

# Metagenomics as a tool to uncover ecological diversity in Mangrove

Amélie LAPORTE

Olivier GROS

Silvina GONZALEZ-RIZZO



# 1. Introduction

$10^{11}$  stars in the galaxy.



$10^{13}$  microbial cells in 1kg of soil.



Microbial communities are underestimated.

# 1. Introduction

Most microbes do not grow in lab culture.

Most bacteria do not have a cultivated representative.

- Difficult nutritional requirements.
- Symbiotic system.



## 2. Problematic

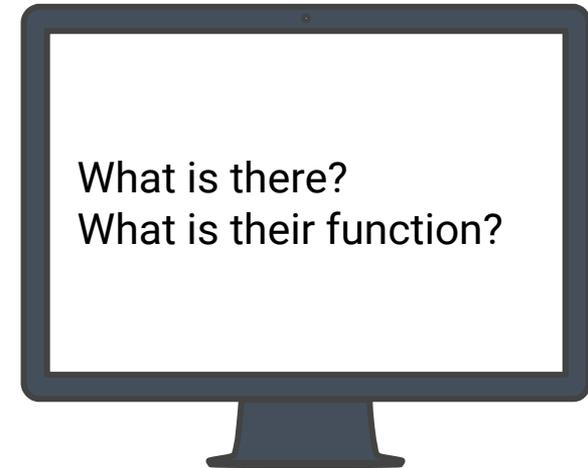


Poor understanding of microbial community.

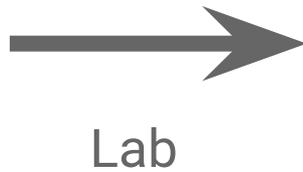
What can we do?

Find new techniques that do not rely on cultivation and isolation of microorganisms.

### 3. Metagenomics



Environment  
(eDNA)



Lab

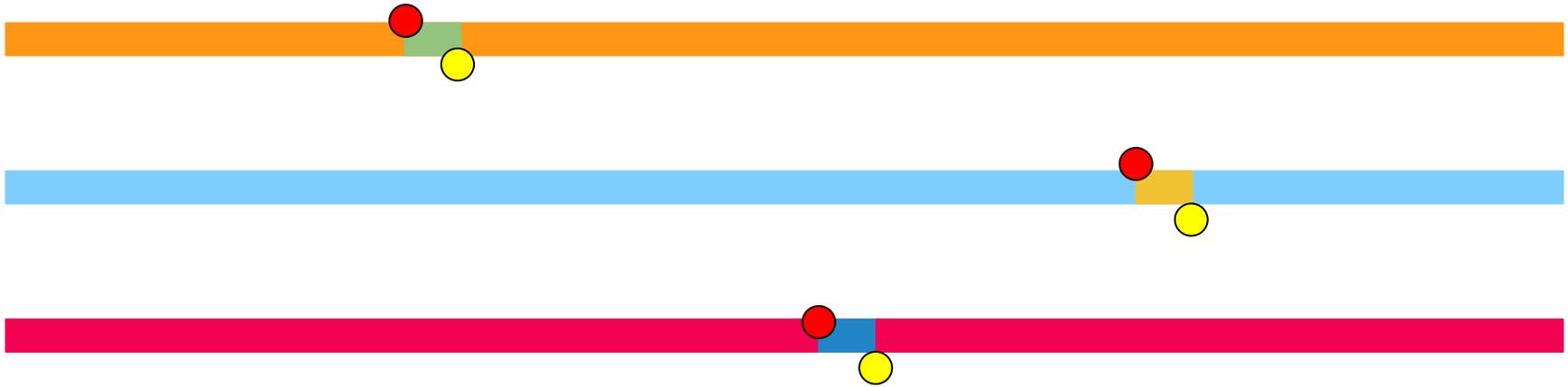
High  
throughput  
sequencing  
technologies



Bioinformatics

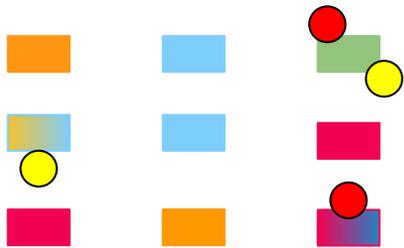
### 3. Metagenomics

e  
D  
N  
A

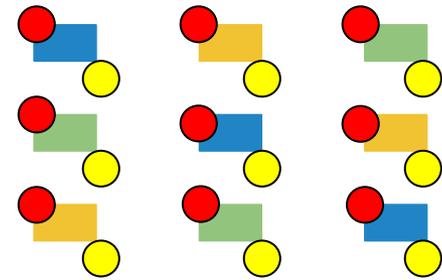
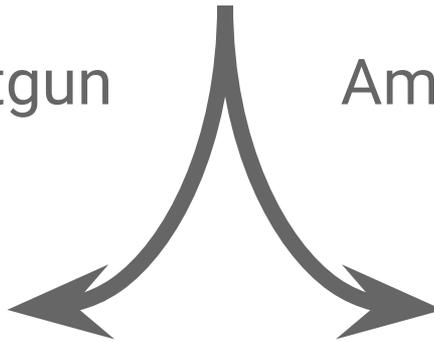


Shotgun

Amplicon-based



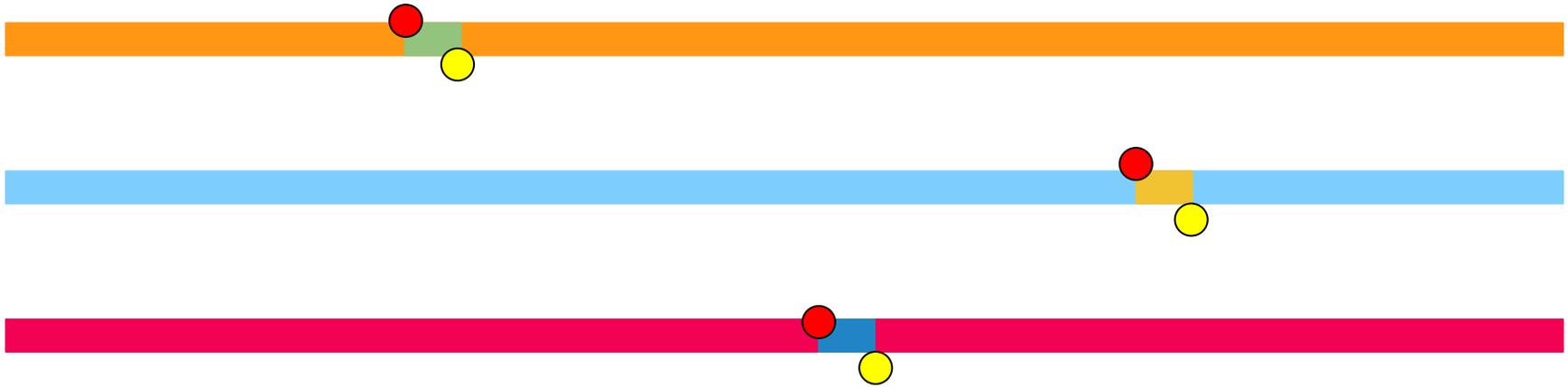
Functional analysis



Taxonomic analysis

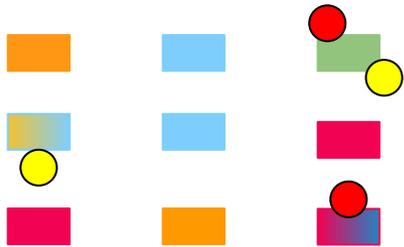
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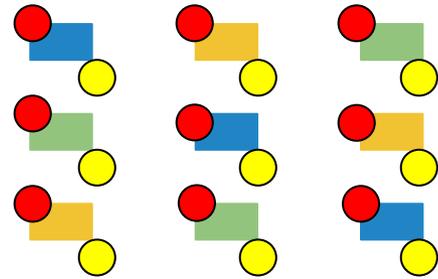
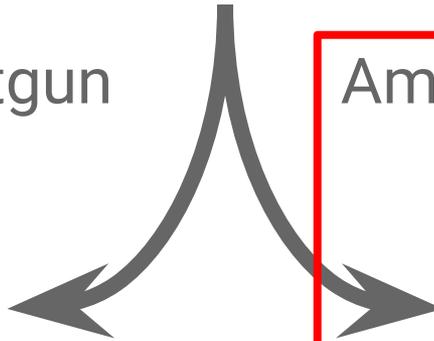


Shotgun

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Functional analysis



Taxonomic analysis

## 4. Applications in microbial ecology



Diversity

Taxonomy

Function

Microbial community:

- Maintains biogeochemical cycles.
- Involved in all levels of ecosystems and trophic-chains.

**Metagenomics is a basis for more in depth research in ecology.**

## 5. Project: Marine mangrove sediments

Mangrove ecosystem is a sulfide environment and:

- a hotspot of microbial diversity.
- a shelter for the fauna.
- a protection for our coasts.

Marine mangrove sediment is composed of an:

- Aerobic top layer.
- Anaerobic bottom layer:  $\text{CO}_2$  production by sulfate reducing bacteria (SRB).

## 5. Project: Marine mangrove sediments

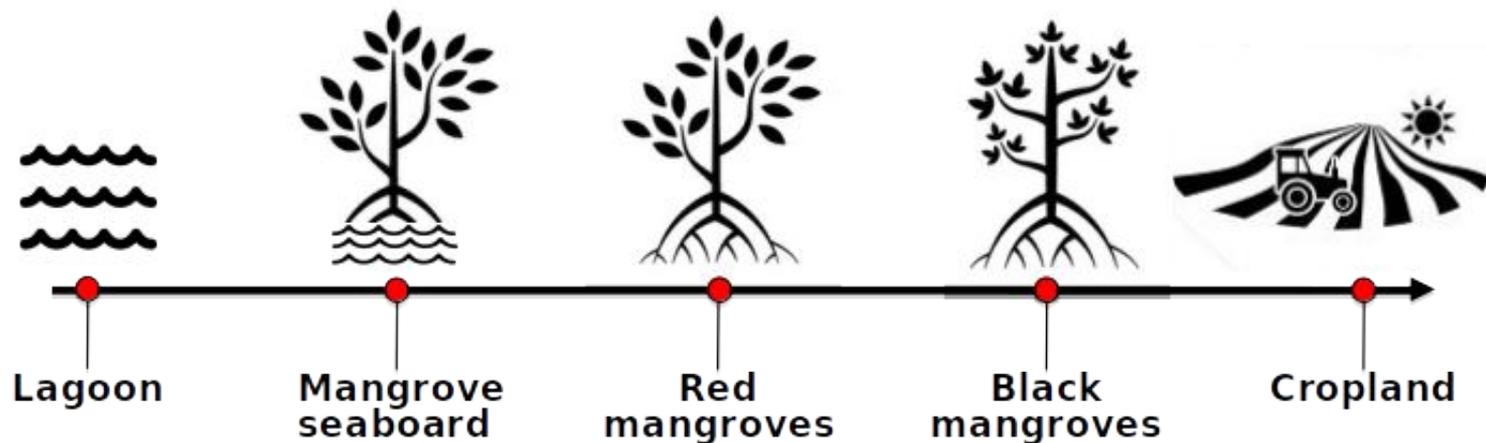
Objectives of the project:

- Insight of the microbial community within marine mangrove sediments.
- Searching for putative pathogens as expected by the MALIN consortium.

## 5. Project: Data

We sampled 5 different types of sediments in Manche à Eau, Guadeloupe.

Anaerobic phase.



Dry and wet seasons

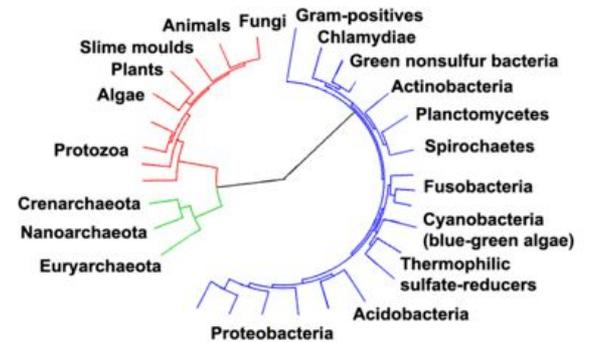
Amplicon-based metagenomics : targeting a region of the 16S rRNA gene -> **Bacterial analysis.**

# 6. Results

1. Statistical diversity analysis.



2. Taxonomic analysis.



## 6.2 Statistical analysis

### Bioinformatics

Total: 127,052 sequences

→ 2000 - 4000 OTUs (Operational Taxonomic Units):  
Group of similar sequences that are considered as one specie.

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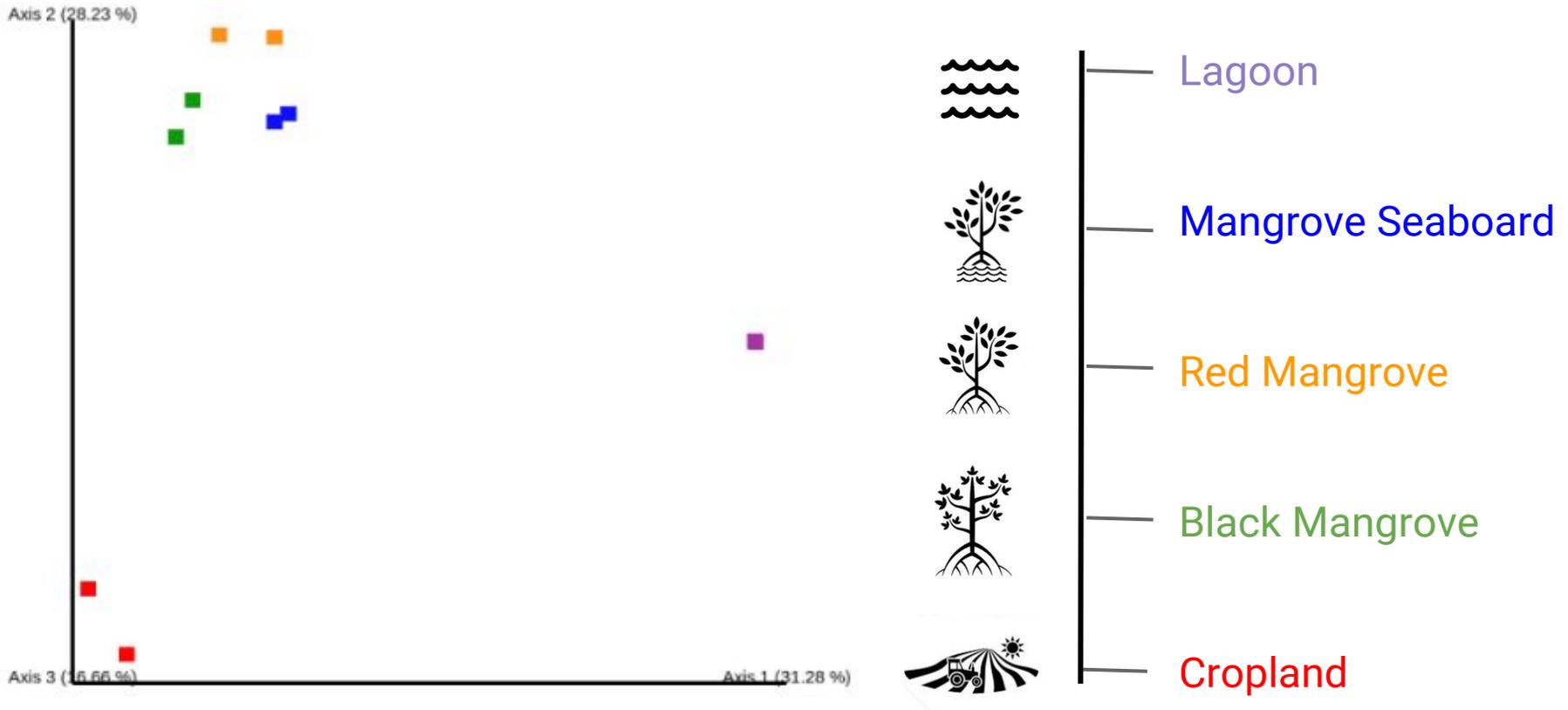
### Statistical analysis

$\alpha$  diversity: Diversity inside one sample.

$\beta$  diversity: Diversity between different samples.

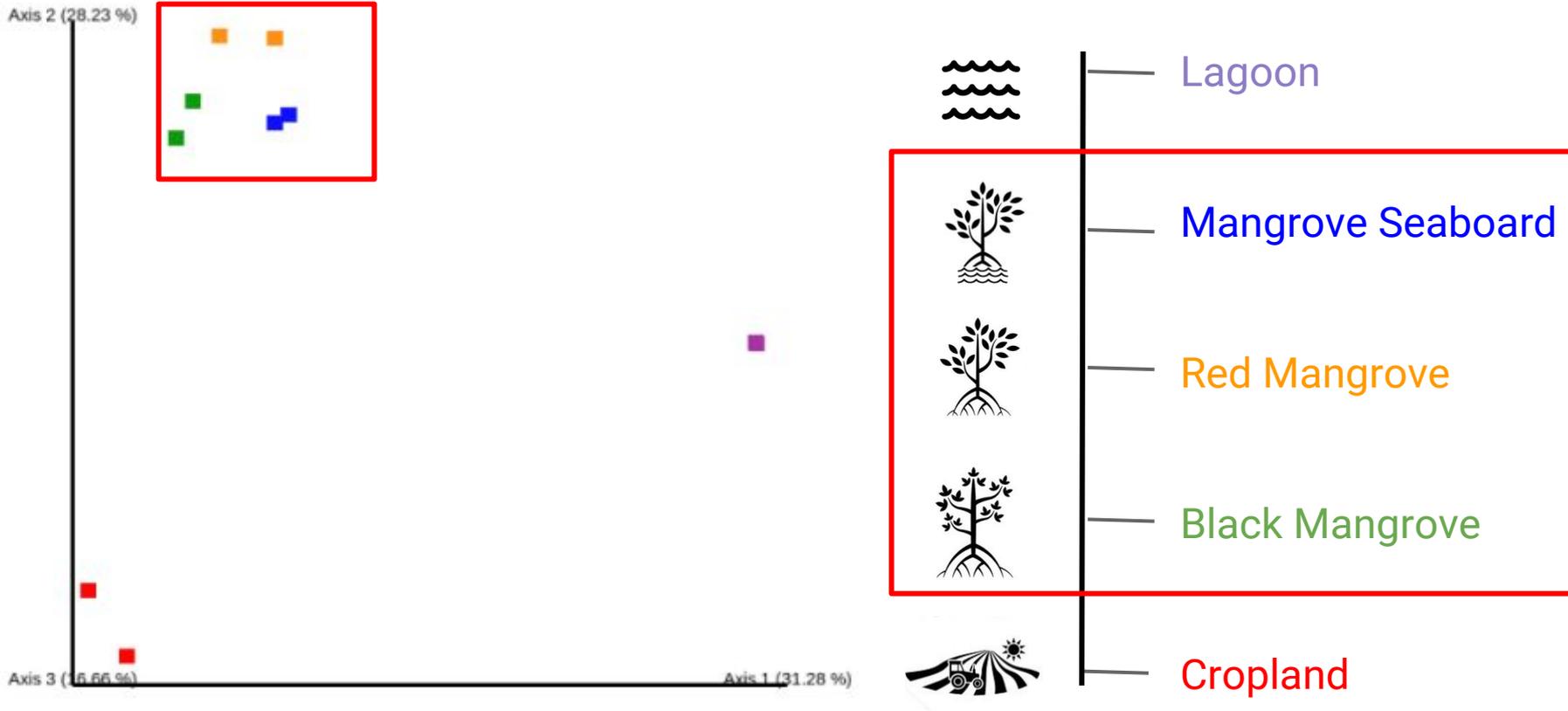
$\beta$  diversity → Principal Coordinate Analysis (PCoA)

# 6.1 Statistical diversity analysis



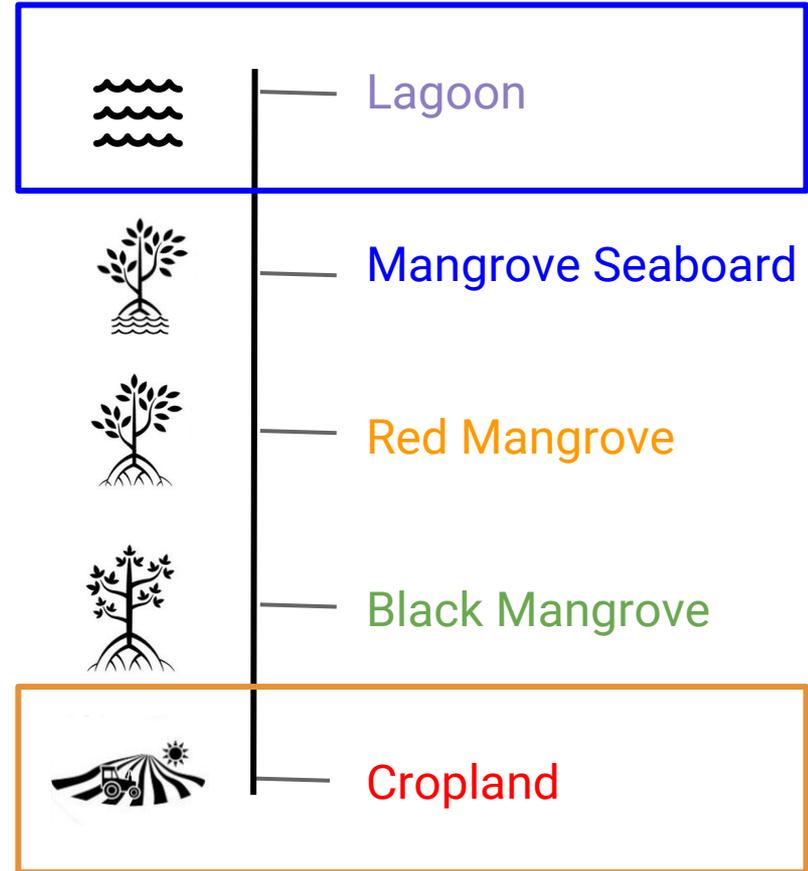
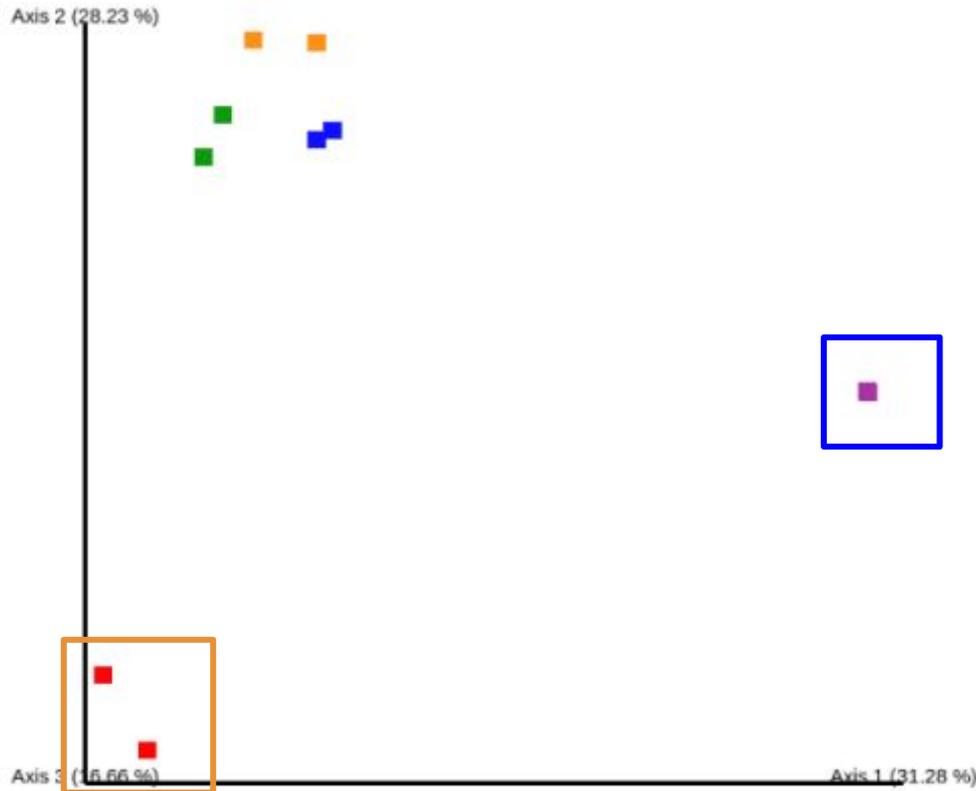
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## 6.2 Taxonomic analysis

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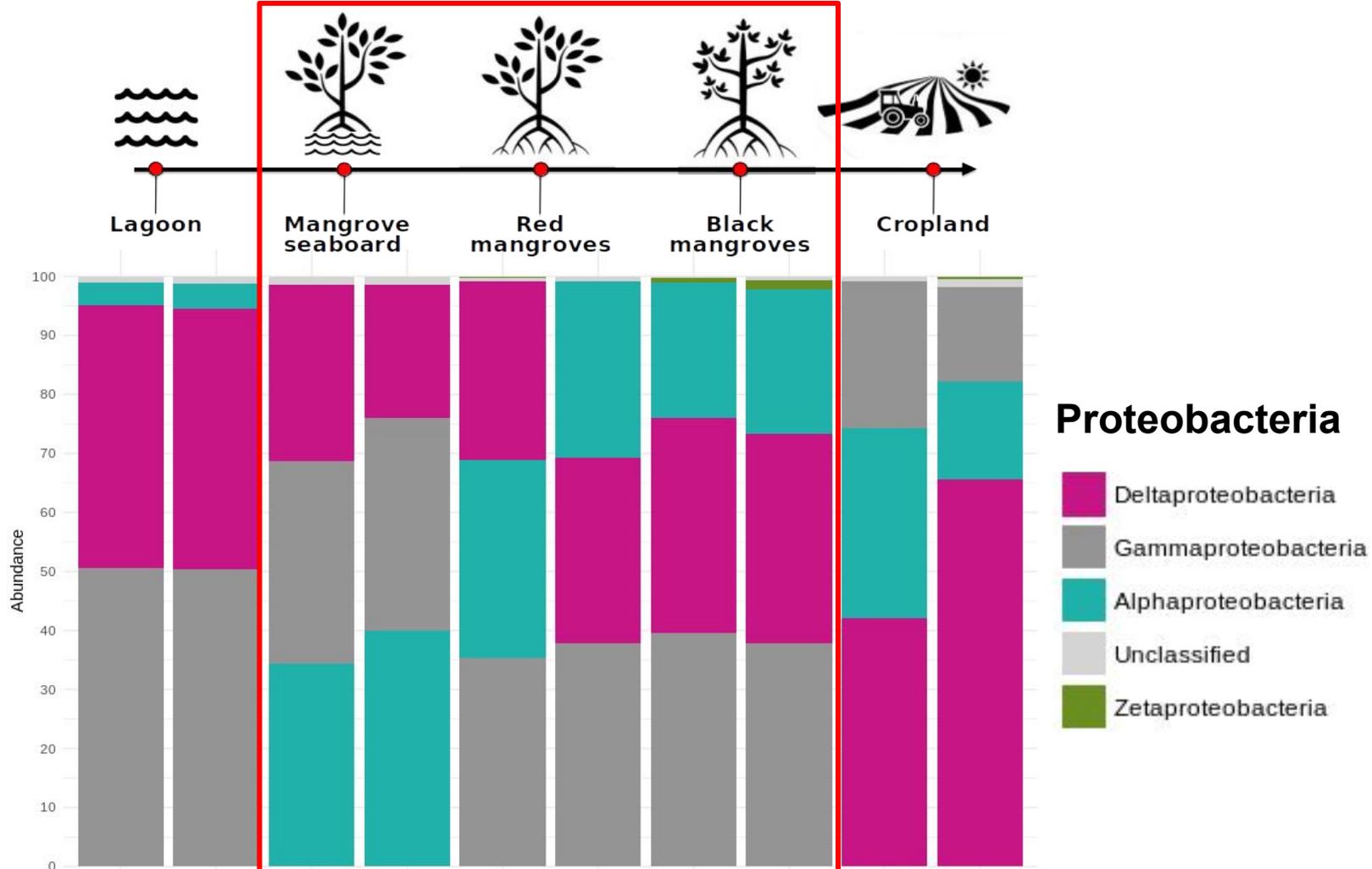
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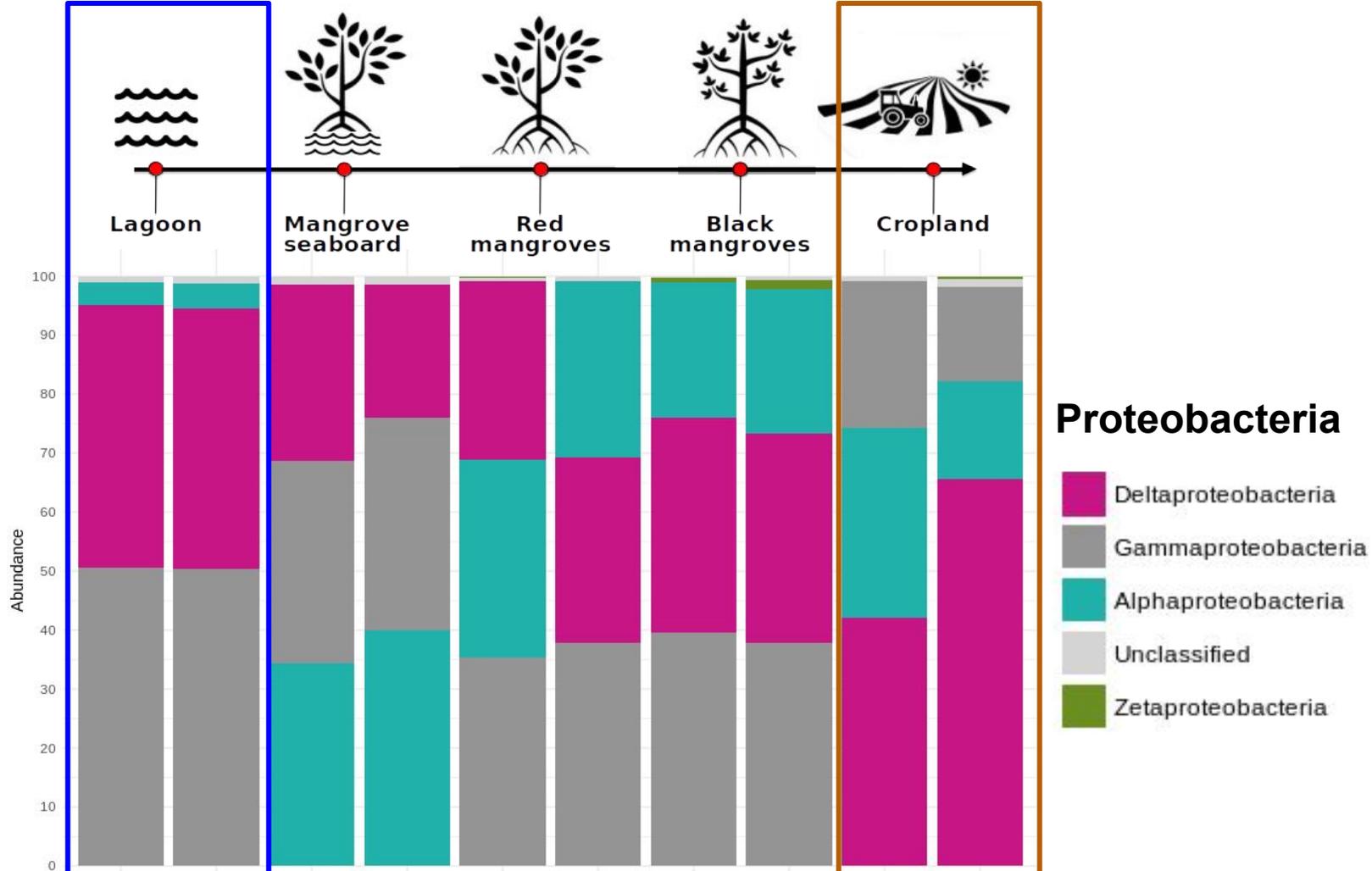
### Taxonomic analysis

Taxonomic classification of the OTUs in 69 phyla.  
Abundance calculation of each phylum.

**Most abundant bacterial group: Proteobacteria.**



Taxon	8A	8B	1H	1S	2H	2S	3H	3S	4H	4S
Deltaproteobacteria	44.47	44.14	29.99	22.52	30.29	31.45	36.55	35.65	42.02	65.63
Gammaproteobacteria	50.58	50.47	34.23	36.07	35.33	37.89	39.48	37.76	24.83	16.06
Alphaproteobacteria	3.86	4.18	34.37	39.90	33.58	29.85	22.93	24.46	32.32	16.49
Unclassified	1.08	1.21	1.30	1.48	0.57	0.65	0.35	0.58	0.83	1.27
Zetaproteobacteria	0.00	0.01	0.11	0.04	0.23	0.16	0.69	1.55	0.00	0.55



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## 7. Discussion

The database are not precise enough for the study at specie level for this type of environment.

We found bacteria involved in sulfur and iron cycles.  
We did not find abundant pathogens.

Each sampling possess a specific bacterial composition.

Further research needs to be conducted in order to understand the functional activity of the bacterial community.

## 8. Conclusion

- Metagenomic is a powerful tool.
- Allows a new multidimensional understanding of an ecosystem.
- Is important for ecological, biodiversity and conservation researches.

# Acknowledgements

Before heading to the questions I would like to express my appreciation to :

**MALIN** for financing this project

**Université des Antilles**

And the **laboratory of Mangrove biology**

**Université de Bordeaux**



Thanks!

**Any questions?**

*You can contact me at [amelie.lpe@sfr.fr](mailto:amelie.lpe@sfr.fr)*