



# Exploring Resistance Genes In Ocean Samples Using Python

Patricia Vera-Wolf<sup>1</sup>, Felipe Melis<sup>1</sup> and Juan A. Ugalde<sup>1</sup>

<sup>1</sup>Centro de Bioinformática y Biología integrativa, Universidad Andrés Bello, Chile



Universidad  
Andrés Bello

## Introduction

There is worldwide concern about the potential consequences of dispersion of antibiotic and metals resistance genes (RG). Because of horizontal gene transfer, most of the genes that provide resistance can be acquired from the environment. There is evidence that the ocean could play an important role as reservoir of resistance genes, but the genetic information from these types of biological samples tends to encompass big volumes of data and their management can be chaotic and hazy.

In this aspect, the Tara Oceans project generated a 7.2 TB catalog of oceanic genomic content spanning the oceanic regions of the world, where Python can be an efficient tool to automate the estimation of resistance genes by comparing the genetic information of the samples with existing resistance databases.

## Aims

- Validate a RG estimation method from NGS data for environmental samples.
- Generate an oceanic georeferential map of antibiotics and metals resistance genes.

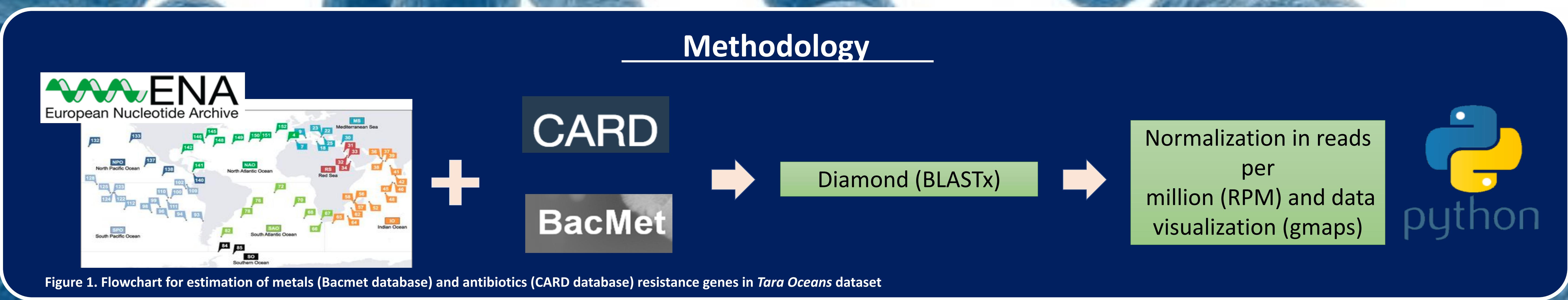


Figure 1. Flowchart for estimation of metals (Bacmet database) and antibiotics (CARD database) resistance genes in *Tara Oceans* dataset

## Methodology

According to Tara Ocean sampling design, samples proceed from different ocean provinces and deepness. Out of 315 samples, only 179 mapped antibiotics or metal resistance genes and the higher levels of RG relative abundance were observed when the reads were compared with the antibiotics database. Relative abundance fluctuated between provinces and sample types, but the highest concentrations of metals and antibiotics were observed in the South Pacific Subtropical and Indian Monsoon Gyres, along with coastal samples from the Indian Ocean and the Mediterranean and Black sea.

## Results and Discussion

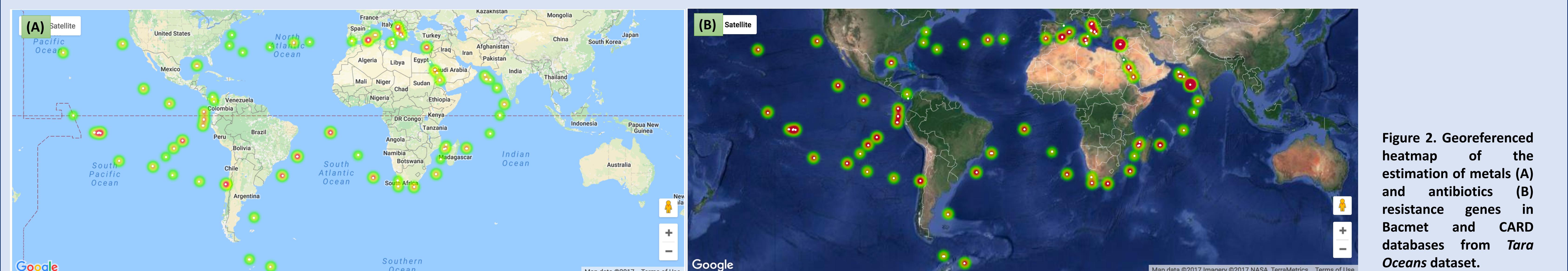


Figure 2. Georeferenced heatmap of the estimation of metals (A) and antibiotics (B) resistance genes in Bacmet and CARD databases from *Tara Oceans* dataset.

## Conclusion and Perspectives

Python demonstrated to be a powerful method to handle normalization of genomic environmental samples and visualization (gmaps library) of RG. In addition to estimate RG relative abundances, it has allowed us to explore what type metals and antibiotics are present in each geographical regions and has opened many hypothesis in relation to the origin of the components, wondering if they are naturally present in the oceans or if they presence have had anthropogenic influence.

### References:

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