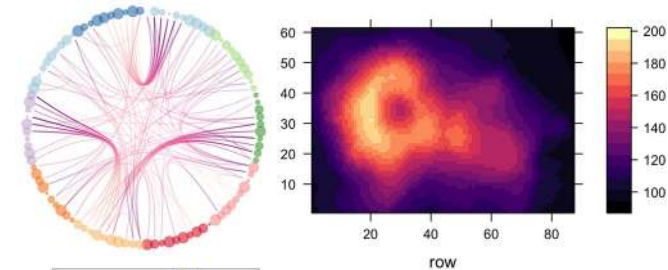
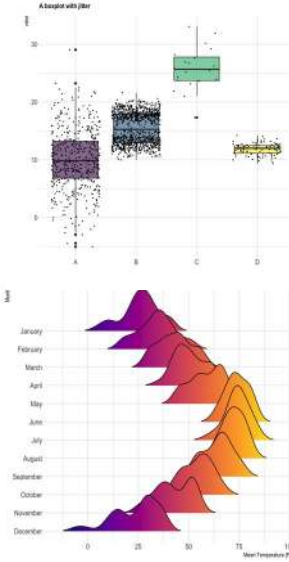
## INTRODUCTION, SYLLABUS AND GENERAL INFORMATION

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# MY BACKGROUND

**2005** – B.Sc. (L) in Biological Science, Università Politecnica delle Marche

**2007** – M.Sc. (LS) in Marine Biology, Università Politecnica delle Marche

**2013** – PhD in Applied Biology, Università di Napoli “Federico II”

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**2016-2018** Researcher, Earth-Life Science Institute, Japan



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**2019-present** RTDb, University of Naples Federico II



# MY BACKGROUND

*I am fundamentally interested in the co-evolution of the biosphere and the geosphere and how life influences planetary-scale processes. My current research focuses on:*

*1) the microbial diversity and ecosystem functioning of extreme environments and their role in global biogeochemistry;*

*2) reconstructing the emergence and evolution of metabolism.*

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*2) reconstructing the emergence and evolution of metabolism.*

*Three basic assumptions underlying my research:*

*i) prokaryotes dominated the evolutionary history of our planet;*

*ii) they are responsible for the bio in biogeochemistry both at the ecosystem level and through time; and*

*iii) extremophilic prokaryotes living in extreme environments resembling early Earth analogs, despite being extant organisms, retain a higher number of ancestral metabolic traits.*









Poas Hyperacidic Volcanic Lake – Costa Rica 2017





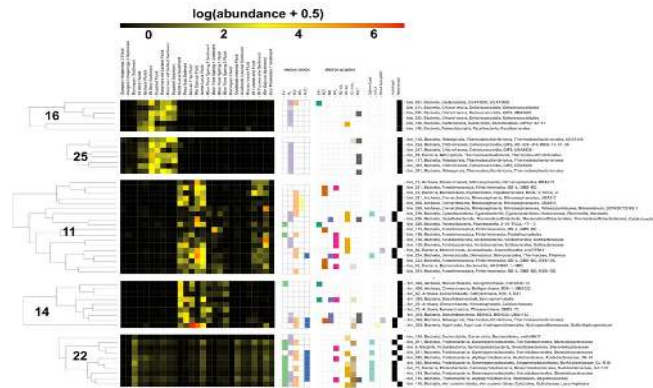
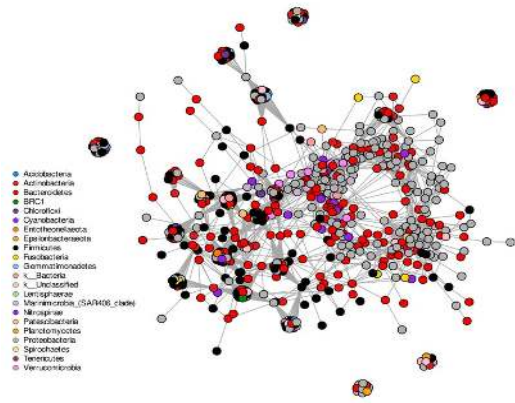
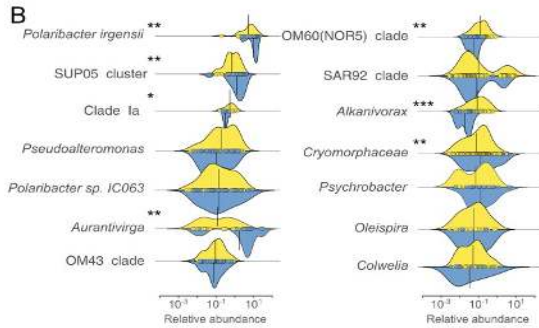
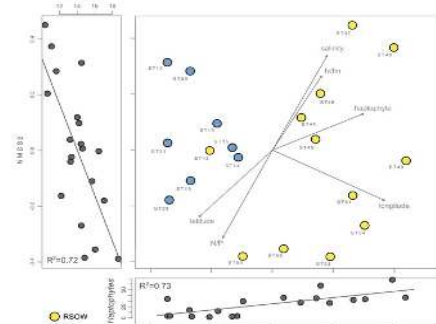
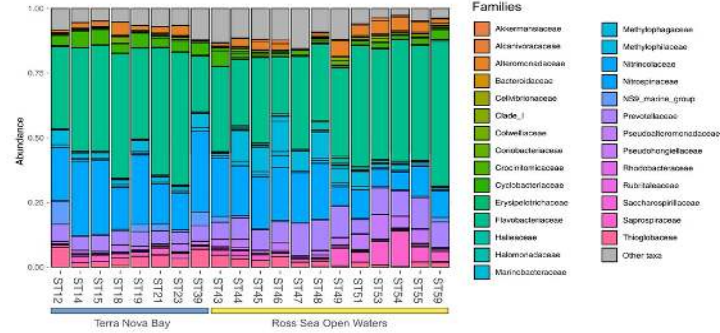
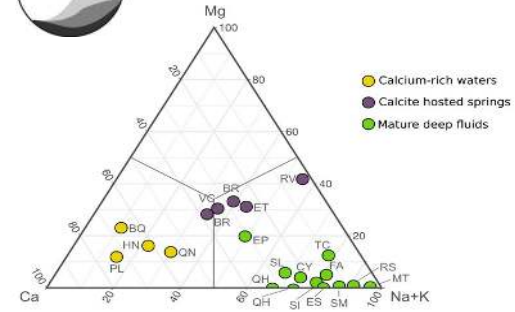
Bottaro Shallow Vents – Aeolian Islands 2019



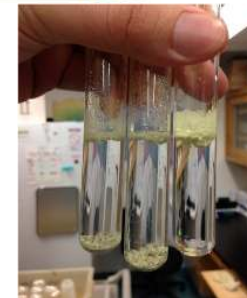
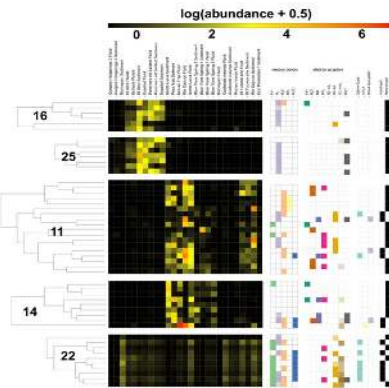
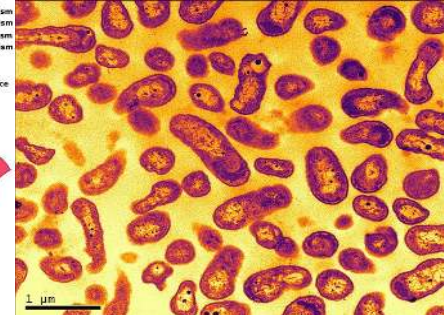
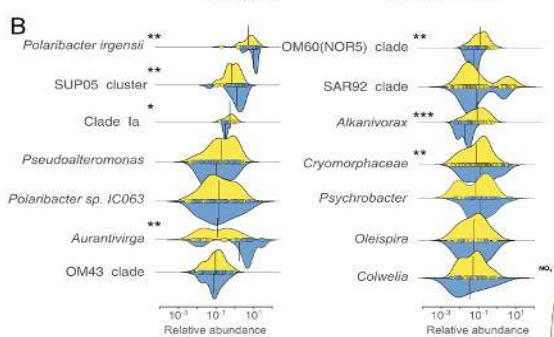


East Pacific Rise 9.50°N – Pacific Ocean 2015

# culture-independent

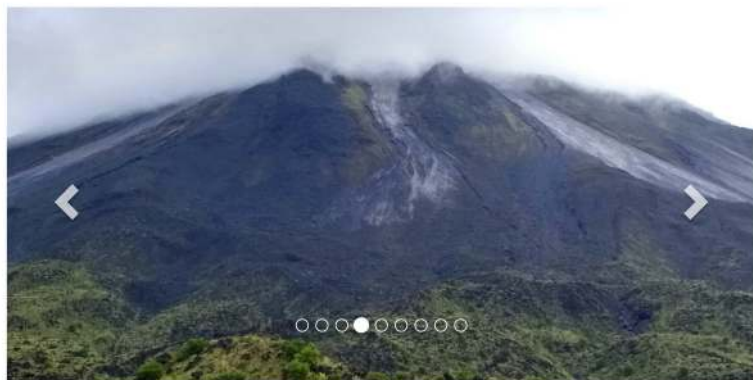






# Welcome to the Giovannelli Lab

I am an Assistant Professor at the [Department of Biology](#) of the [University of Naples "Federico II"](#), in Italy. My group aims to explore and understand [the emergence and evolution of life](#) and the [co-evolution of the Geosphere and the Biosphere](#). I've been recently awarded a **ERC Starting Grant** to look at the co-evolution of biogeochemically-relevant proteins and trace metal availability in the environment called CoEVOLVE. Read more about [the CoEVOLVE project](#) [here](#).



To this end in my lab we combine classic microbiology techniques with data from comparative genomic, phylogenetic, environmental surveys and computational approaches to reconstruct

## News

2. Dec 2020

*And I am on Netflix! As part of the Strobilology series Alien Worlds I went to Iceland to shoot a segment. Watch the entire series on [Netflix](#). I'm on Episode 2 - Janus*

1. Dec 2020

*The registration for the 9th ELSI Symposium Science in Society is now open! The symposium has a very innovative structure this year. Check it out and register here <https://symposium2021.elsi.jp/>*

23. Nov 2020

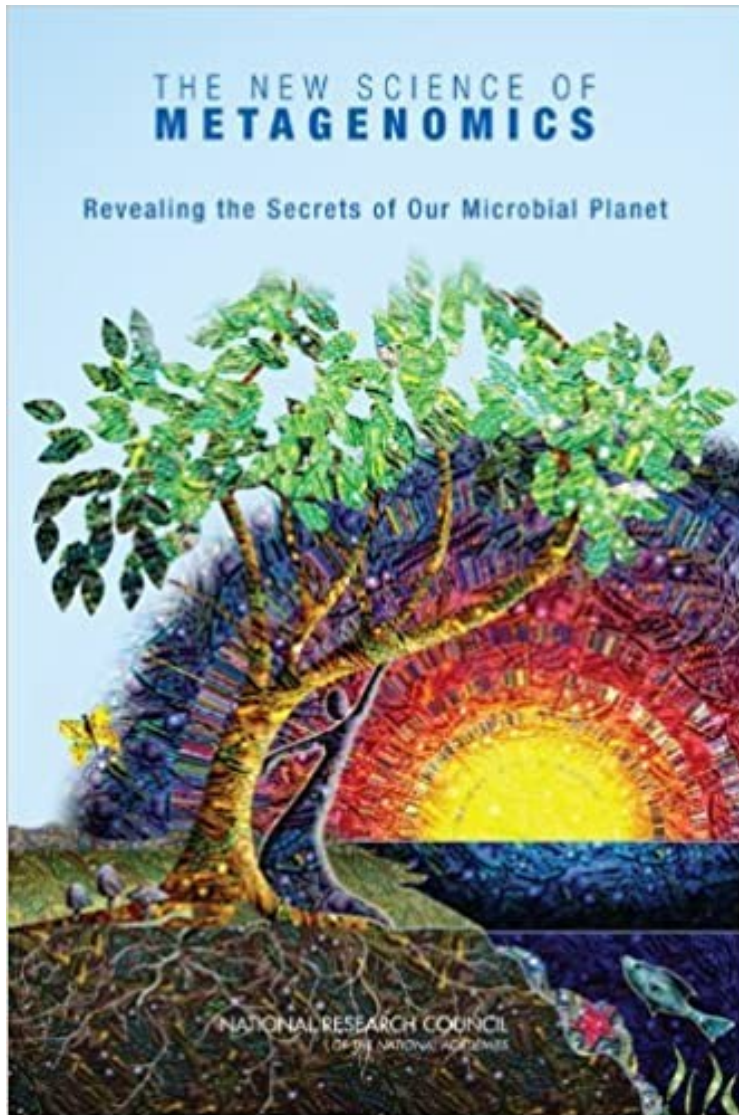
*Today the First Online Italian Congress on the Evolution of Marine Organisms starts! I'm one of the co-organizer. Check it out at [www.evolmar.it](http://www.evolmar.it)*

25. Nov 2020

*Our recent Nature Communication article about deep sources of energy*







*Portions of this course will be based on  
the following FREE book*

***The New Science of Metagenomics:  
Revealing the Secrets of  
Our Microbial Planet***

*The National Academies Press  
2007*

***Download it for free at***  
[https://www.nap.edu/catalog/11902/  
the-new-science-of-metagenomics-  
revealing-the-secrets-of-our](https://www.nap.edu/catalog/11902/the-new-science-of-metagenomics-revealing-the-secrets-of-our)





*Introduction to microbiology based on  
the following textbook*

***Brock Biology of Microorganisms***

*Madigan, Bender, Buckley, Sattley, Stahl*

*Pearson Edition*

# Course Objectives

*Provide you with a general overview of the possible applications of metagenomic, showcasing use cases*

*Provide you with an overview of the techniques and approaches used to study and apply metagenomic*

*Provide you with the basic concepts necessary for the use of -omic approaches*

*Being able to ask relevant questions in environmental microbiology and identify the correct tools to answer them*

*Give you hands-on experience in dealing with basic metagenomic data and their biological interpretation*

# Course Program

## *Module 1: Basic environmental microbiology concept refresher*

*Microorganisms – Microbial Metabolism – Microbial Diversity – Microbial Genetic – Microbial Ecology – Sampling for environmental metagenomic*

## *Module 2: Basic bioinformatic and statistical knowledge*

*Sequencing and data – Computer skills – Reading common diversity plots – Questions in Environmental Metagenomic – Omics approaches*

## *Module 3: Environmental Metagenomic case studies*

*Reading a research paper – Reading and discussing case studies – Guest lectures in Metagenomic: Dr. Karen Lloyd (UTK, USA), Prof. Costa Vetriani (Rutgers, USA), Prof. Brett Baker (UAT, USA)*

## *Module 4: Hands-on training and data analysis*

*Analyzing and discussing a metagenomic dataset*



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***Final grade** is based on class participation and discussion and the metagenomic project presentation*



# What you need

## **Theoretically:**

*A Linux install (e.g. Ubuntu), a functional install of R, dada2 and phyloseq, a basic knowledge of multivariate statistics, a basic knowledge of bioinformatic jargon, a working knowledge of R and experience with command line-like environments*

## **Practically:**

*A computer with a internet connection, working knowledge of Excel or Google Drive, a strong will to spend a few ours learning and wrangling data, PowerPoint or Google Slide skills*

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# Resources

## **16S rRNA sequence analysis**

dada2 – <https://benjjneb.github.io/dada2/index.html>

SilvaNGs – <https://ngs.arb-silva.de/silvangs/>

## **16S rRNA abundance data analysis**

AmpiVar – <https://kasperskyte.shinyapps.io/shinyampvis/>

## **Exploring public metagenomes**

JGI-IMG – <https://img.jgi.doe.gov/>

MetaSeek – <https://www.metaseek.cloud/>

## **Full blown metagenome analysis**

KBase – <https://www.kbase.us/>

Galaxy – <https://usegalaxy.eu/>

## **Fast functional annotation of metagenomes**

mi-faser – <https://services.bromberglab.org/mifaser/>

## **Analysis and visualization of results**

Excel / Google Sheet

KEGG – <https://www.genome.jp/kegg/>

Krona plots – <https://github.com/marbl/Krona/releases/tag/xl2.5>

Circos Table – <http://mkweb.bcgsc.ca/tableviewer/>