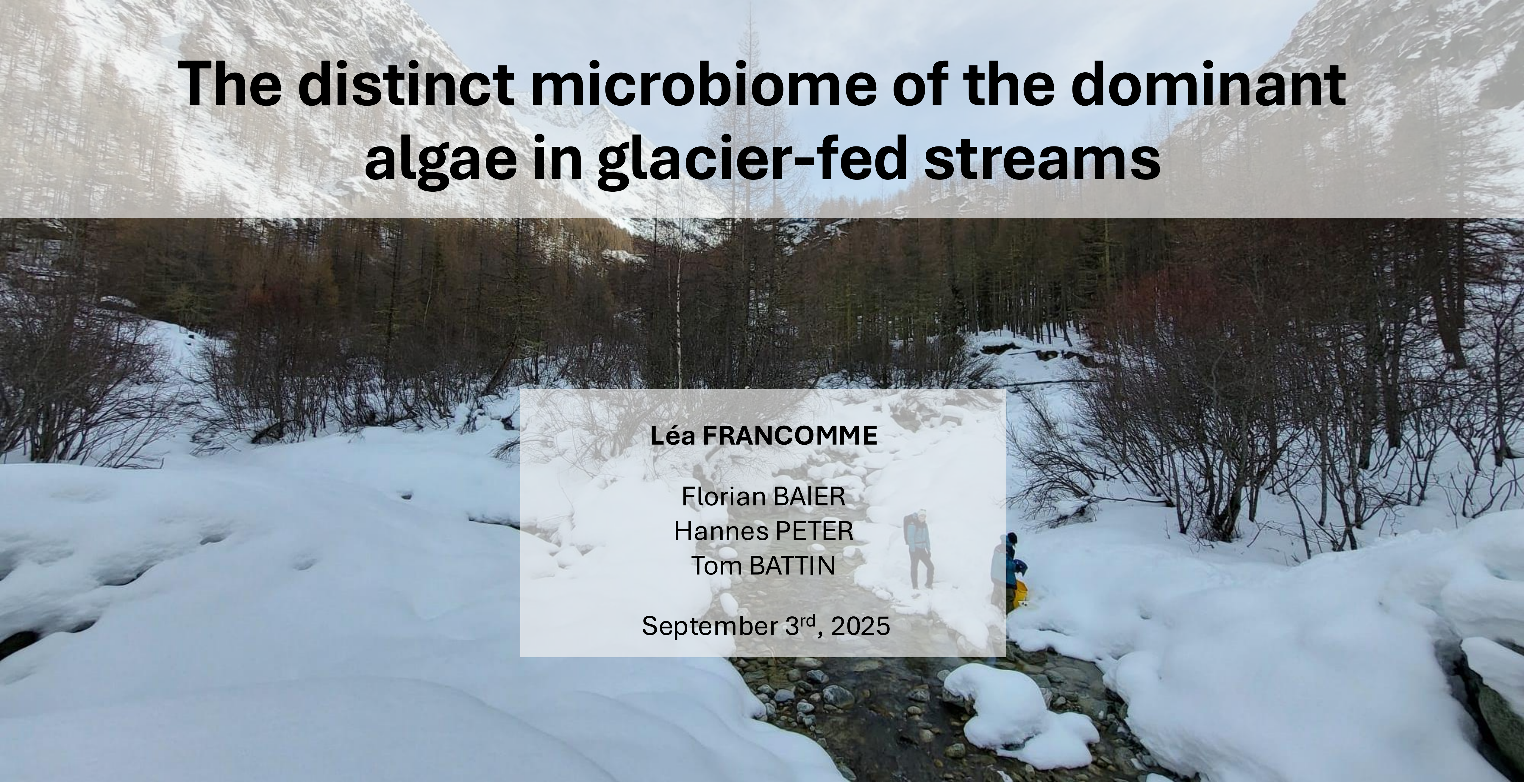

The distinct microbiome of the dominant algae in glacier-fed streams

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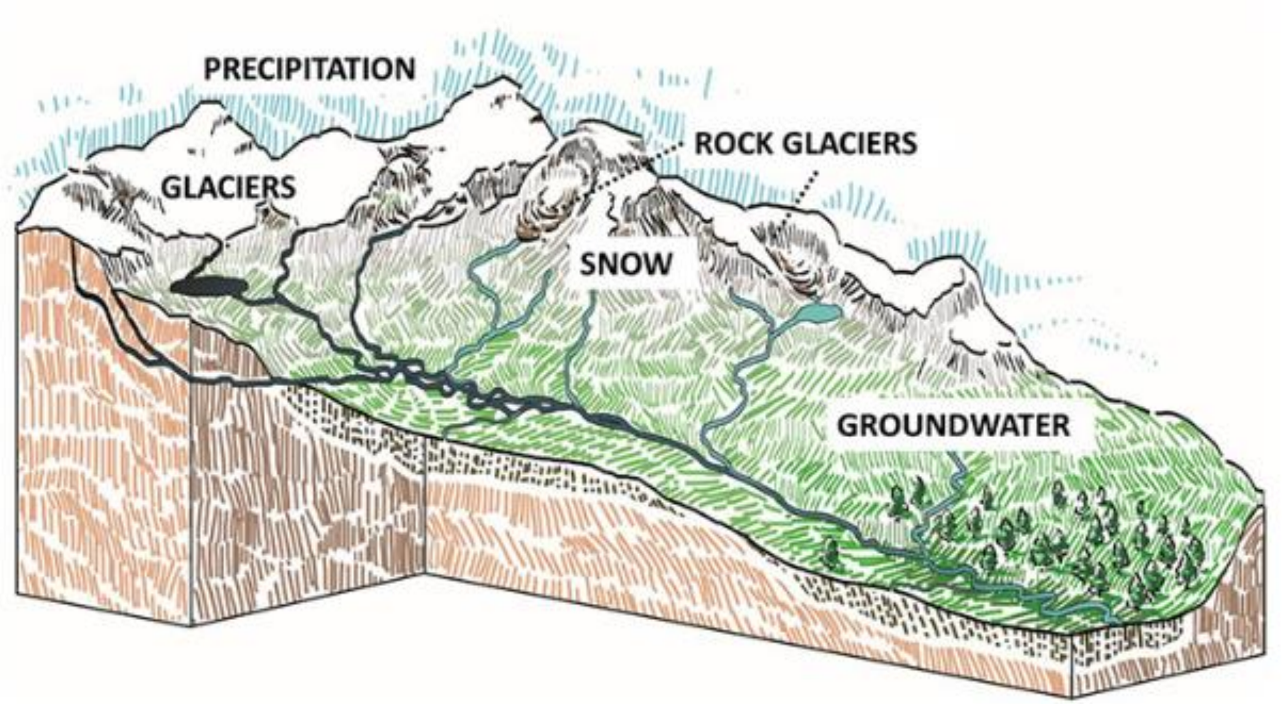
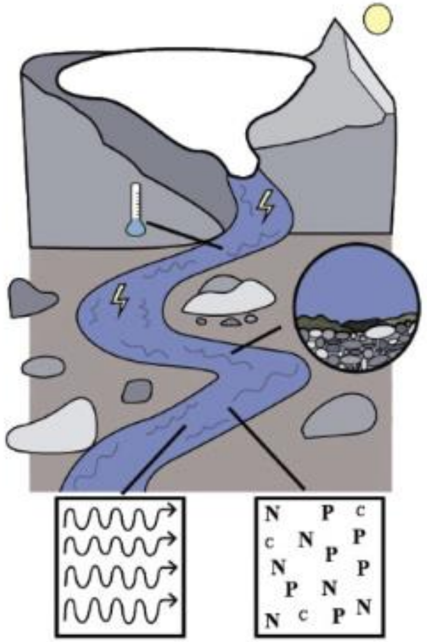
ICEBIO
CRYOSPHERIC ECOSYSTEMS CONFERENCE
EPFL

Glacier-fed streams



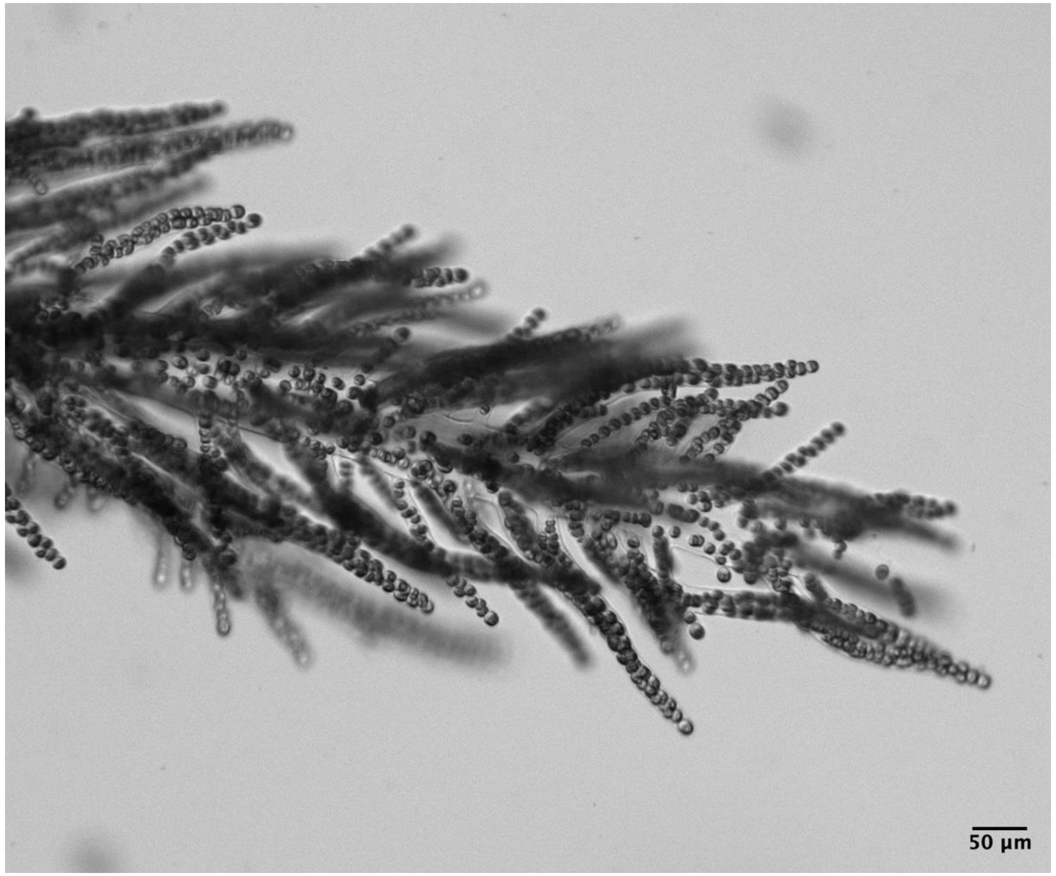
Brighenti et al, 2019

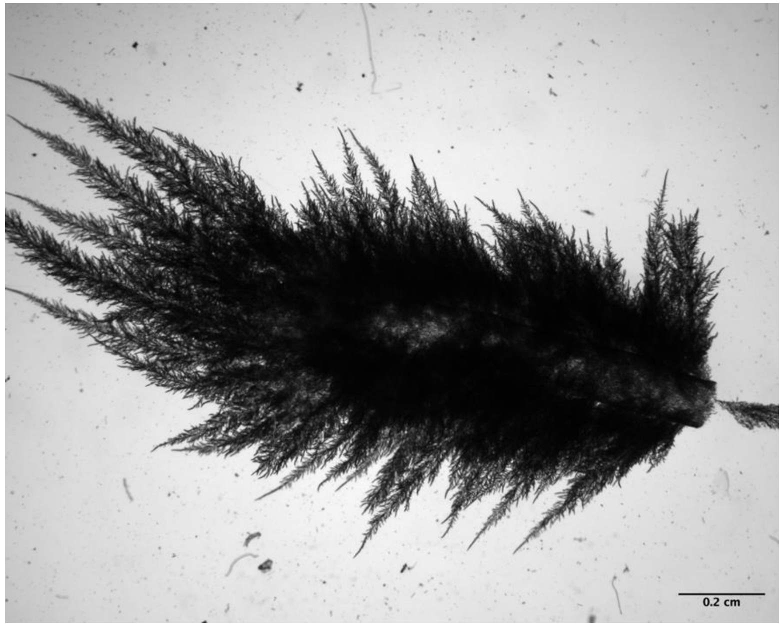


Sudlow et al, 2023

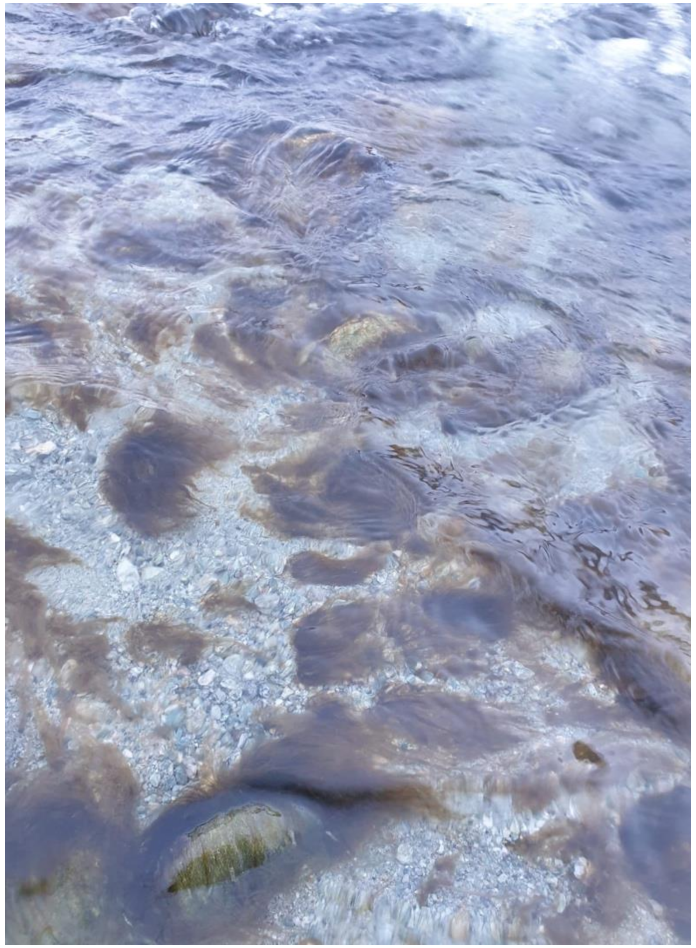
Hydrurus foetidus – the dominant algae in GFS

- *Chrysophyceae* family
- Unicellular organism
- Macroscopic structure
- Up to 30cm long





Hydrurus foetidus – the dominant algae in GFS



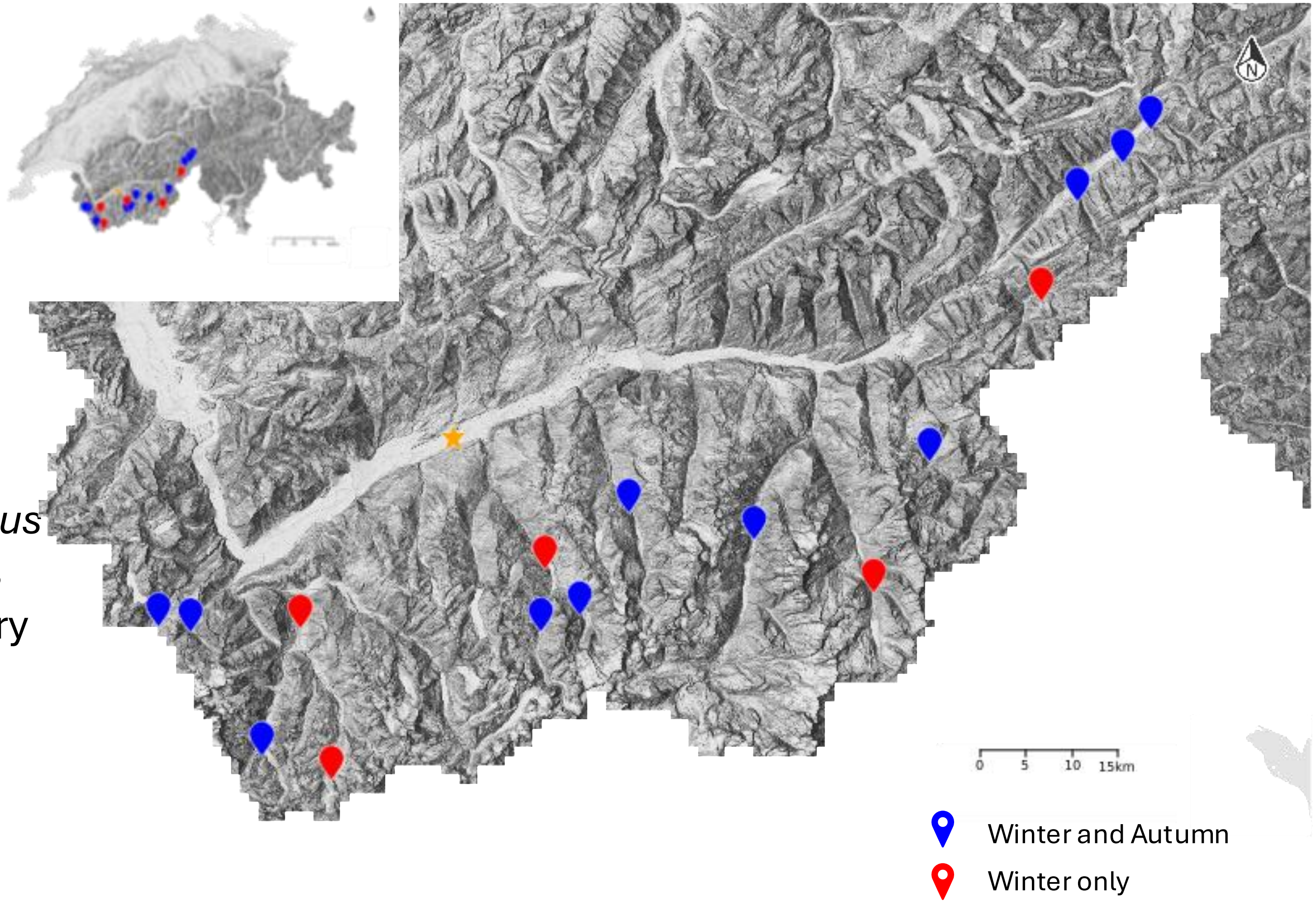
- Seasonal algae (disappears in summer)
- In streamwaters ranging from 0 to 12°C
- At the base of the food web
- Forming blooms under oligotrophic conditions

Hypothesis

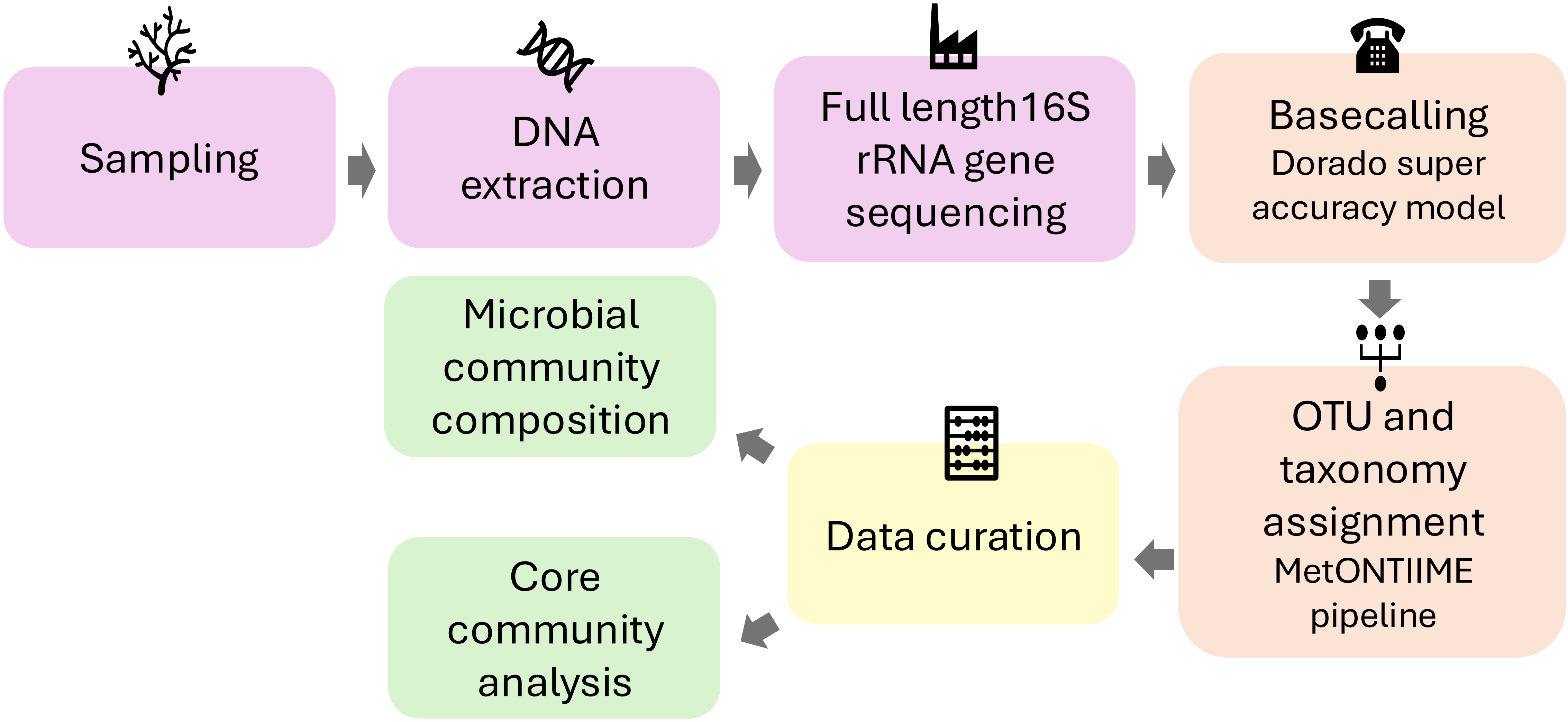
- *H. foetidus* has its own microbiome, which changes across seasons.
- Part of this microbiome is independent of space and time ⟶ core microbiome
- *H. foetidus* interacts with its microbiome ⟶ potential symbiotic organism

Sampling

- 16 streams
- Triplicates of *H. foetidus*
- Streamwater samples
- Streamwater chemistry



Workflow



Sampling

DNA extraction

Full length16S rRNA gene sequencing

Basecalling
Dorado super accuracy model

OTU and taxonomy assignment
MetONTIIME pipeline

Data curation

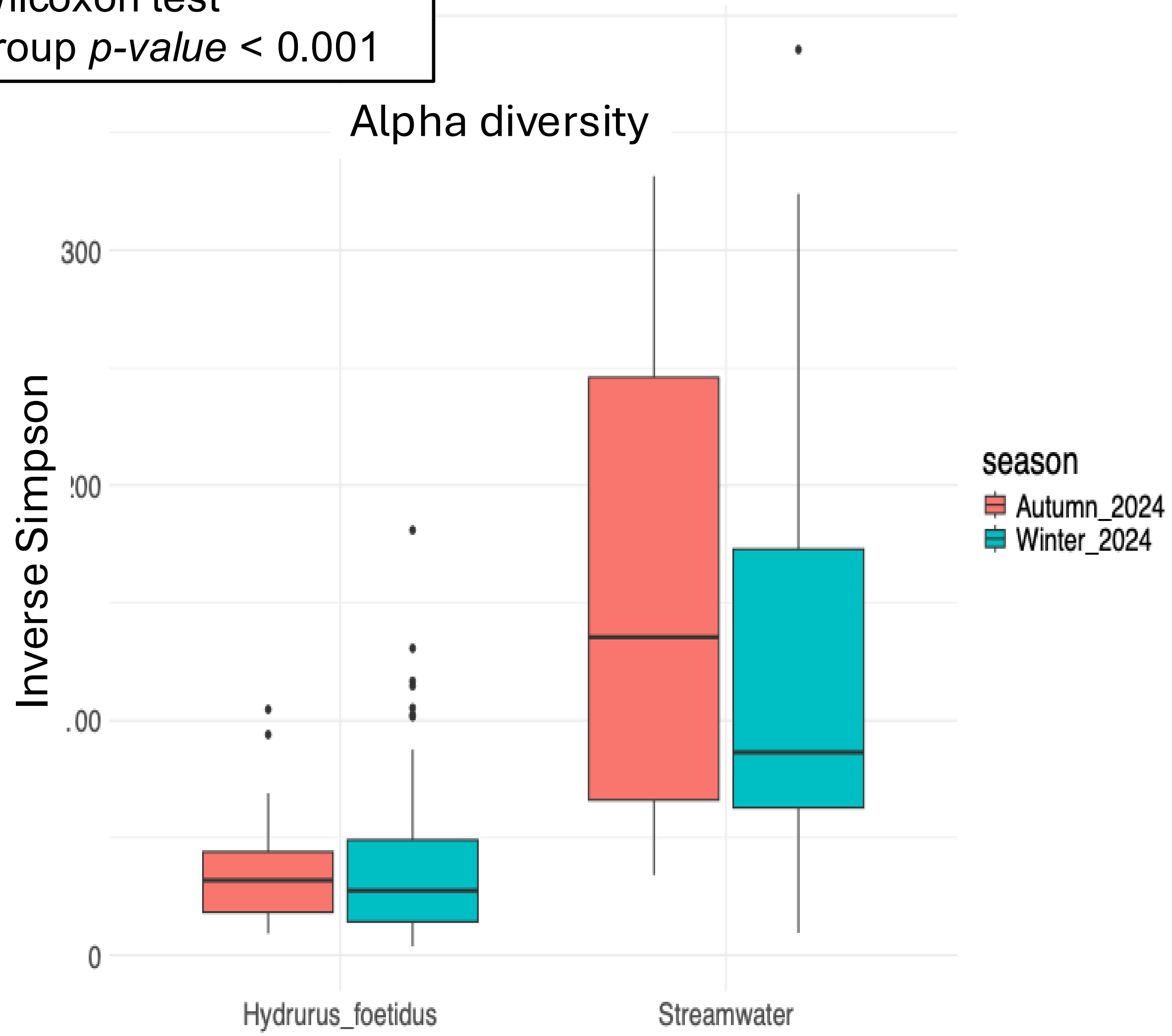
Microbial community composition

Core community analysis

H. foetidus harbours a distinct microbiome

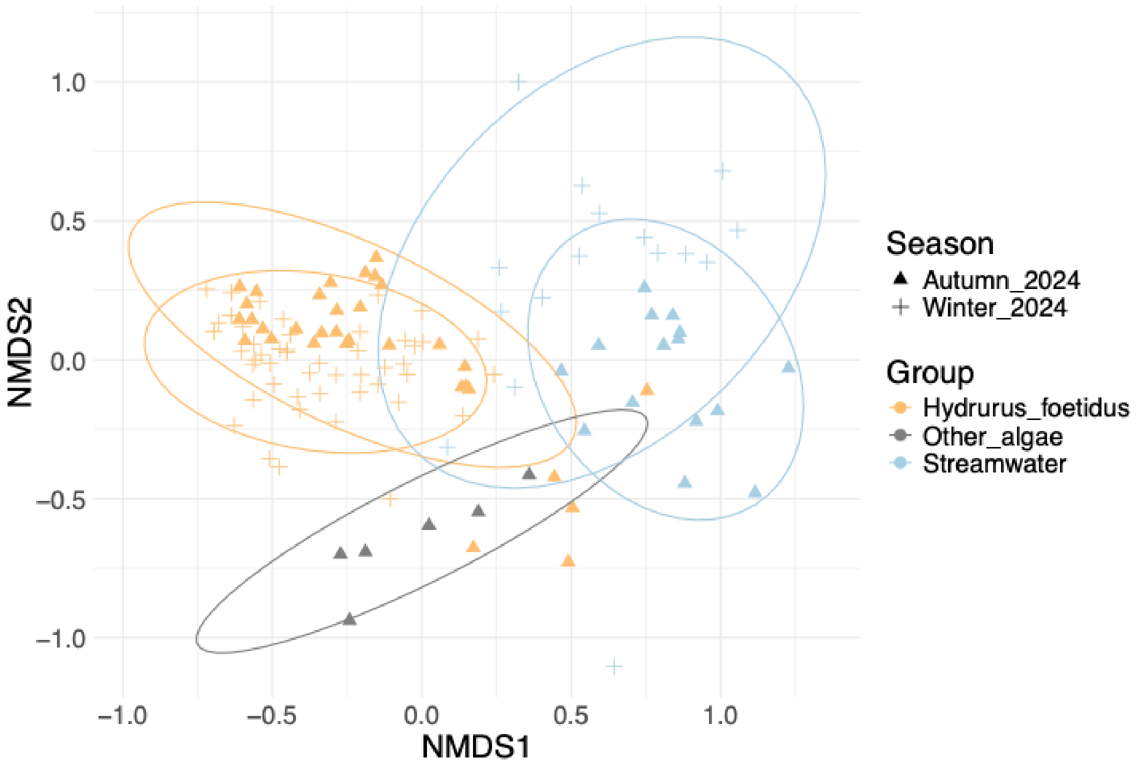
Wilcoxon test
group *p-value* < 0.001

Alpha diversity



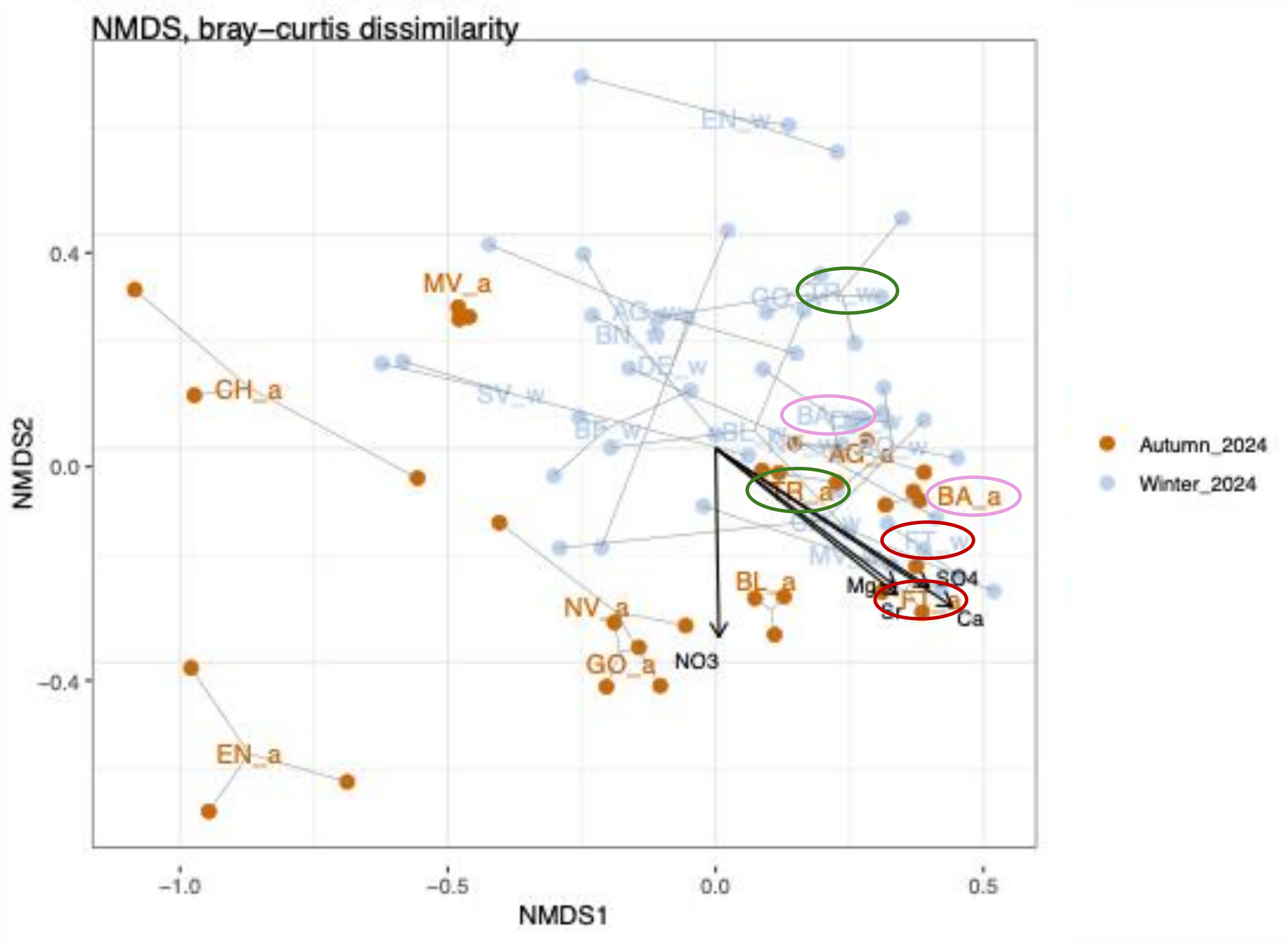
PERMANOVA
p-values < 0.001

Microbial community composition



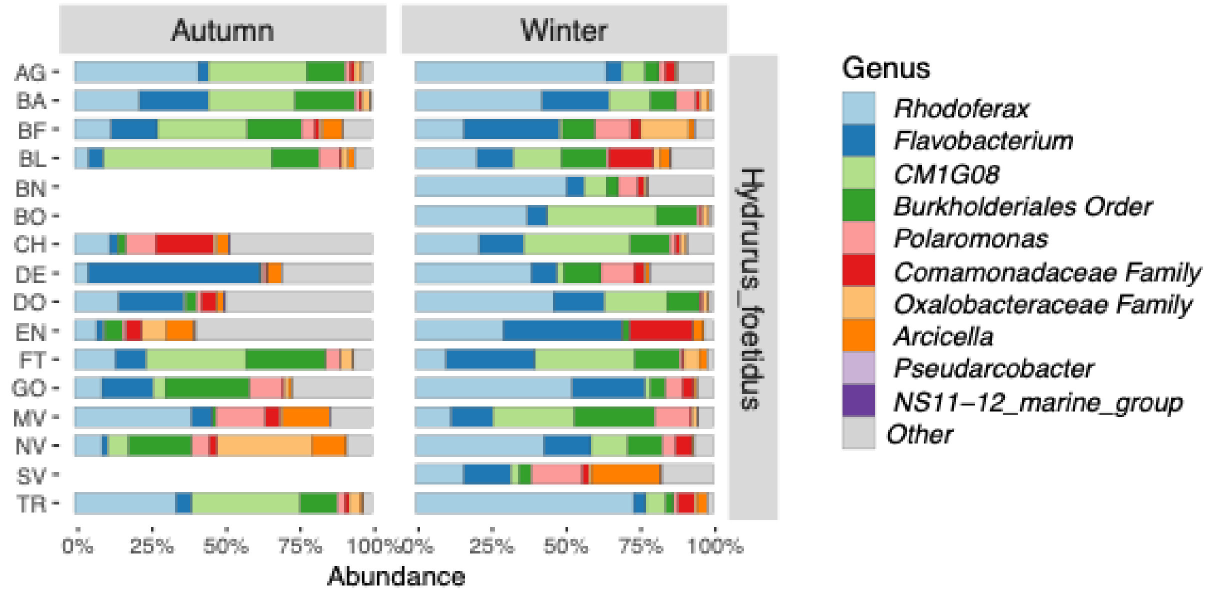
Effect of the environment on *H. foetidus* microbiome

Envfit
p-values < 0.001
NO_3 *p-value* < 0.01



Core microbiome

Genera present in at least 90% of *H. foetidus* samples



On average

- Rhodoferax: 30%
- CM1G08 (*Oxalobacteraceae* fam.): 17%
- Flavobacterium: 11%
- Polaromonas: 5%
- Arcicella: 2%
- Pseudorhodobacter: 1%

Conclusion

- *H. foetidus* microbiome ≠ streamwater one ≠ other algae

  ⟶ *H. foetidus* harbours its **own** microbial community
- *H. foetidus* microbiome season
- *H. foetidus* core microbiome

  ⟶ is independent of space and time

  ⟶ represents most of the total microbiome relative abundance

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