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# Seasonal dynamic of benthic communities in coastal marshes (Charente-Maritime, France)

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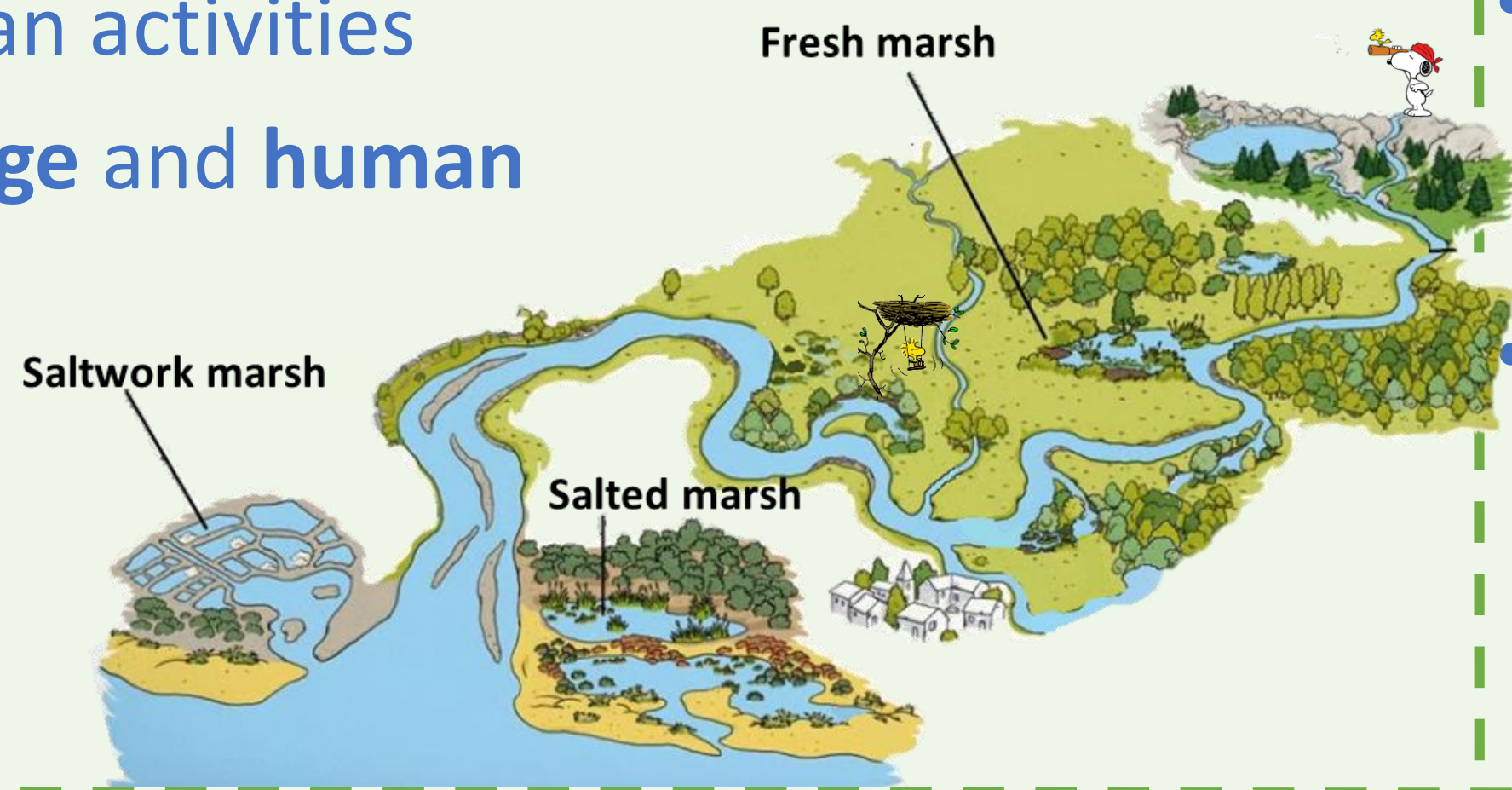
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INTRODUCTION

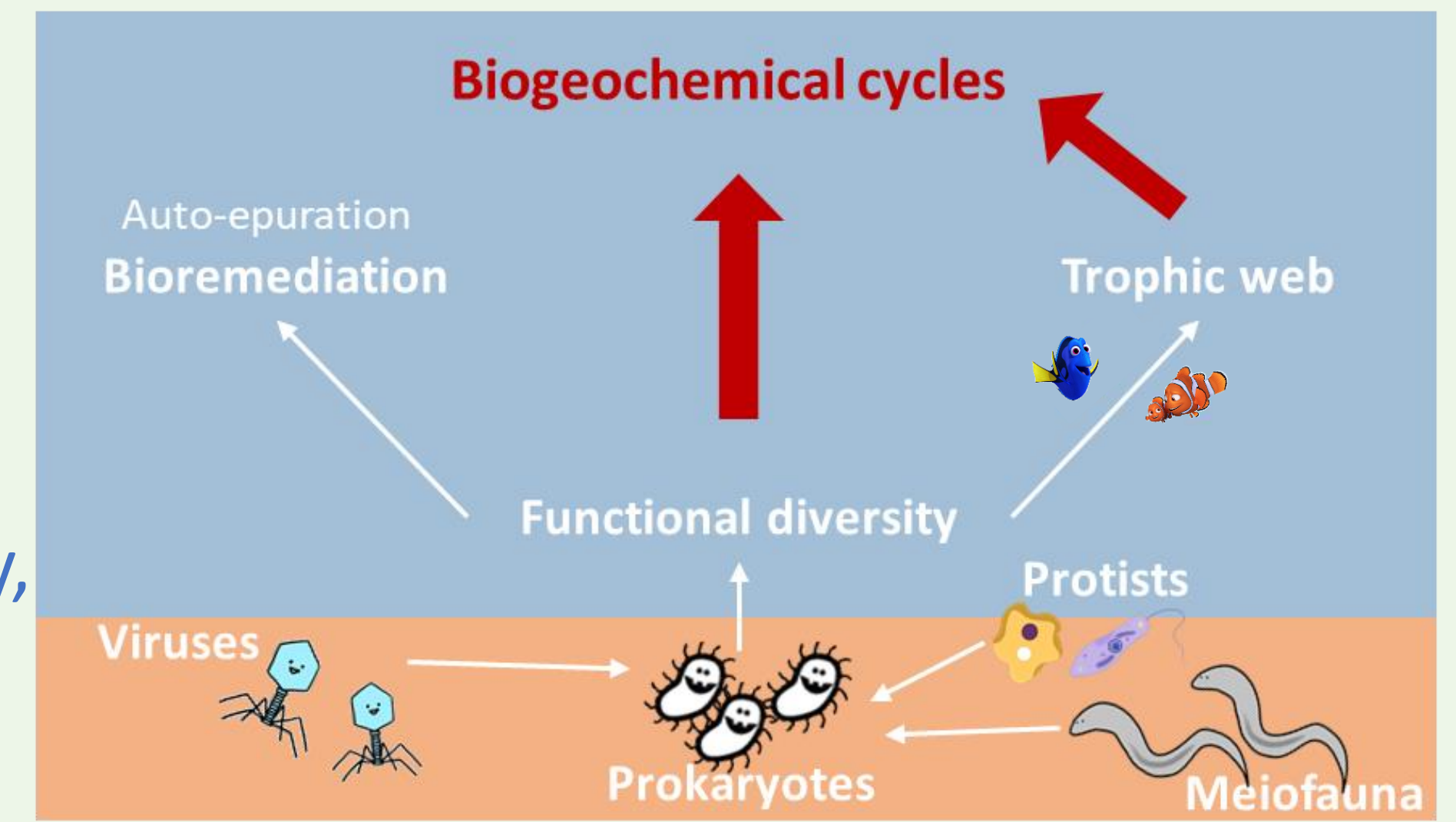
## Marshes environments

- Vast diversity of environment and habitats
- Ensure ecosystem services thanks to their microbial communities
- Largely exploited for human activities
- Impacted by climate change and human activities



## Microbial benthic communities

- Are at the basis of trophic webs in sediments thanks to their functional diversity
- Regulated by biotic parameters such as trophic interactions
- Affected by abiotic parameters (e.g. salinity, temperature, light, nutrients, pollutants,...)



## Assessing the seasonal dynamics of marshes with different salinities in order to better understand parameters regulating benthic communities interaction and abundances

METHODS

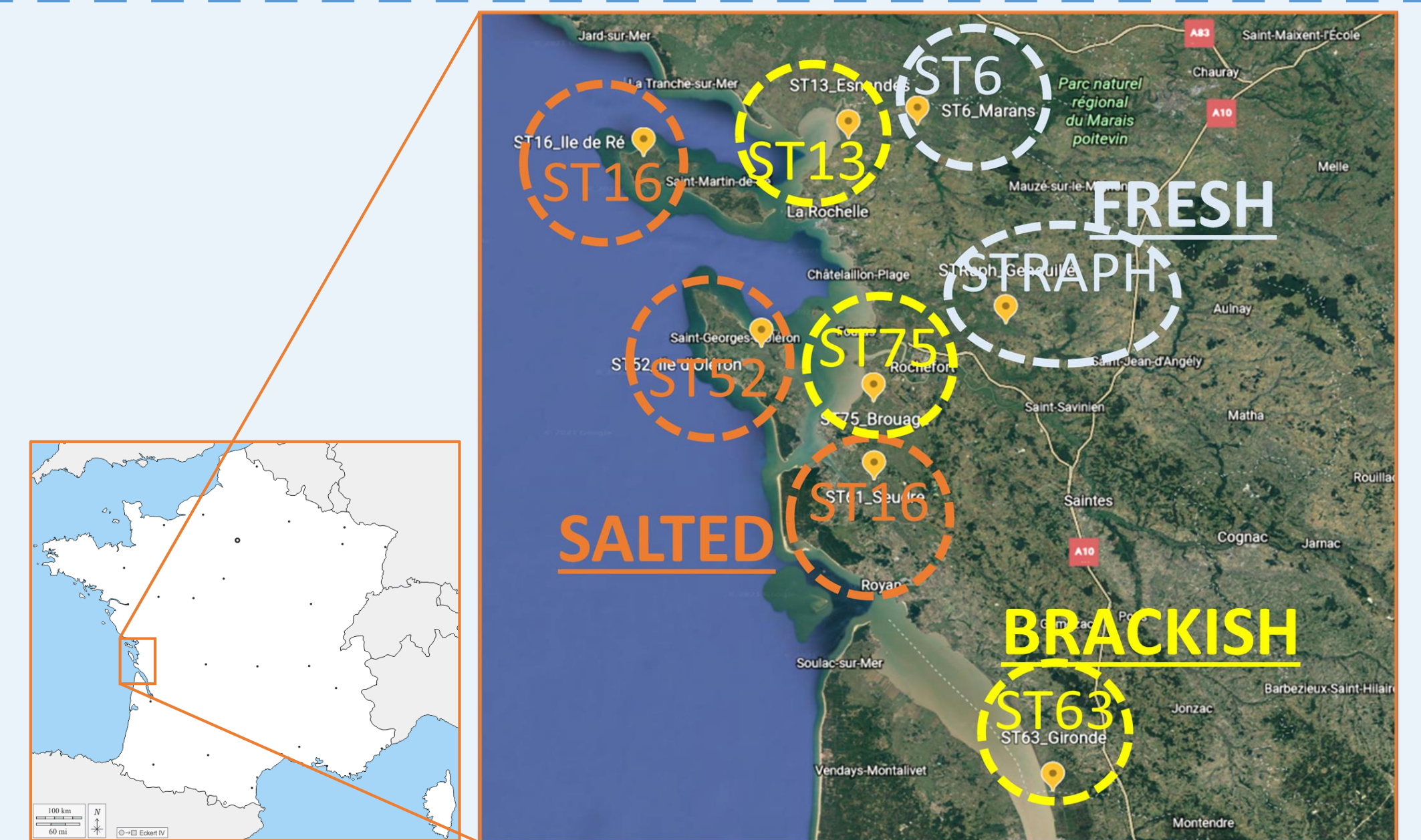
### A four season monitoring comparing 8 Marshes of various salinities analysing

#### Biotic parameters

- Prokaryotic abundance (flow cytometry)
- Meiofaunal abundance and diversity (magnifying glass)
- Chlorophyll *a* biomass (fluorimetry)

#### Abiotic parameters

- Nutrients ( $\text{NH}_4^+$ / $\text{NO}_3^-$ / $\text{NO}_2^-$ / $\text{PO}_4^{3-}$ / $\text{Si}$ )
- *In situ* parameters (pH/RedOx/Salinity/Temperature)
- Metals
- Granulometry
- Water content
- Dissolved Organic Carbon (DOC)



RESULTS

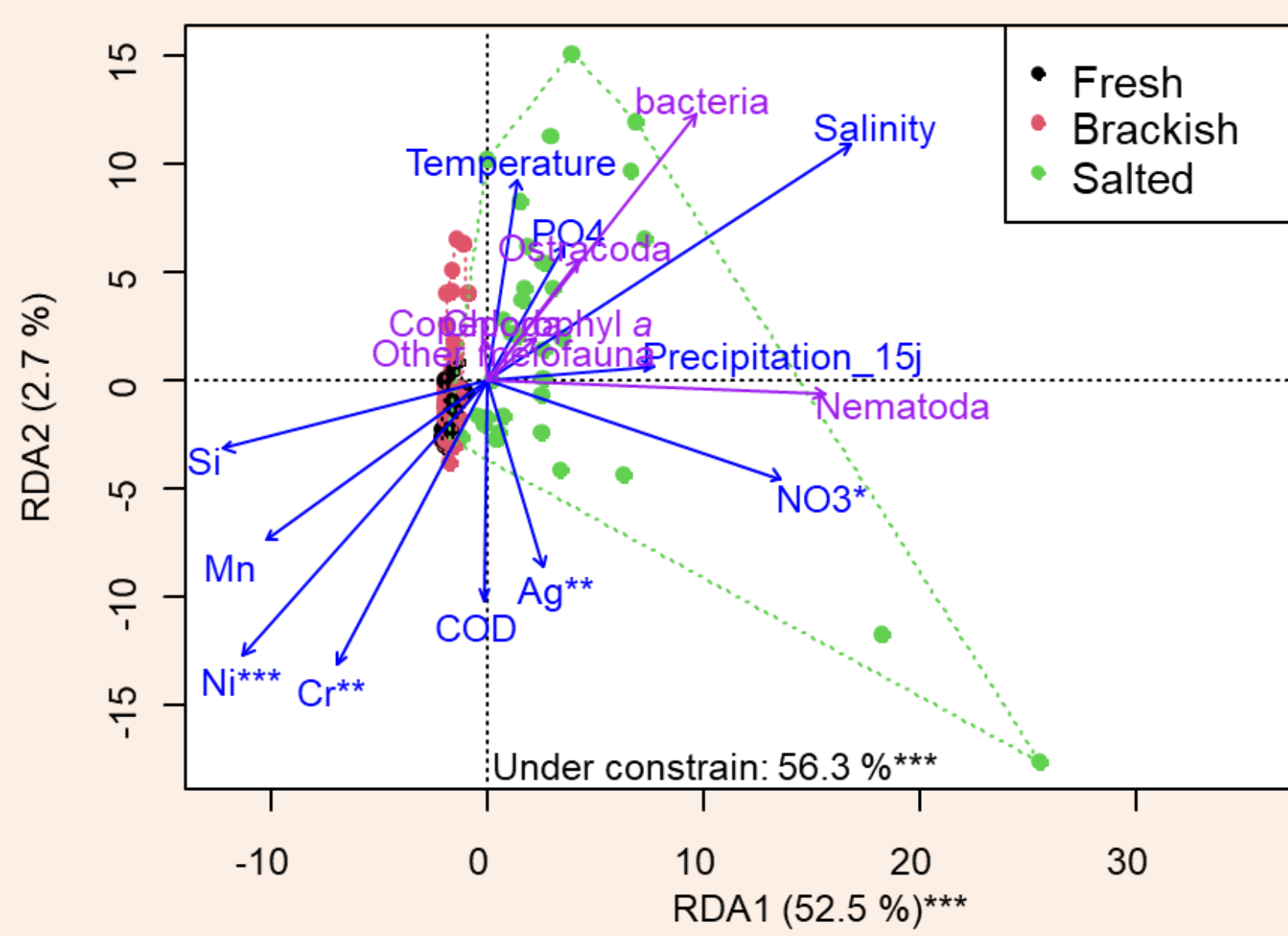


Fig 1: RDA analysing biotic parameters against abiotic factors for all sites. Significativity was tested with ANOVA (\*\*\*)  $< 0.001$ ; \*\*  $< 0.01$ ; \*  $< 0.05$ .

Separation of the samples depending on salinity

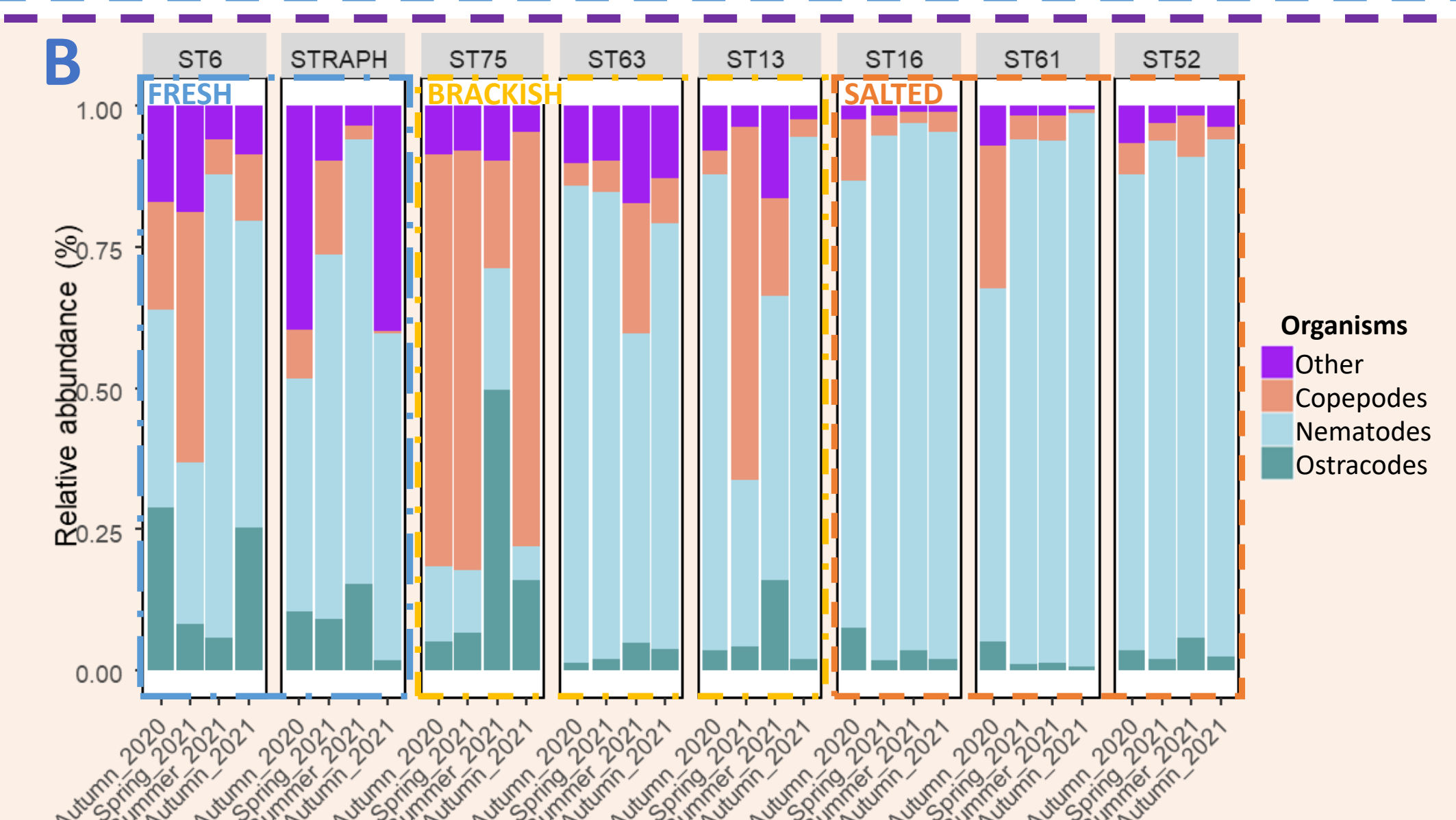
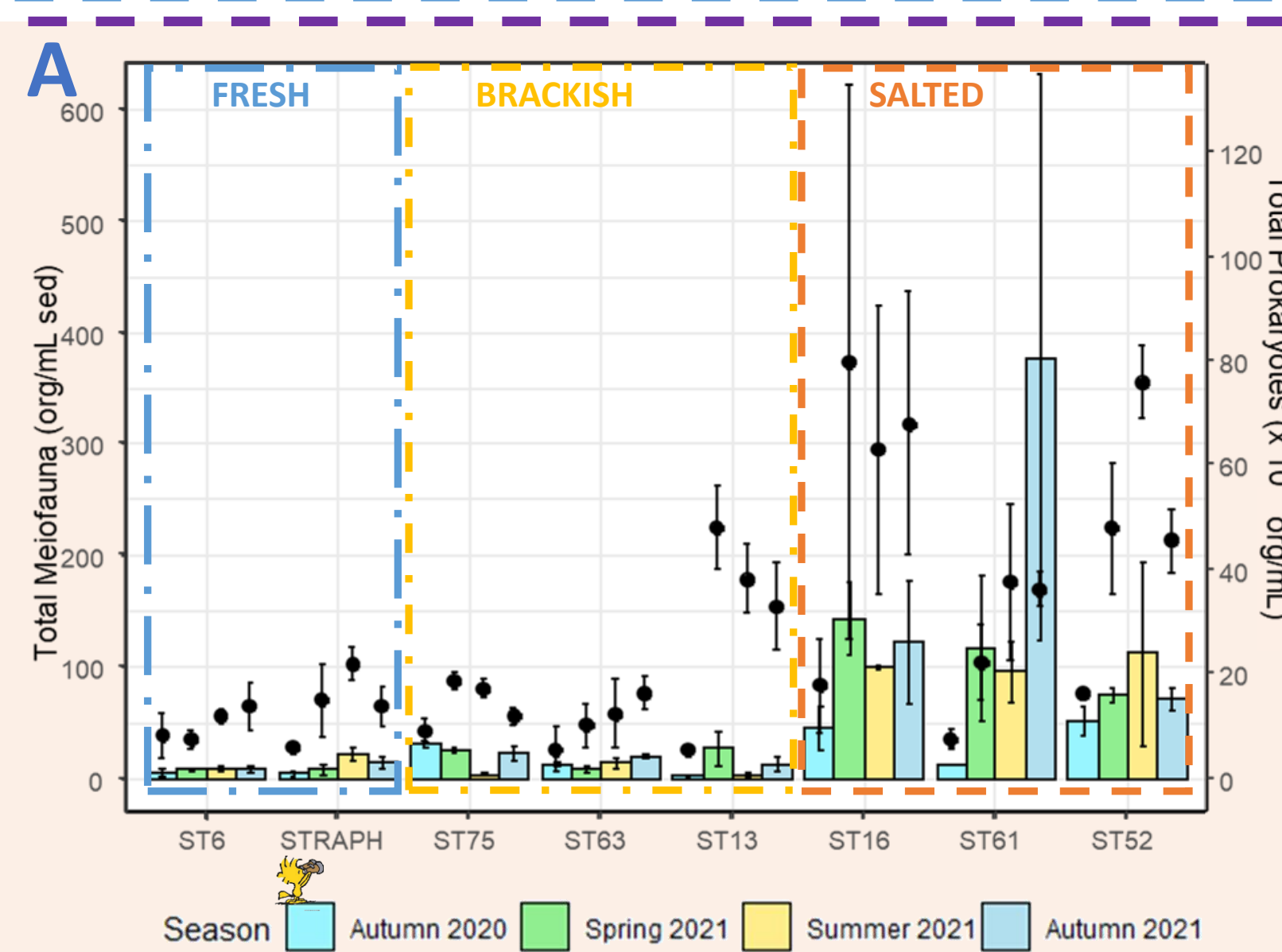


Fig 2: Meiofaunal (bars) and prokaryotic (dots) abundances (A) and meiofaunal composition (B) for all sites.

- Salted sites presented a higher meiofaunal abundance\*\*\* dominated by Nematodes.
- Fresh and brackish samples had lower meiofaunal abundance with higher proportion of copepods\*, ostracods\*\* and other organisms\*\*\*.
- Prokaryotic abundance was high in all sites but higher in salted stations\*\*\*.

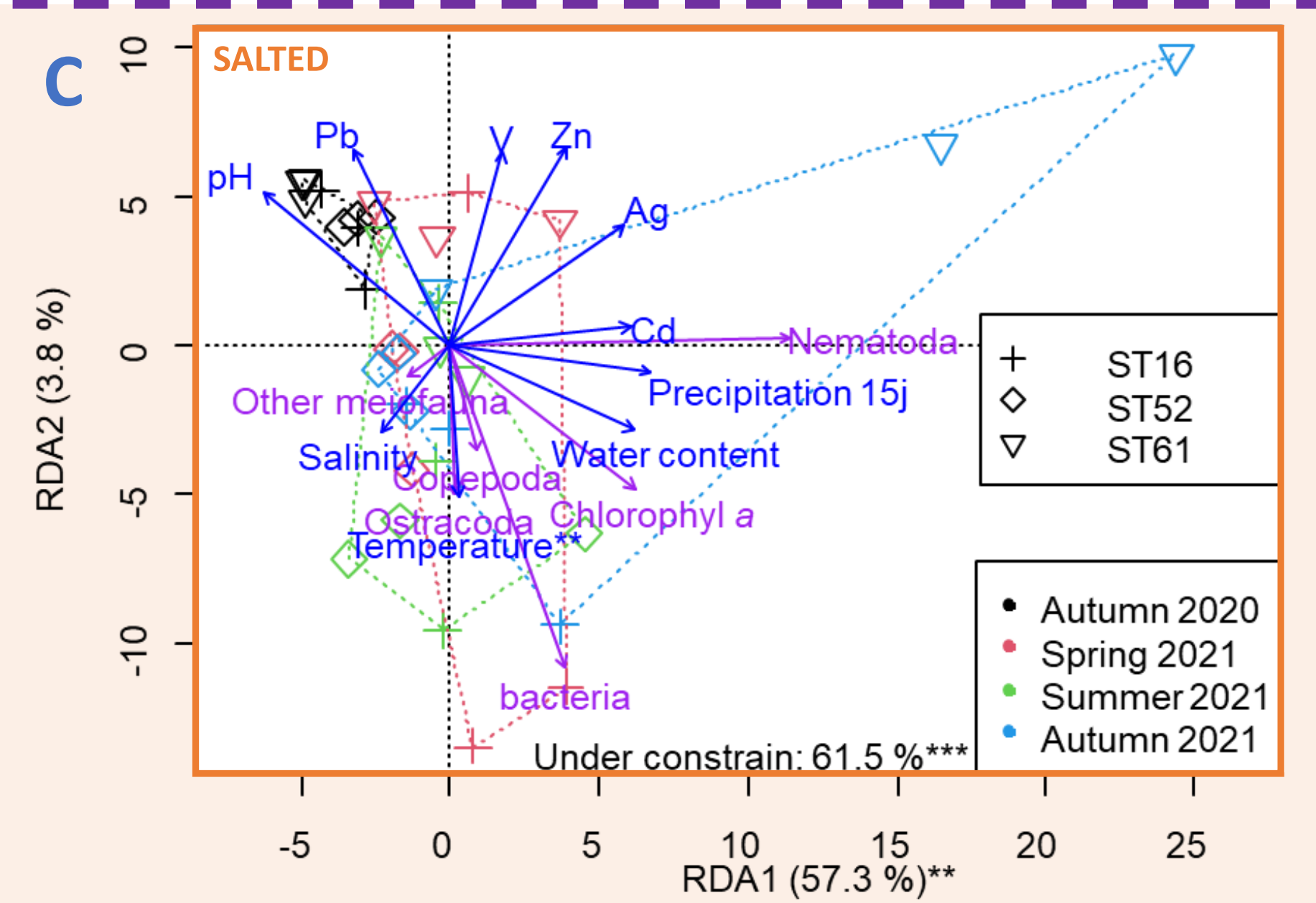
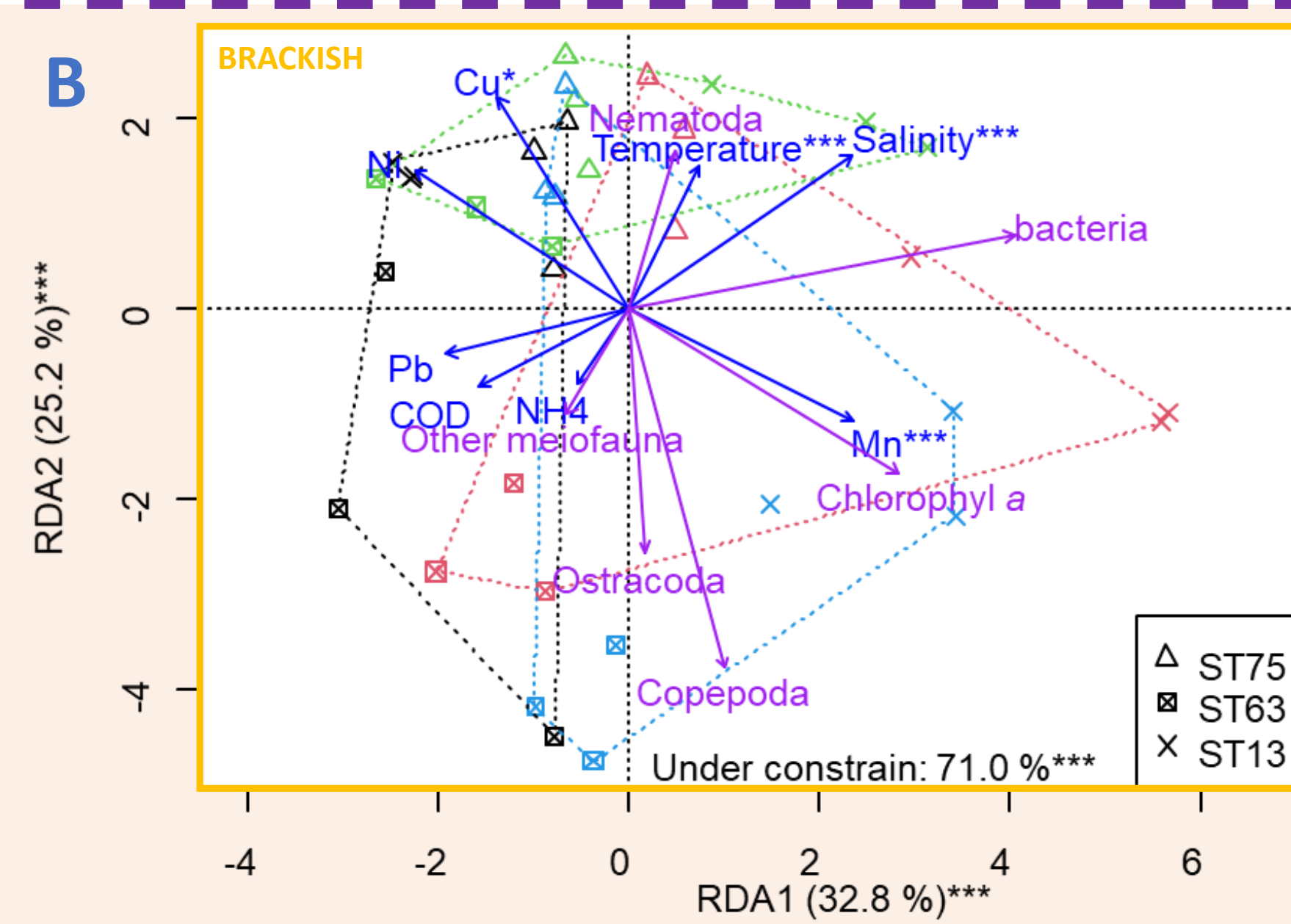
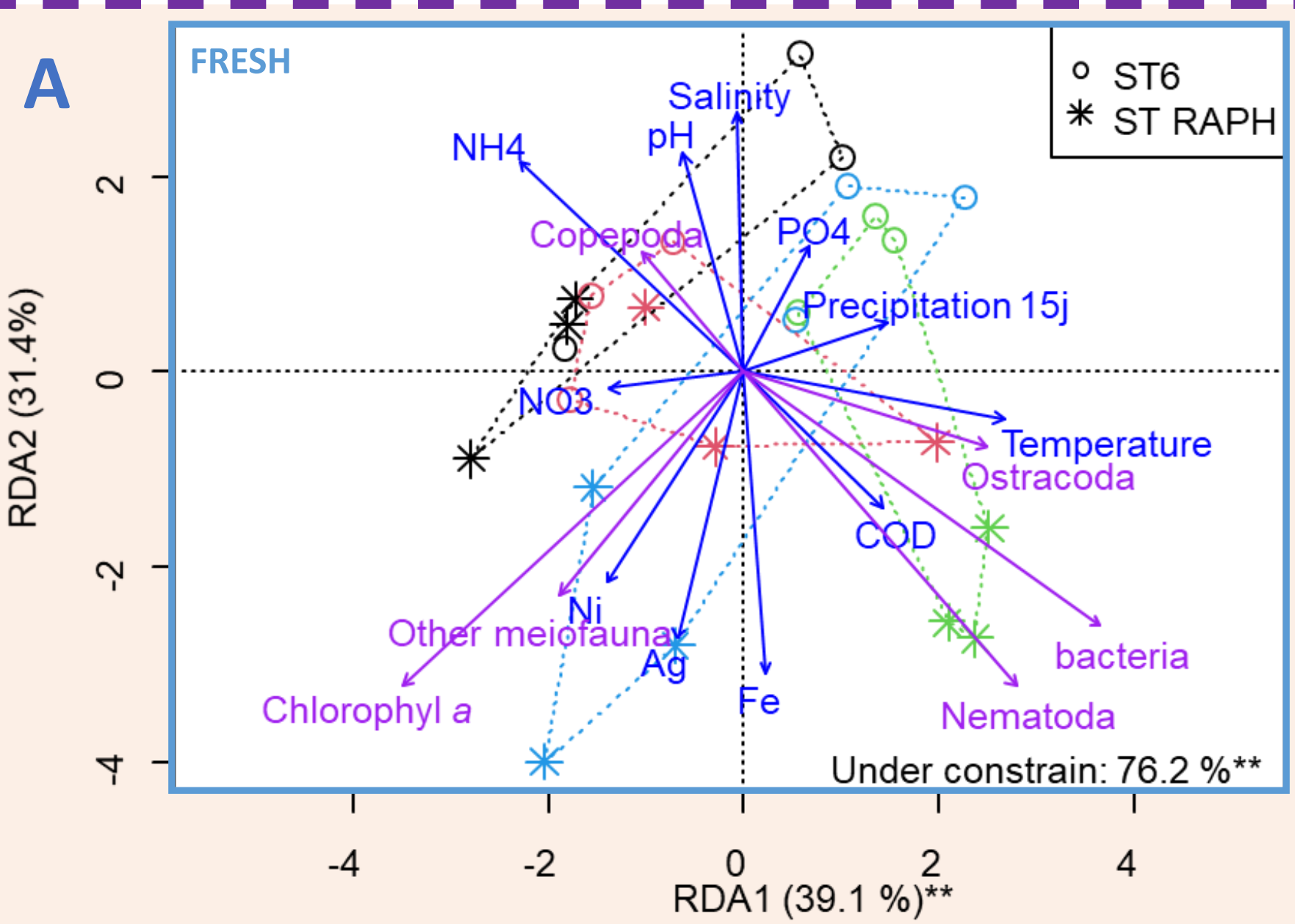


Fig 3: RDA analysing biotic parameters against abiotic factors was conducted separately for fresh (A), brackish (B) and salted (C) sites. Significativities were tested for the total model, axis and variable with ANOVA (\*\*\*)  $< 0.001$ ; \*\*  $< 0.01$ ; \*  $< 0.05$ .

Fresh sites showed the highest seasonal effect. Prokaryotes were more abundant in seasons with higher DOC and temperature and lower  $\text{NH}_4^+$  concentrations.

In brackish sites prokaryotic abundance decreased with salinity and for seasons with high level of Pb and  $\text{NH}_4^+$ . Chlorophyll *a* was lower in sites with high metal concentrations.

The lowest seasonal effect was observed in salted sites. Prokaryotic and meiofaunal abundances were lower in samples with higher metal concentration.

CONCLUSION

- Salinity is the main driver of community variation depicting a clear separation of salted and fresh/brackish marshes with a more pronounced seasonal effect that can be observed in fresh sites.
- Organisms abundances suggest that prokaryotes could be used as good indicators of ecological status in all marsh types and meiofauna in salted marshes.
- Meiofauna, prokaryotes and chlorophyll *a* hinted a sensitivity to metals in brackish and salted sites.
- Environmental DNA analysis will be conducted to understand factors controlling community composition.
- All information gathered will be useful to define potential bioindicators evaluating ecological statuses.