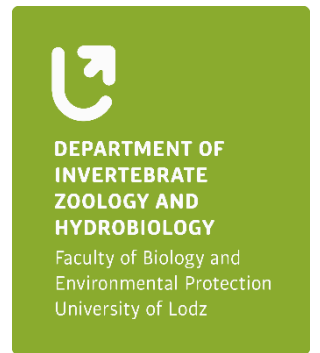


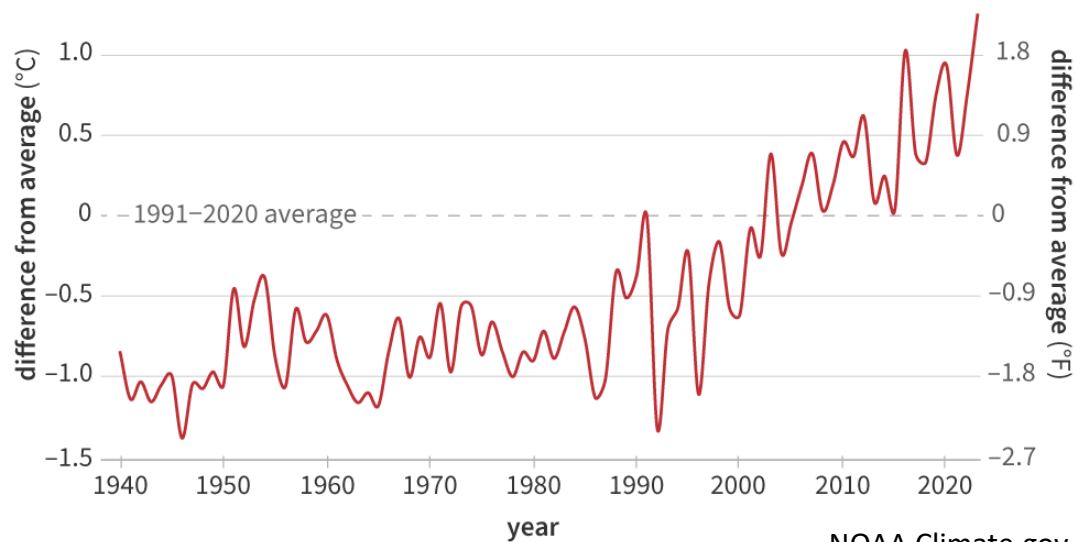
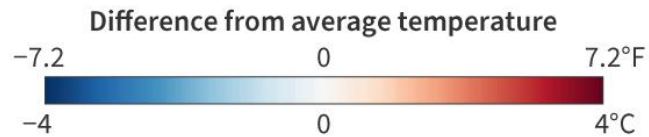
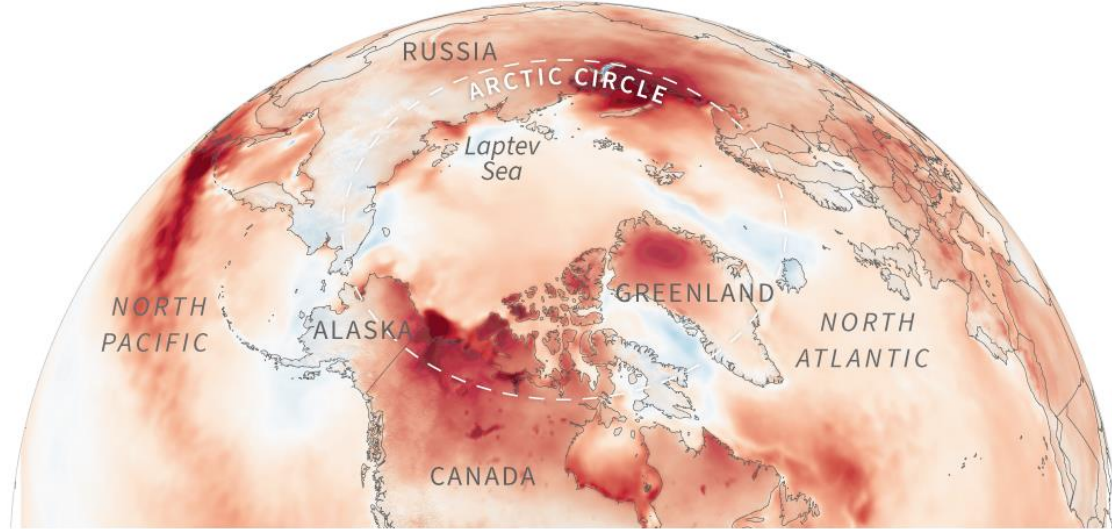
Response of macrofaunal, eukaryotic and prokaryotic diversity to environmental stressors in Arctic coastal waters



Mikołaj Mazurkiewicz, Agata Zaborska, Joanna
Legeżyńska, Ksenia Pazdro, Anna Pouch, Jan
Pawłowski, Maria Włodarska-Kowalczyk



Climate Change in the Arctic and Its Effects



NOAA Climate.gov

Some of key drivers

- Glaciers retreat and melting
- Increased sediment loads
- Coastal „darkening”
- Sea currents range
- Reduction of sea ice extent and thickness
- Thawing of permafrost
- Increasing pollution from multiple sources
- Primary production changes
- Borealisation of marine fauna

Pollution in Arctic

Heavy metals

Black carbon

Persistent organic pollutants (POPs)

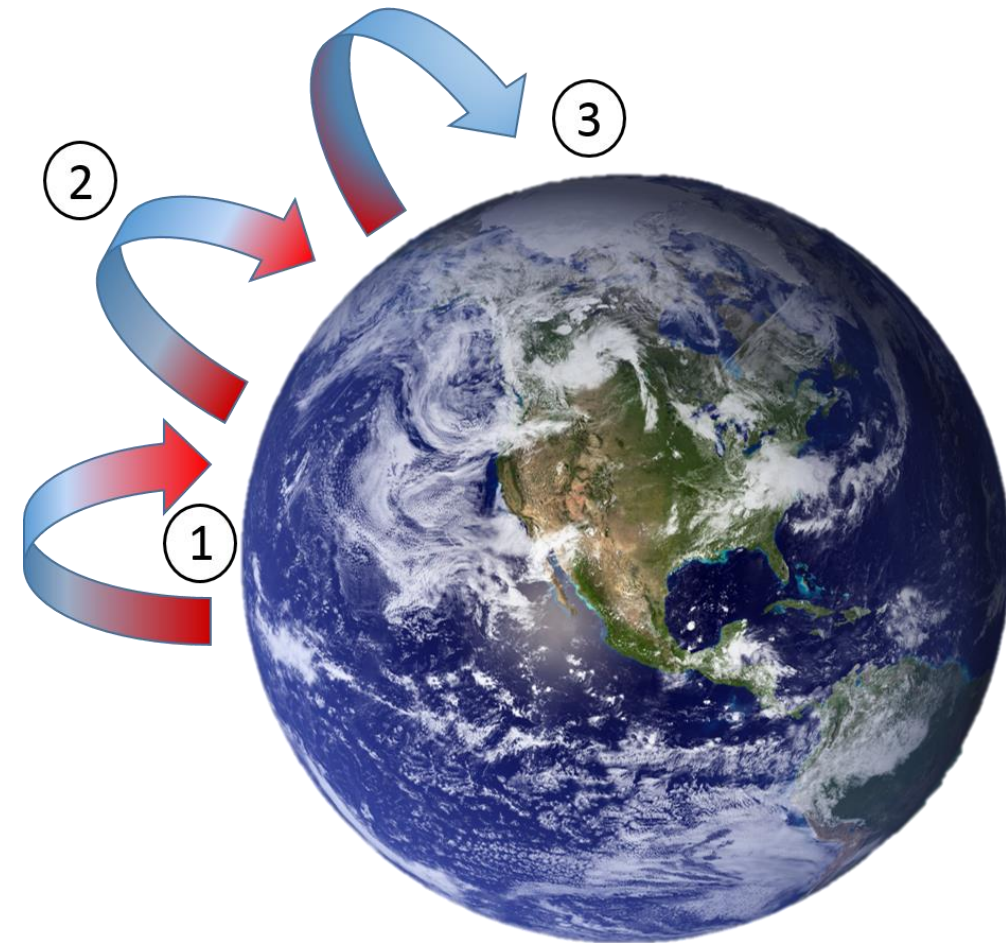
Garbage & plastic

New emerging pollutants e.g.,
pharmaceuticals



Sources

- ❑ Pollutants are transported to the Arctic through atmospheric circulation, oceanic currents and rivers from distant sources.
- ❑ Local human activity is increasing e.g., tourism, cargo traffic, oil and gas exploitation, extensive fisher
- ❑ Secondary sources: glaciers melting and thawing of permafrost



GLOBAL DISTILLATION

<https://earthlyhorizon.wordpress.com/>

Aim

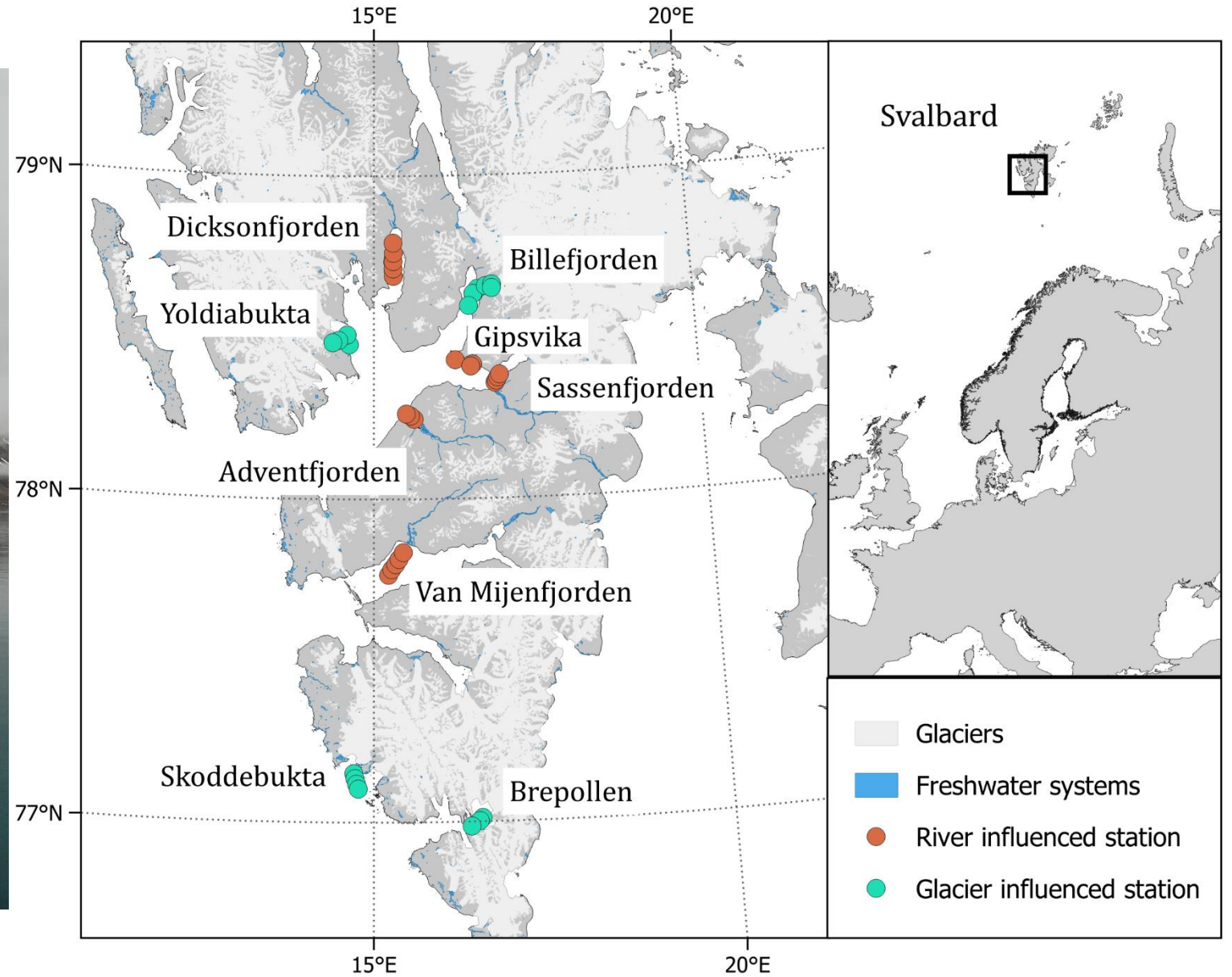
- compare the environmental conditions and macrofaunal (assessed morphologically) and eukaryote and bacterial (sediment eDNA) composition and diversity in glacial and glaciofluvial bays,
- explore the relationships between the biotic communities and environmental variability to assess the response of various taxonomic groups to environmental conditions and determine their sensitivities to natural and anthropogenic stressors



Study area



r/v Oceania (photo K. Deja)



Research methods



van Veen grab



Box corer



Nemisto corer

☐ Macrofauna

☐ Sediments

■ Environmental parameters

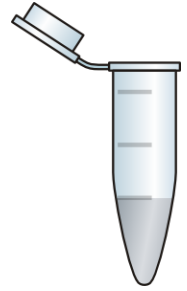


■ eDNA

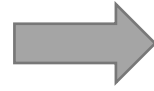
- (~10g of sediments)
- 3 replicates / station

- Chl a, pheophytin
- Grain size
- Sediment accumulation rate
- POC, TOC, TN, $\delta^{13}\text{C}$, $\delta^{15}\text{N}$
- Heavy metals
- PCBs
- PAHs

Molecular methods



DNA extraction using
Qiagen PowerMax Soil Kit
~10g of sediments



PCR amplification with 3
different markers:

- mtCOI
- 18S V1V2 (Eukaryota)
- 16S V3V4 (Bacteria)



NGS sequencing on
Illumina MiSeq



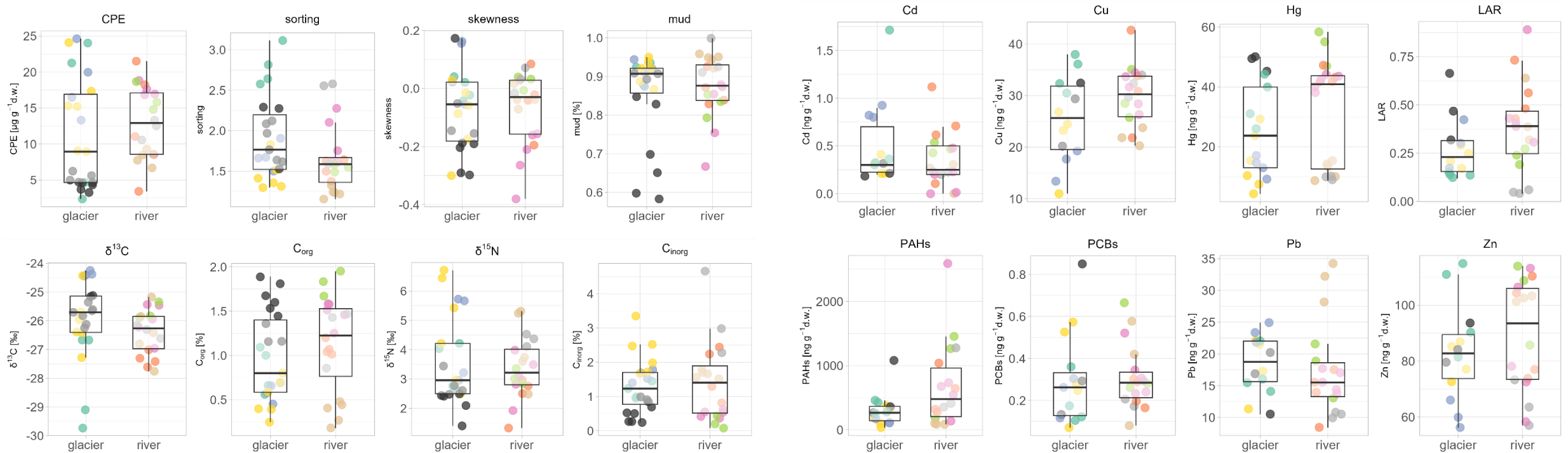
Bioinformatics



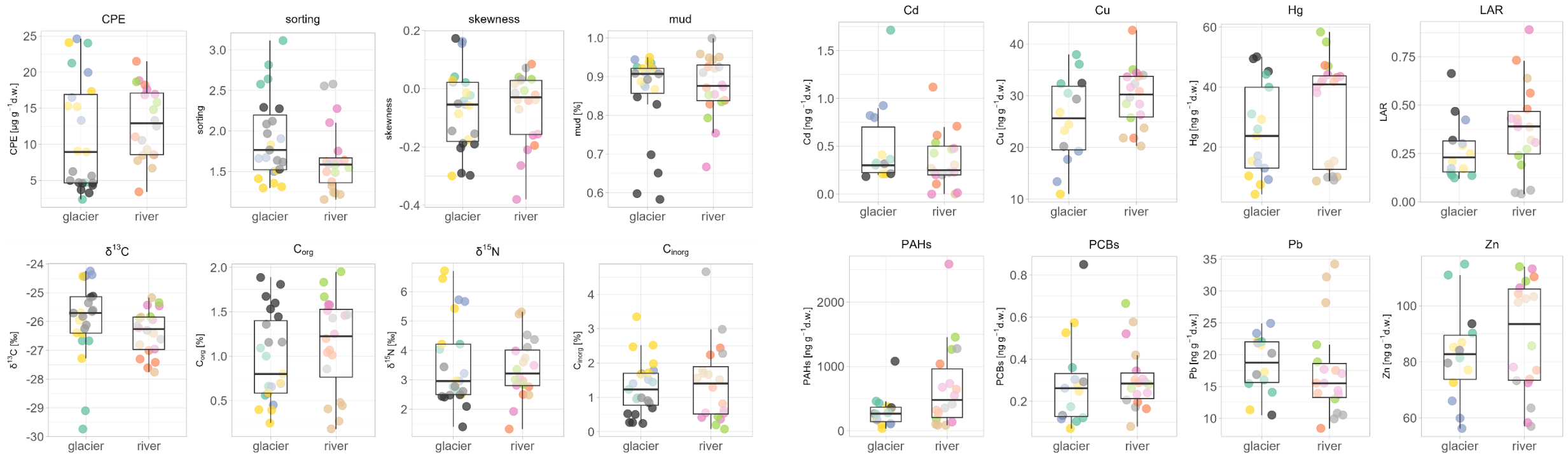
Taxonomic assignment
based on reference
databases



Environmental conditions at studied locations

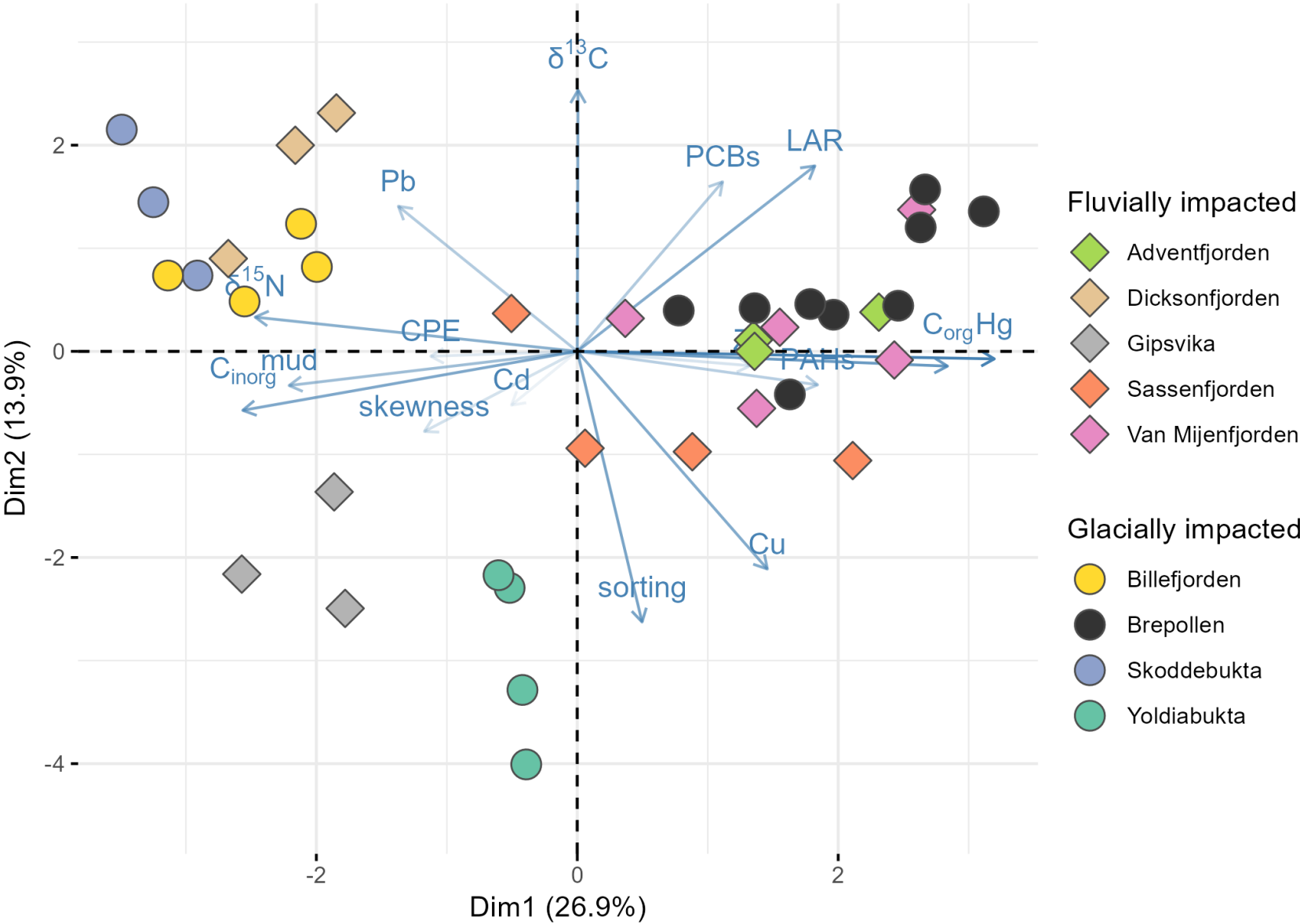


Environmental conditions at studies locations

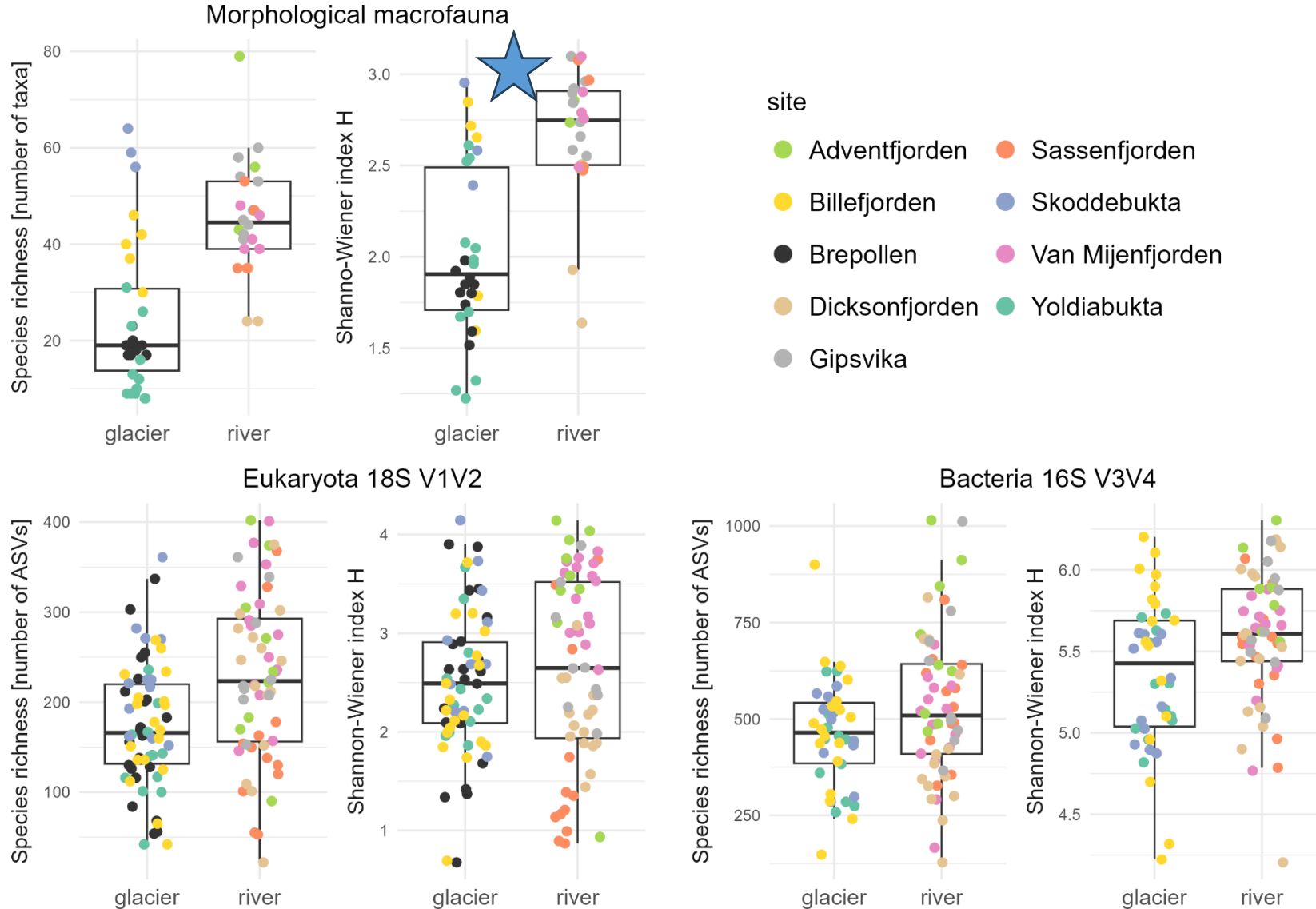



No statistically significant difference between glacier and river in all cases (indicated by Linear Mixed Models)

Environmental conditions at studies locations

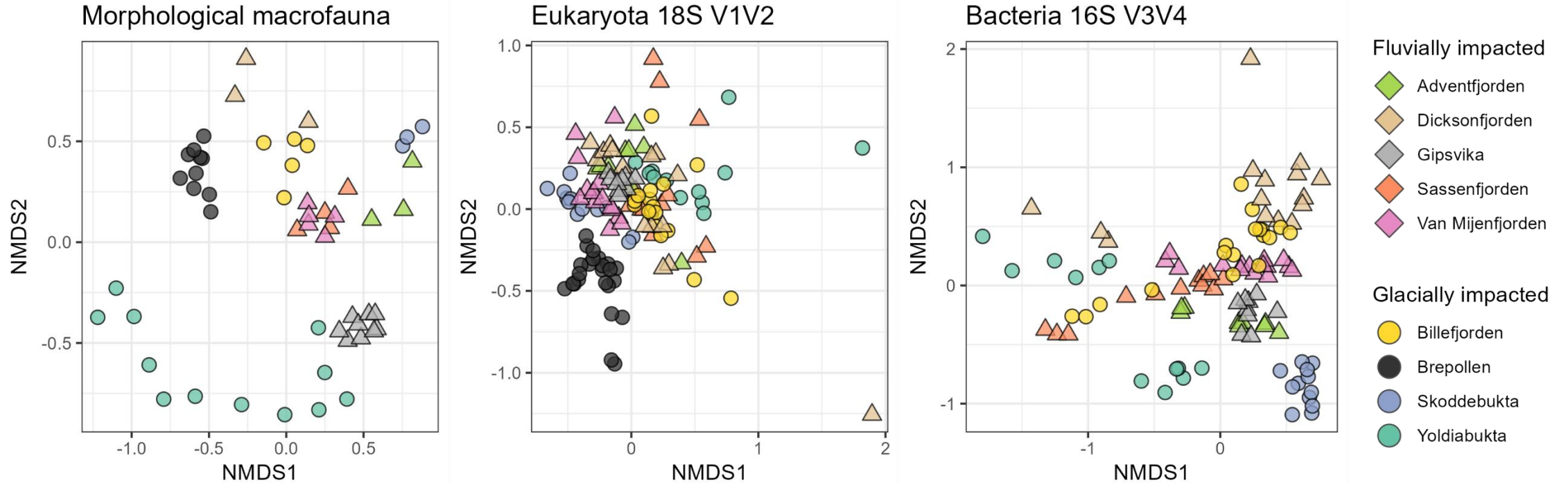


Alpha diversity



 $p < 0.05$

Beta diversity



Step-wise DistLM based on BIC

Variable	Pseudo-F	R2	R2 cum
CPE	8	0.14	0.14
sorting	8.2	0.12	0.26
C_{inorg}	5.7	0.08	0.33
C_{org}	5	0.06	0.4
δ¹³C	4.1	0.05	0.45

Variable	Pseudo-F	R2	R2 cum
δ¹³C	9	0.08	0.08
CPE	9.7	0.08	0.15
C_{org}	7.2	0.05	0.21
Hg	5	0.04	0.24
C_{inorg}	4.6	0.03	0.27
sorting	4.9	0.03	0.31

Variable	Pseudo-F	R2	R2 cum
δ¹³C	11.4	0.12	0.12
Cd	7.4	0.07	0.19
C_{org}	6.5	0.06	0.25
PCBs	6	0.05	0.3
sorting	4.9	0.04	0.34
skewness	5.3	0.04	0.38
C_{inorg}	5.1	0.04	0.42
Zn	4.9	0.03	0.45

Summary



There is no significant difference between glacier and river-influenced locations; site-specific characteristics are more pronounced



Macrofauna alpha diversity differs between glacier and river-impacted locations, with no effect on Eukaryotic and Bacterial eDNA



The taxonomic composition of macrofauna seems site-specific, contrary to eDNA data



Distinct environmental variables shape each community

Thank you!

