Stronger effects of salinity on bacterial than protist beta but not alpha diversity in the DNA-monitored Baltic Sea area

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Background:

- Well-studied **separation of freshwater** and **marine bacterial communities**.
- **Distinct brackish bacterial species** (Hugerth et al. 2015).
- **No signs of local adaptation of bacteria after the Baltic Sea salination** (Jurdzinski, Mehrshad et al., 2023).
- **Bacterial** and **protist community composition shift along the brackish salinity gradient** (Herlemann et al. 2011, Hu et al. 2016).

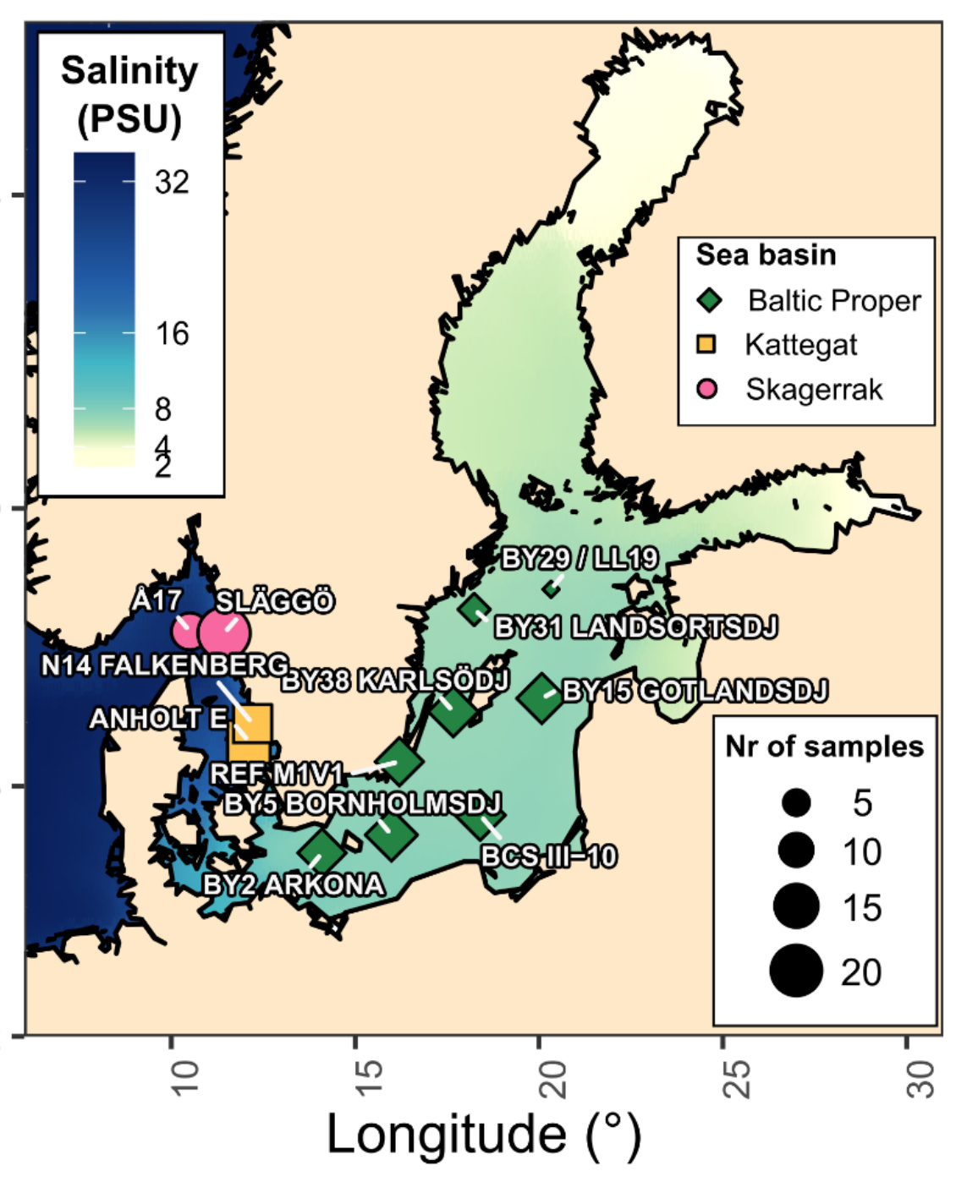
Conclusions:

- **Salinity** has a **dominant** impact on **bacterial but not protist beta diversity.**
- **Protist alpha diversity increases with salinity**, while **bacterial alpha diversity increases in winter.**
- **Protist diversity pattern** can be explained by **gradual local adaptation**, and **bacterial diversity pattern** by **niches being filled by migration.**

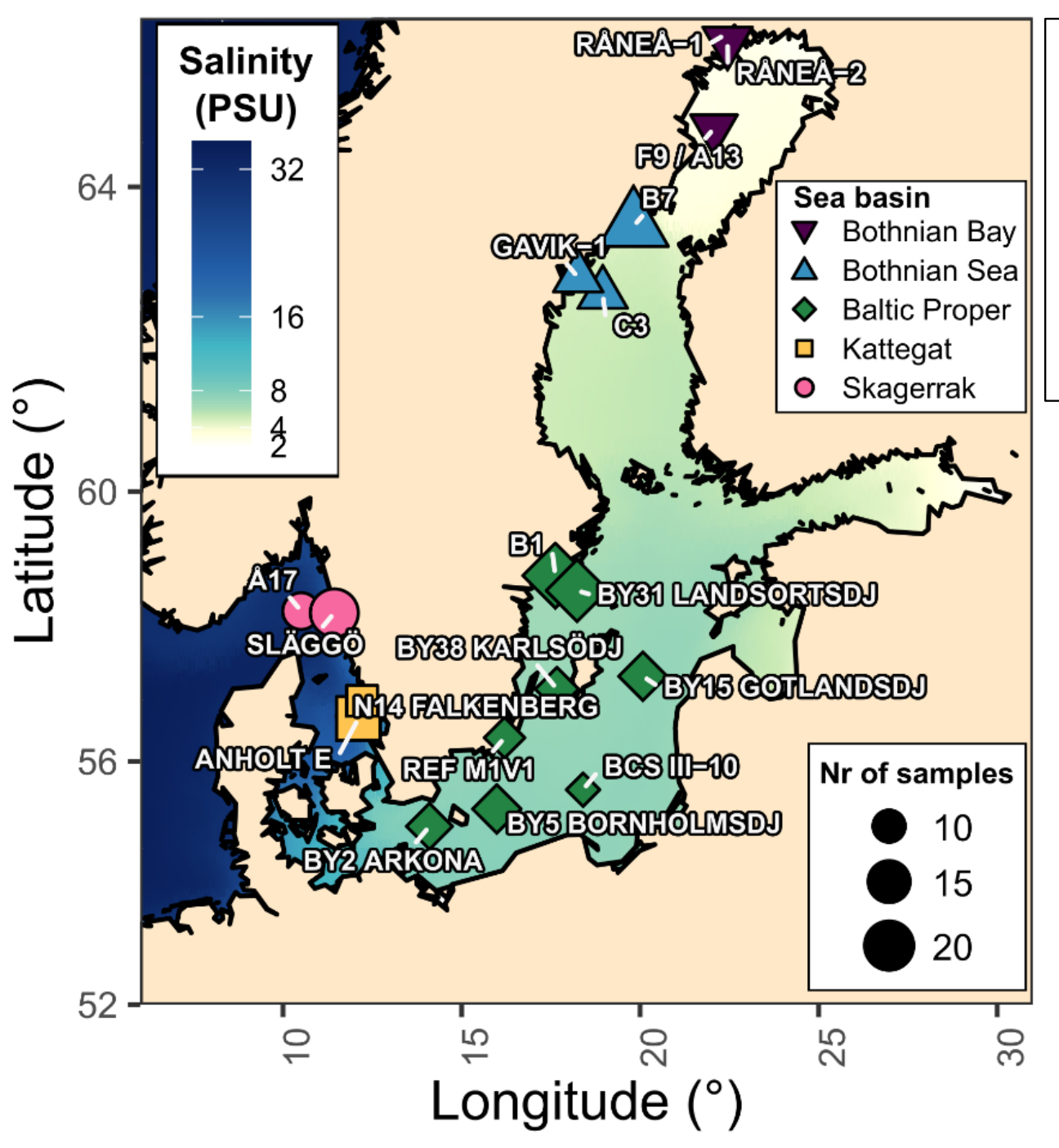
Material and methods

16S and 18S metabarcoding combined with Swedish marine monitoring program

2016-2017 (new)



2019-2020
available at: scientific **data**



Seq. data

Sequencing data processing

- **Denoise**, **infer amplicon sequence variants (ASVs)**, and **taxonomically annotate** using: DADA2

Implemented using nf-core/ ampliseq

Reference databases:

18S PR2

16S GTDB

Remove chloroplasts and mitochondria silva

- Additional **chimera removal** UCHIME
- **Cluster ASVs by sequence and distribution similarity** into **dbOTUs**. dbOTU3

dbOTUs should represent **species or higher taxonomic levels** (no intraspecies variation; usually genera)

Full study: **Distinct bacterial and protist plankton diversity dynamics uncovered through DNA-based monitoring of the Baltic Sea**

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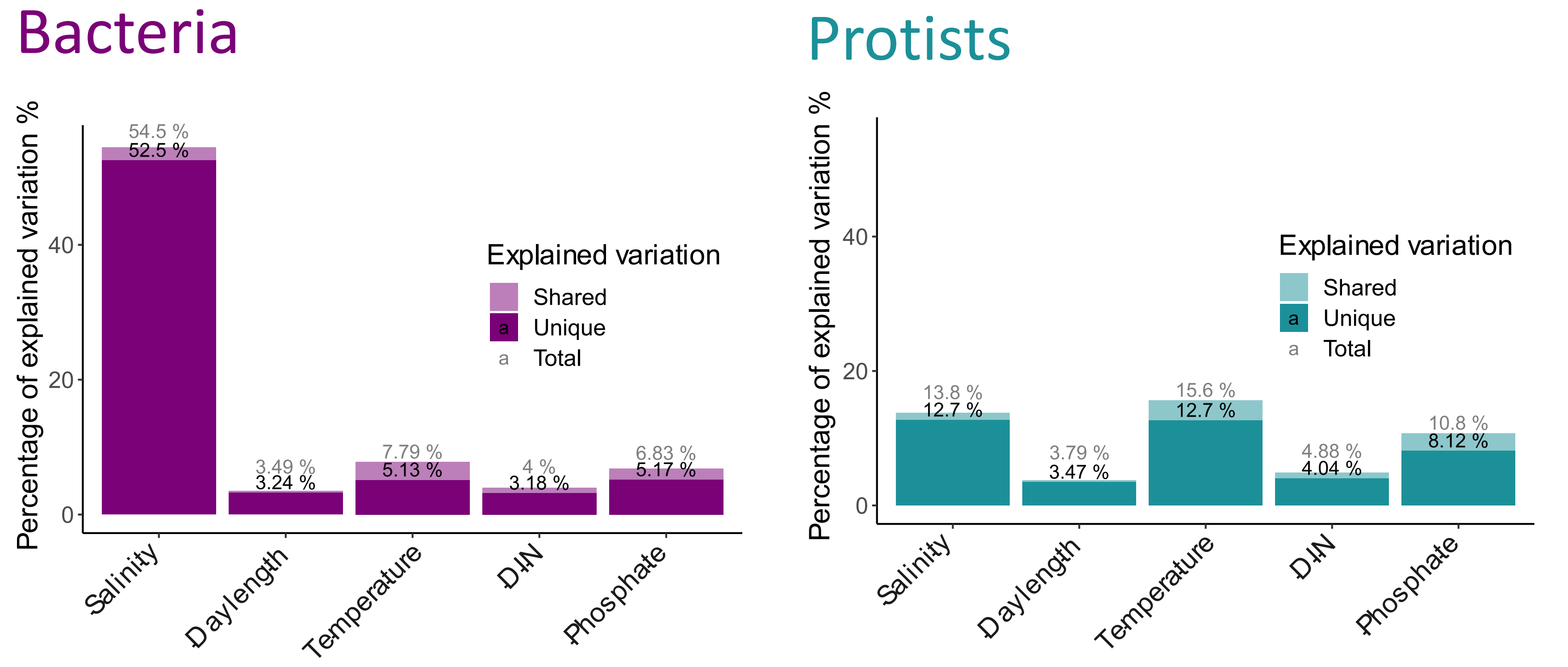
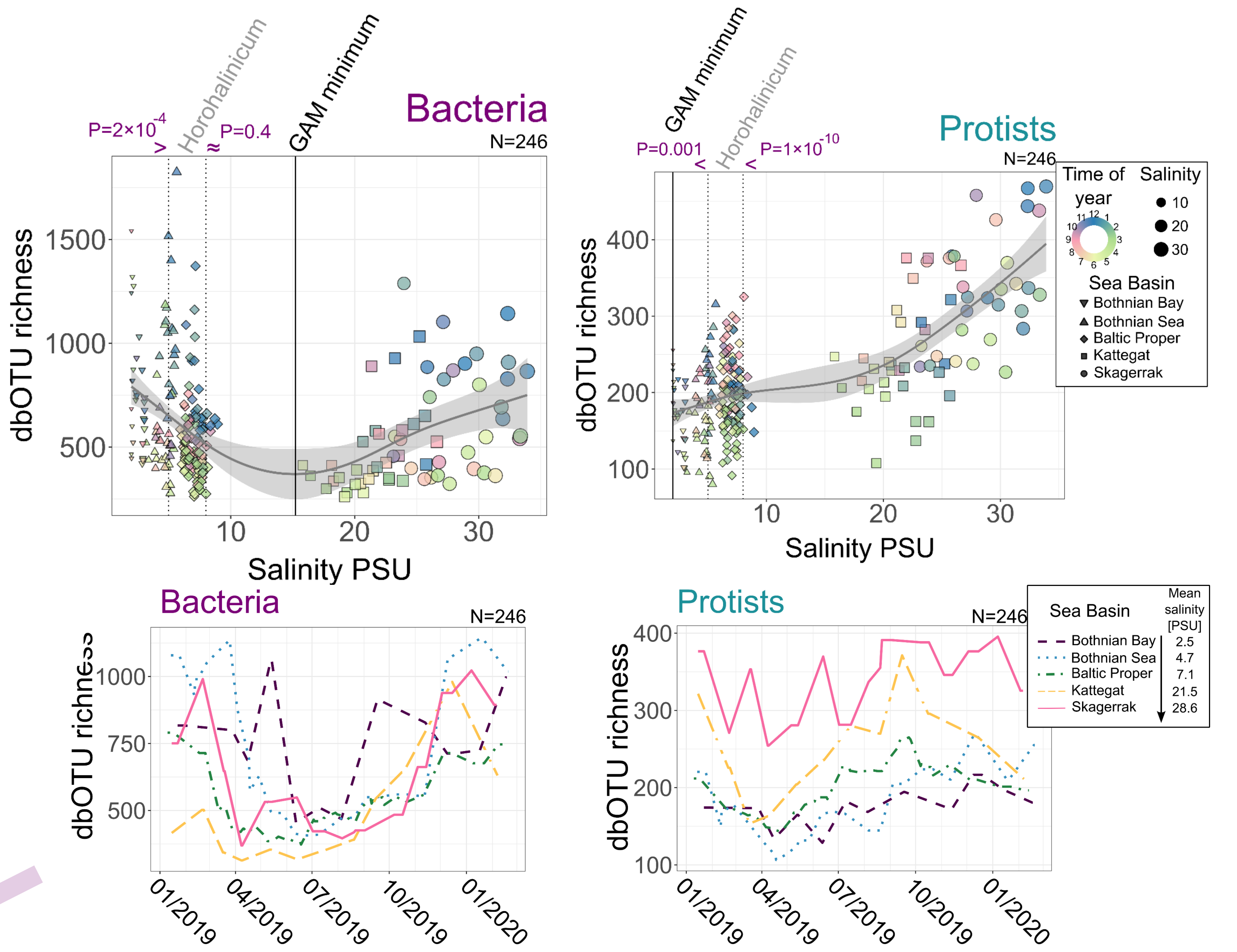
Results

1. Higher impact of salinity on bacterial than protist beta diversity



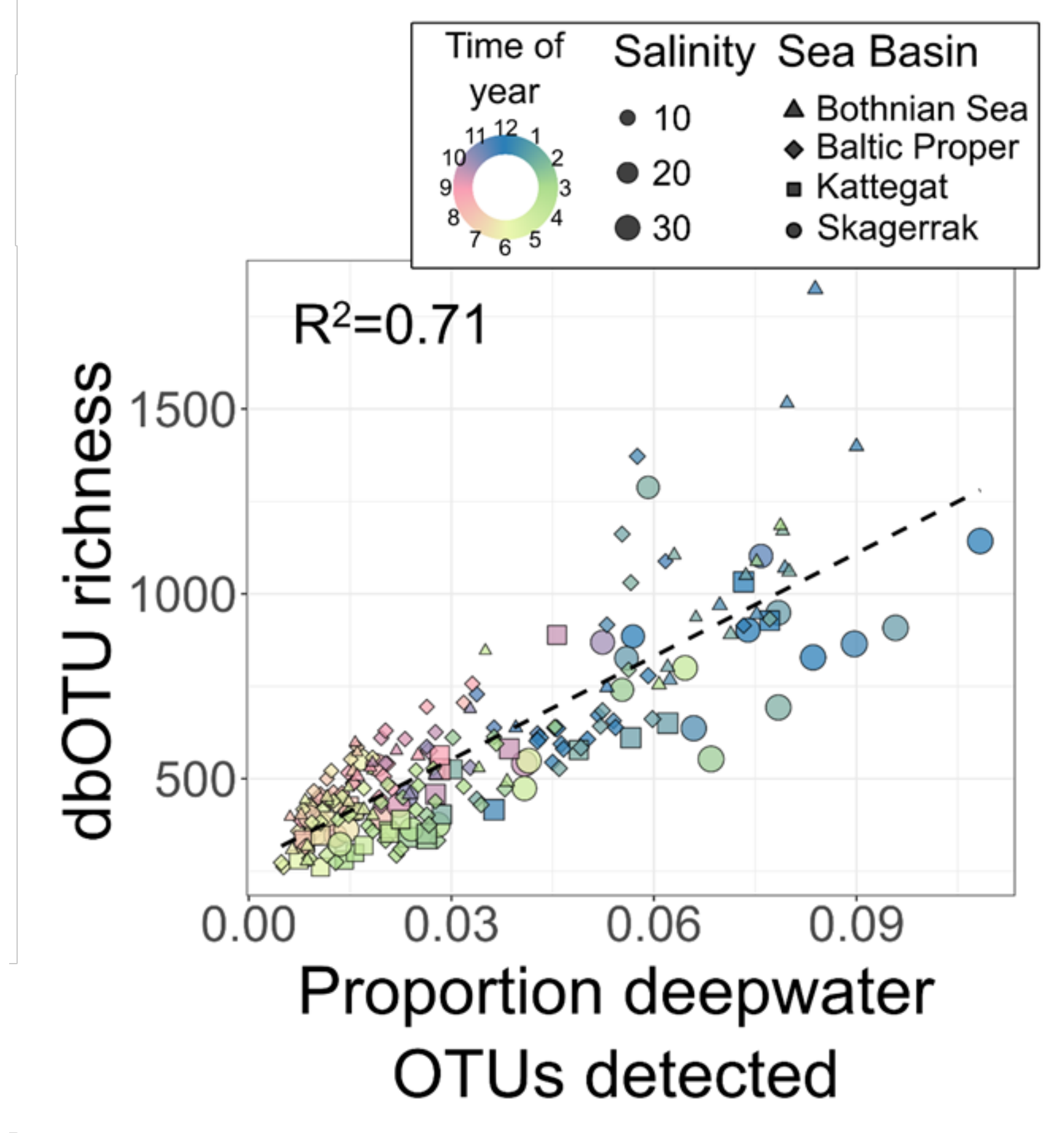
dbRDA-based variance partitioning of impacts of selected environmental variables on bacterial and protist dbOTU-based community composition

2. Protist but not bacterial alpha diversity increases with salinity



Salinity-dependent (top) and seasonal patterns (bottom) of bacterial and protist alpha diversity

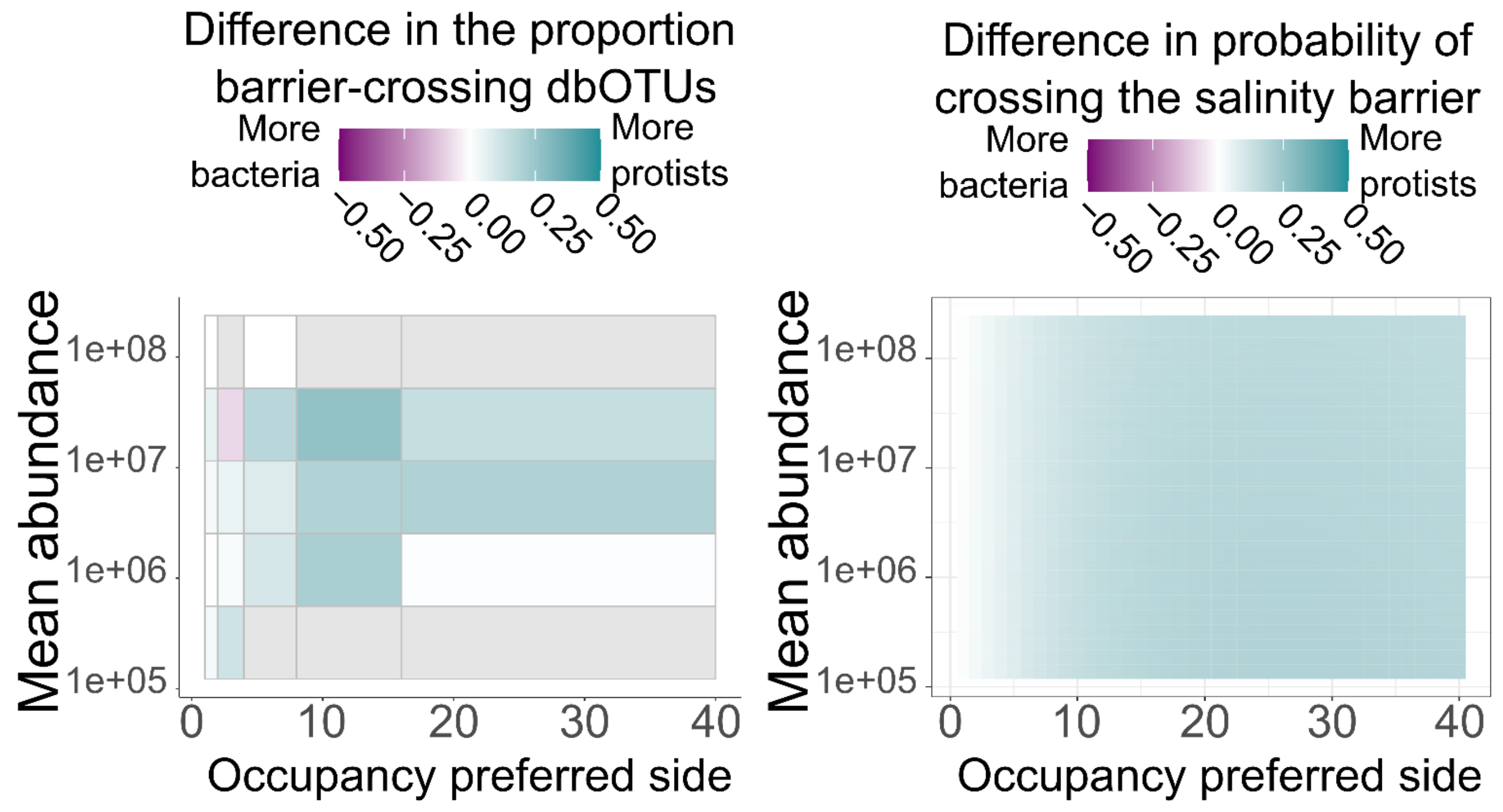
3. Winter convective mixing increases observed alpha diversity



Using data from Herlemann et al. 2016

Bacterial alpha diversity as a function of the proportion of deepwater OTUs from Herlemann et al. 2016 having matches among the dbOTUs in a sample.

4. Protists inhabit both low (<9 PSU) and high (>15 PSU) brackish salinities more often than bacteria



Difference in **proportion of barrier-crossing bacterial and protist dbOTUs (left)** and **probability a dbOTU is found in both low and high brackish salinities (right)**; based on **Bayesian modeling**). Both are given as a function of mean abundance (when present) and maximum abundance at the preferred side of the salinity barrier.

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