

# Downstream results overview

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Institutional organizers



**ciimar**



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Fundação  
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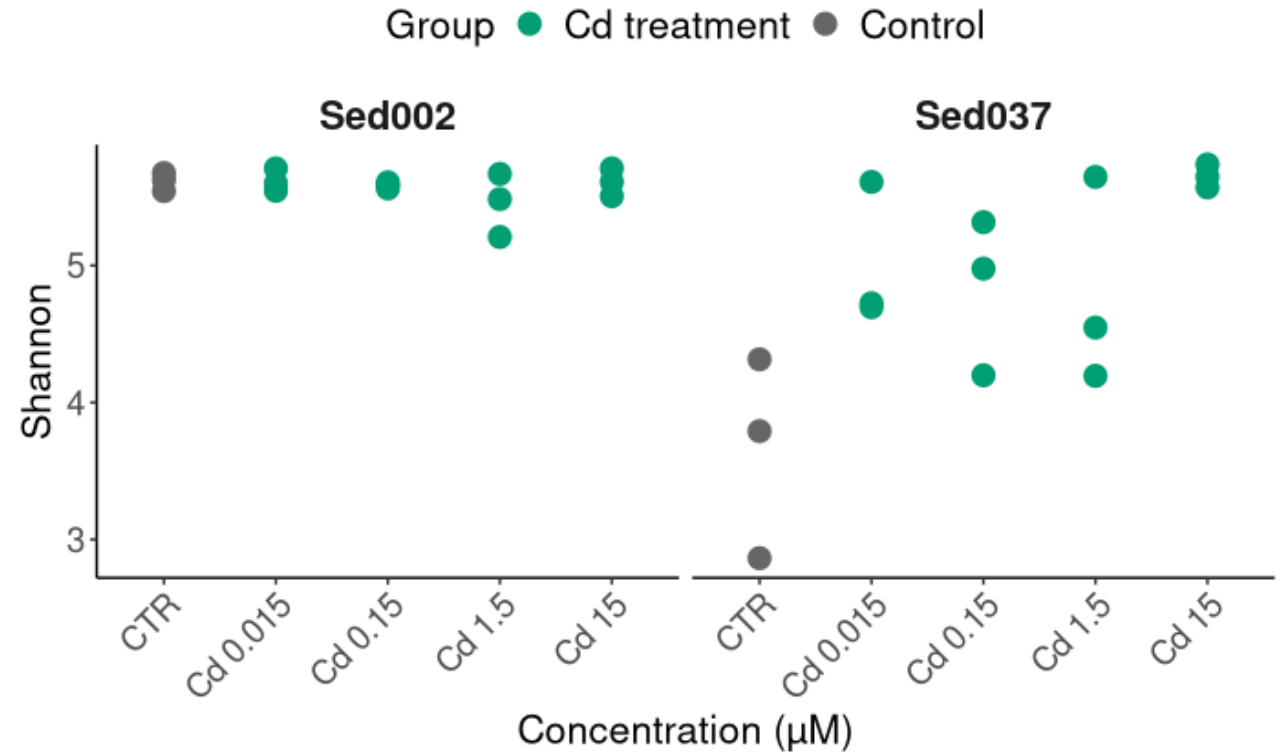
**BIOPORTUGAL**  
Químico, Farmacêutica, Lda.

# Summary of results

- Clean data, which can be readily used for or analyses;
- Alpha diversity;
  - How diverse are our samples;
- Taxonomy;
  - What is present in our samples;
- Beta diversity;
  - What are the shifts in community composition across samples.

# Recall alpha diversity (1)

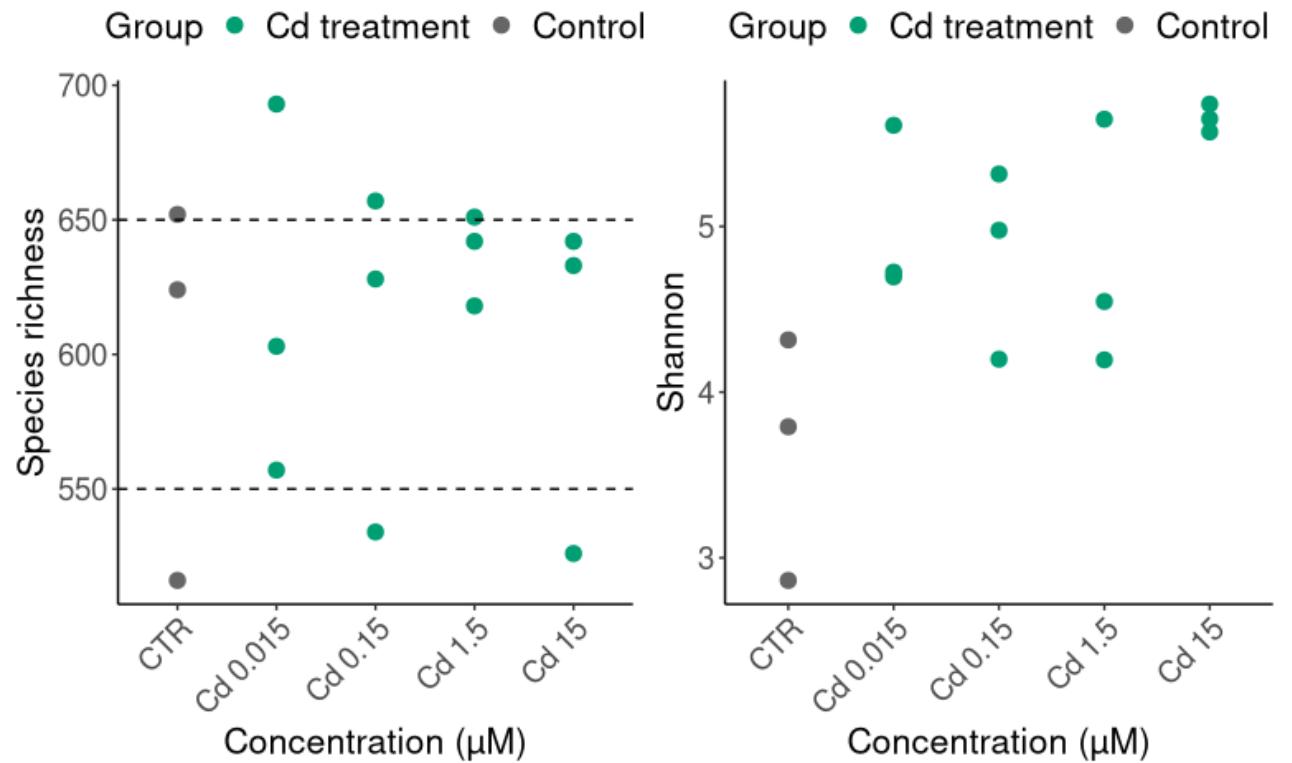
- Shannon index illustrated different diversity trends between Sediments 2 and 37;
  - Constant diversity in Sed002;
  - Increased diversity after treatment in Sed037.



# Recall alpha diversity (2)

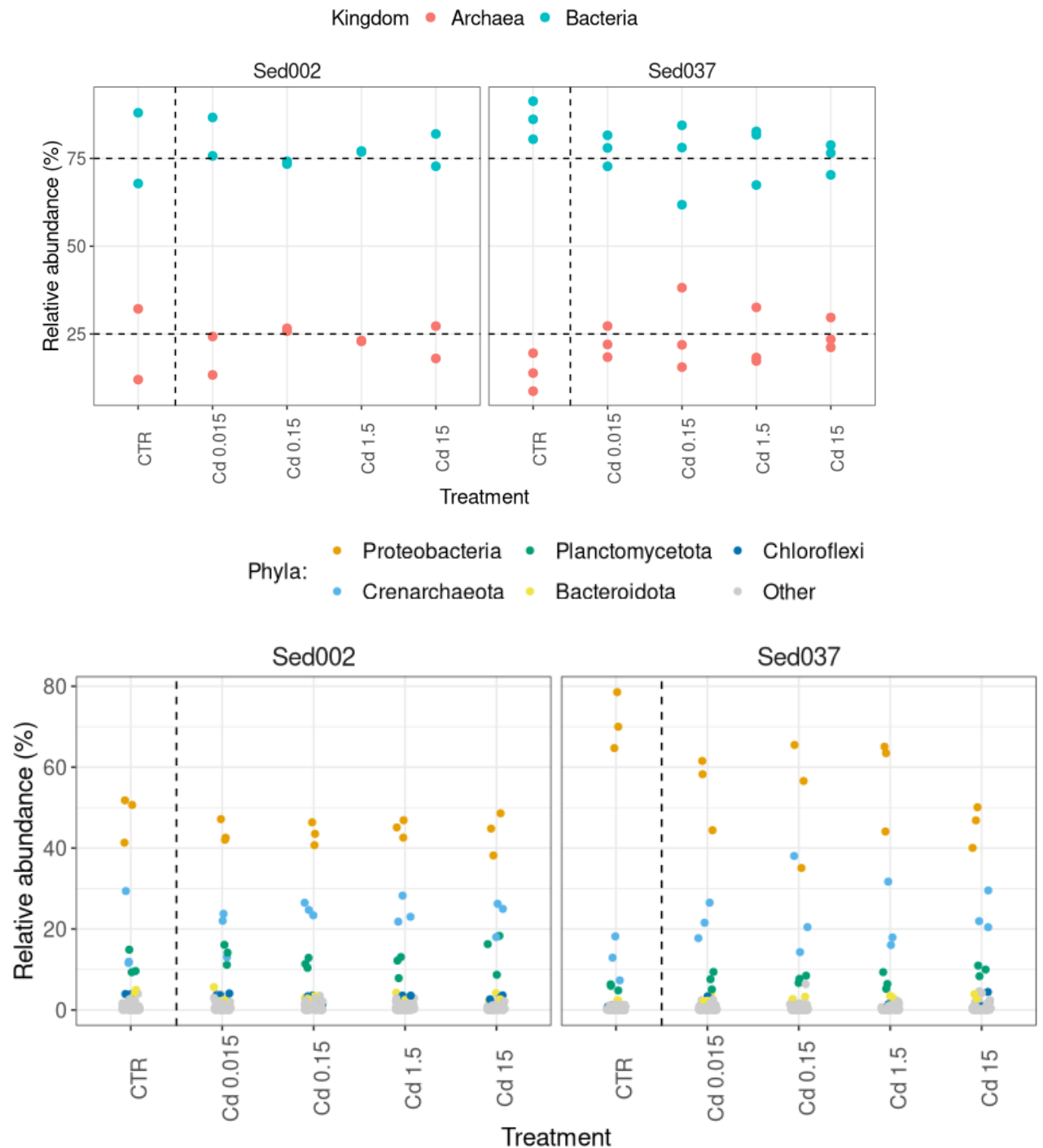
- There was no clear trend in Species richness;
- Shannon index increased after Cd treatment;
  - The Shannon index significantly increased between CTR and Cd 15 (one-way ANOVA + Tukey test).

## Sed 37



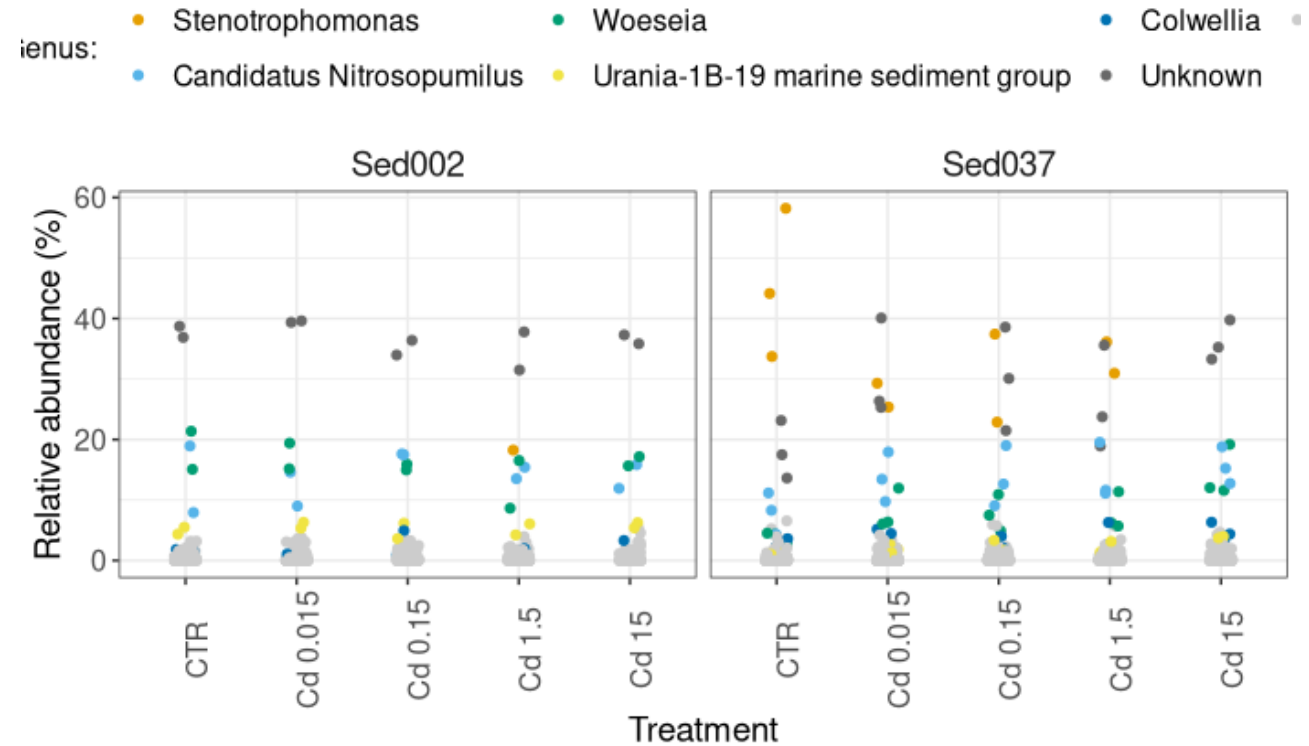
# Recall taxonomy (1)

- At **Domain level**, we can already see differences between Sediments 2 and 37:
  - Bacteria decrease;
  - Archaea increase.
- At **Phylum level**, it becomes clear that some **Proteobacteria** group was responsible for the differences between Experiments 2 and 37.



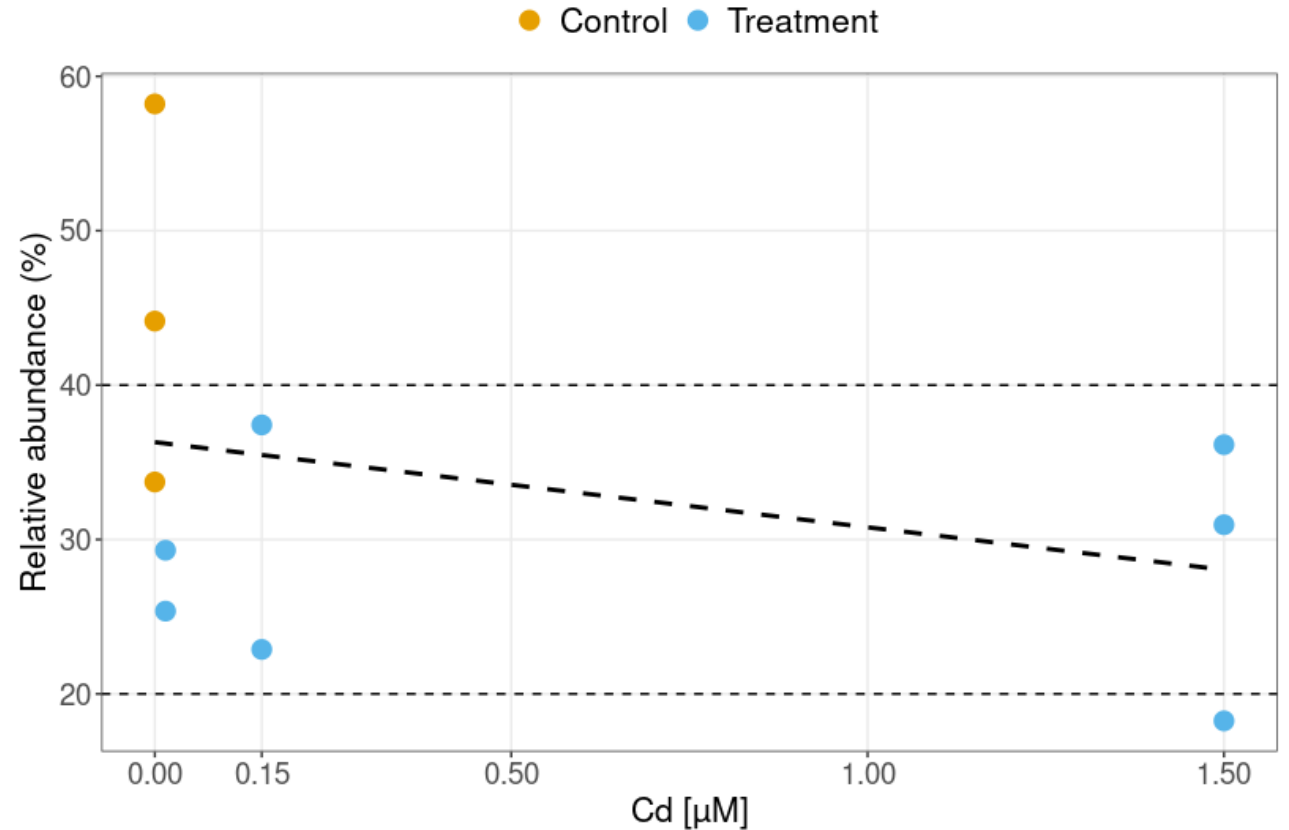
# Recall taxonomy (2)

- An overview of Genus level quickly highlighted **Stenotrophomonas** as the culprit of the major differences between Experiments 2 and 37;
- There was an increase in relative abundance of **unknown genera** after Cd treatment in the sediment 37;
- Candidatus Nitrosopumilus also increased, but it was less visible.



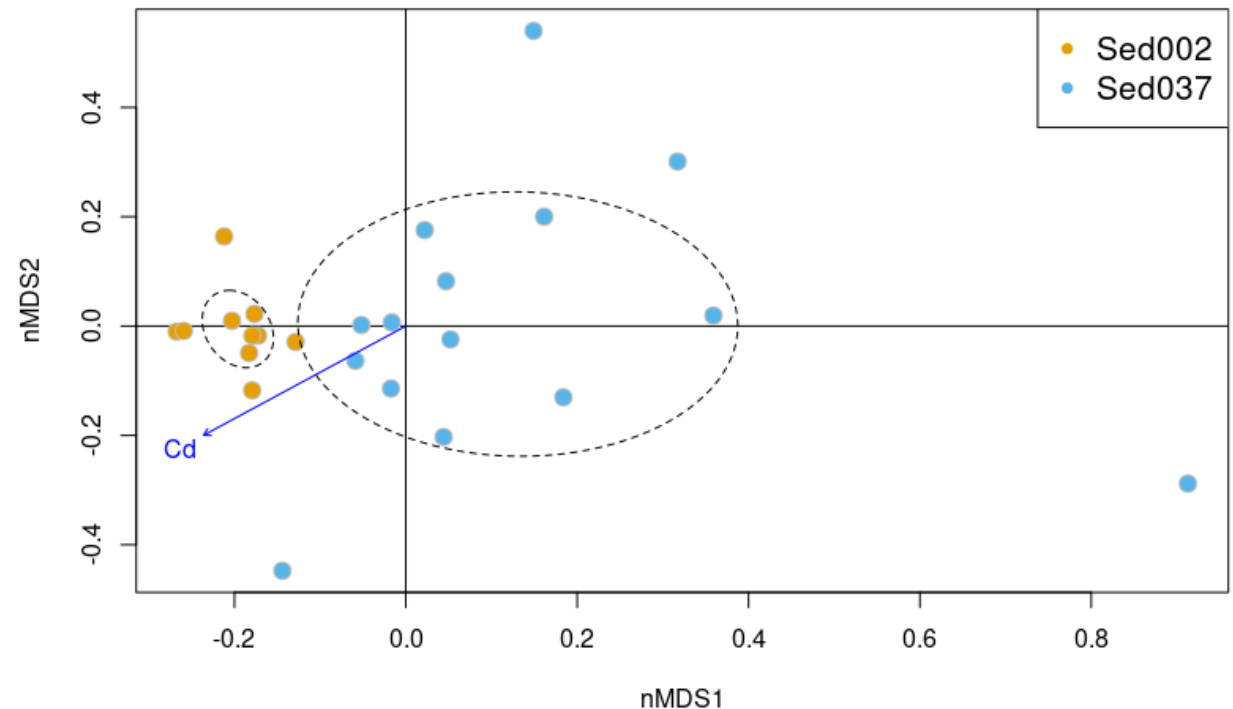
# Recall taxonomy (3)

- After closer inspection, we discovered that *Stenotrophomonas* was more abundant in the Control group, but decreased its relative abundance after Cd treatment;
- However, there was no trend after increasing concentrations of Cd.



# Recall beta diversity (1)

- Both sediments presented distinct community compositions;
- The sediment 37 presented most of the community composition variability.
- PERMANOVA confirmed that any differences in community composition were mostly derived from the source sediment and not from Cd treatments.





# Conclusions

- The two sediments represented different microbial communities, with distinct responses to Cd treatment;
- The sediments were collected at a very similar place, indicating high local heterogeneity;
- The presence of *Stenotrophomonas* in the control group of sediment 37 seems to have been responsible for the major differences.
- The sediment 37 also included more unknown and *Candidatus Nitrosopumilus* genera, which grew upon Cd treatment.