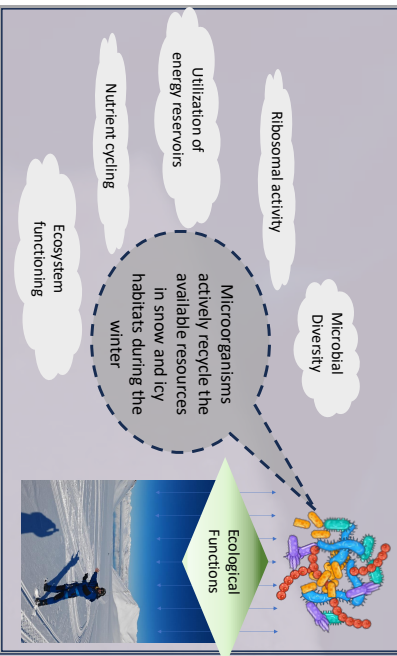


1. Introduction

- Microorganisms have evolved to thrive on limited supplies of energy resources (CO₂, CO, NH₃, CH₄, H₂, VOCs)
- Snow and ice habitats pose physicochemical constraints on microbes which potentially alter their biogeochemical processes
- Our goal is to identify the active microorganisms and their metabolic processes in different habitats during the polar night, which is currently unknown

Hypothesis

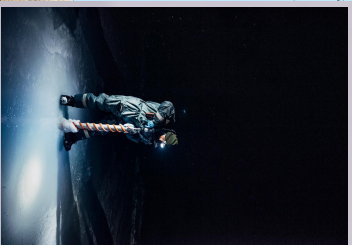


2. Sampling and site description

- Snow, ice, water and soil samples were collected in Ny-Alesund, Svalbard, during the polar night in December.

- All the samples were processed on site and stored in DNA/RNA shield to preserve the RNA and DNA

Sample	Sample type	Site
GLACIAL SNOW	Glacier	Middle boreal forest
GLACIAL ICE	Glacier	Middle boreal forest
LAKE ICE LOWER	Lake	Middle boreal forest
LAKE ICE UPPER	Lake	Middle boreal forest
LAKE SLUSH	Lake	Middle boreal forest
LAKE SNOW	Lake	Middle boreal forest
LAKE WATER	Lake	Middle boreal forest
TERRA SNOW	Terrestrial	Grassland
SOIL	Terrestrial	Middle boreal forest
FJORD WATER	Fjord	Kongsfjorden

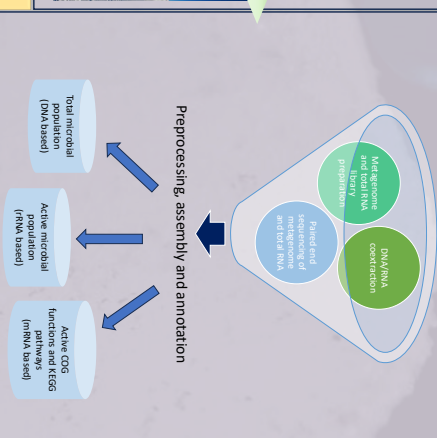


Credits: Daga Wojtanowicz (Norwegian Polar Institute)

3. Research Questions and Methodology

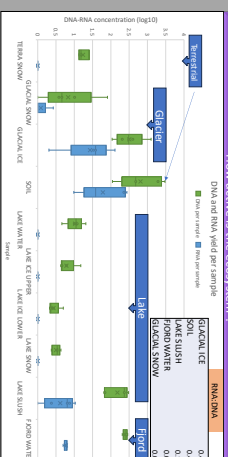
Questions ?

- Which microbial communities are present across different habitats during the polar winter of the Arctic ?
- Which microbial communities are active during the polar winter of the Arctic ?
- What are the active metabolic processes during the polar winter ?

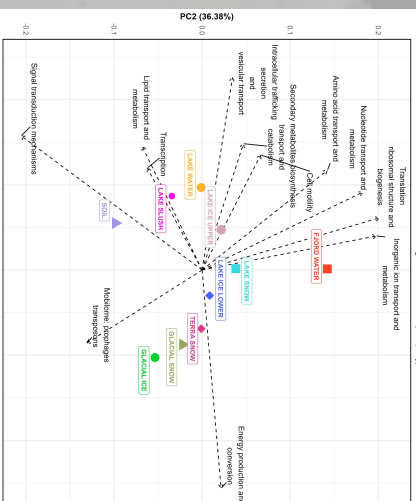


4. Results

How active is the ecosystem ?



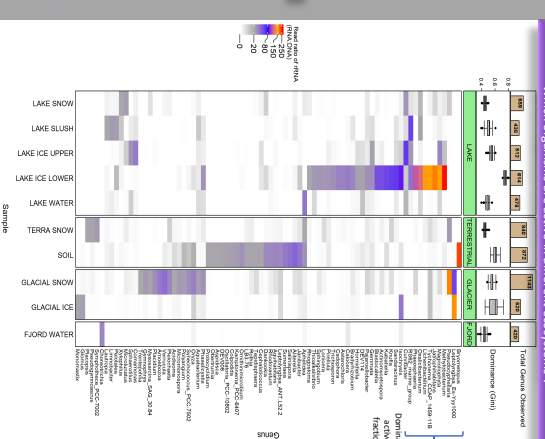
What are the active metabolic processes of microbes in different ecosystems?



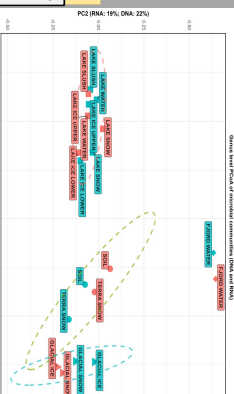
5. Conclusion

- The active communities were more diverse and abundant in lower lake ice core followed by the soil and glacial snow
- The community composition was similar between the metagenomes and metatranscriptomes across all habitats. However, the most active genera were found as rare taxa in the metagenomic data
- The active communities in lake samples were dominated by organic matter degraders and single carbon metabolizers (Methylobacterium), specifically the lower lake ice core
- Endophytic fungi and lichens (Pseudophellaria) associated with cyanobacterium (Laploglymya) were found in glacial (snow and ice) and other habitats
- The genera clustered as per the ecosystem of lake, glacial, terrestrial and fjord based on both the active and total population (RNA vs DNA)
- The active COGs shows no ecosystem-based clustering, suggesting functional variation is driven more by environmental factors than habitat type

Which organisms are active in different ecosystems ?



How do the microbial communities vary among different ecosystems ?





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References: Dziewit et al., 2015, Cordero et al., 2019, Liot & Constant, 2016, Berney et al., 2014, Kleerebezem & Lucker, 2021.

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