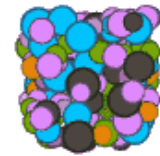


# Paleometagenomic network analysis of ancient DNA from Bering Sea sediments to examine past ecological communities



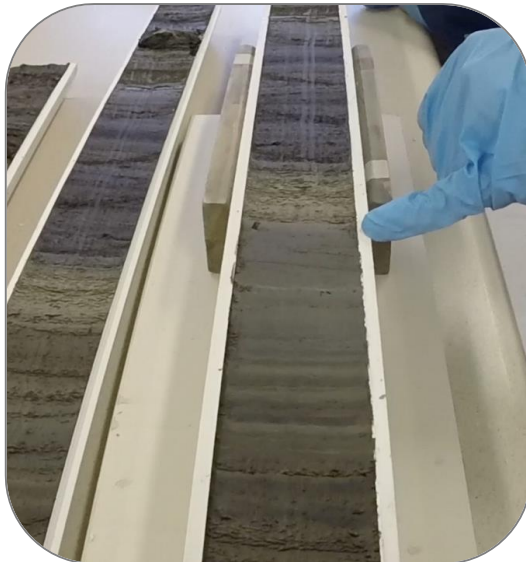
*Viktor Dinkel, Stella Zora Buchwald, Kathleen Stoof-Leichsenring, Marc-Thorsten Hütt, Dirk Nürnberg, and Ulrike Herzsich*

# Motivation

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## Motivation

Study past **biodiversity**  
of **marine**  
**ancient DNA**



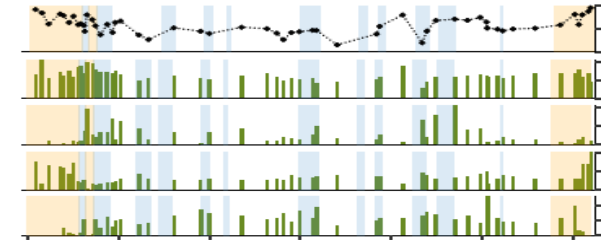
## Methods

Shotgun  
Sequencing

Network Analysis

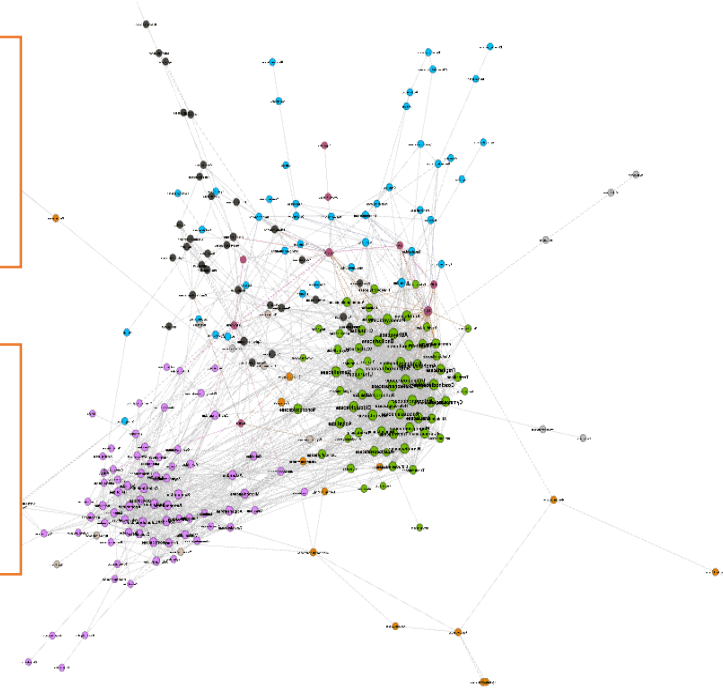
## Aim of research

Understand past  
**changes in  
biodiversity**



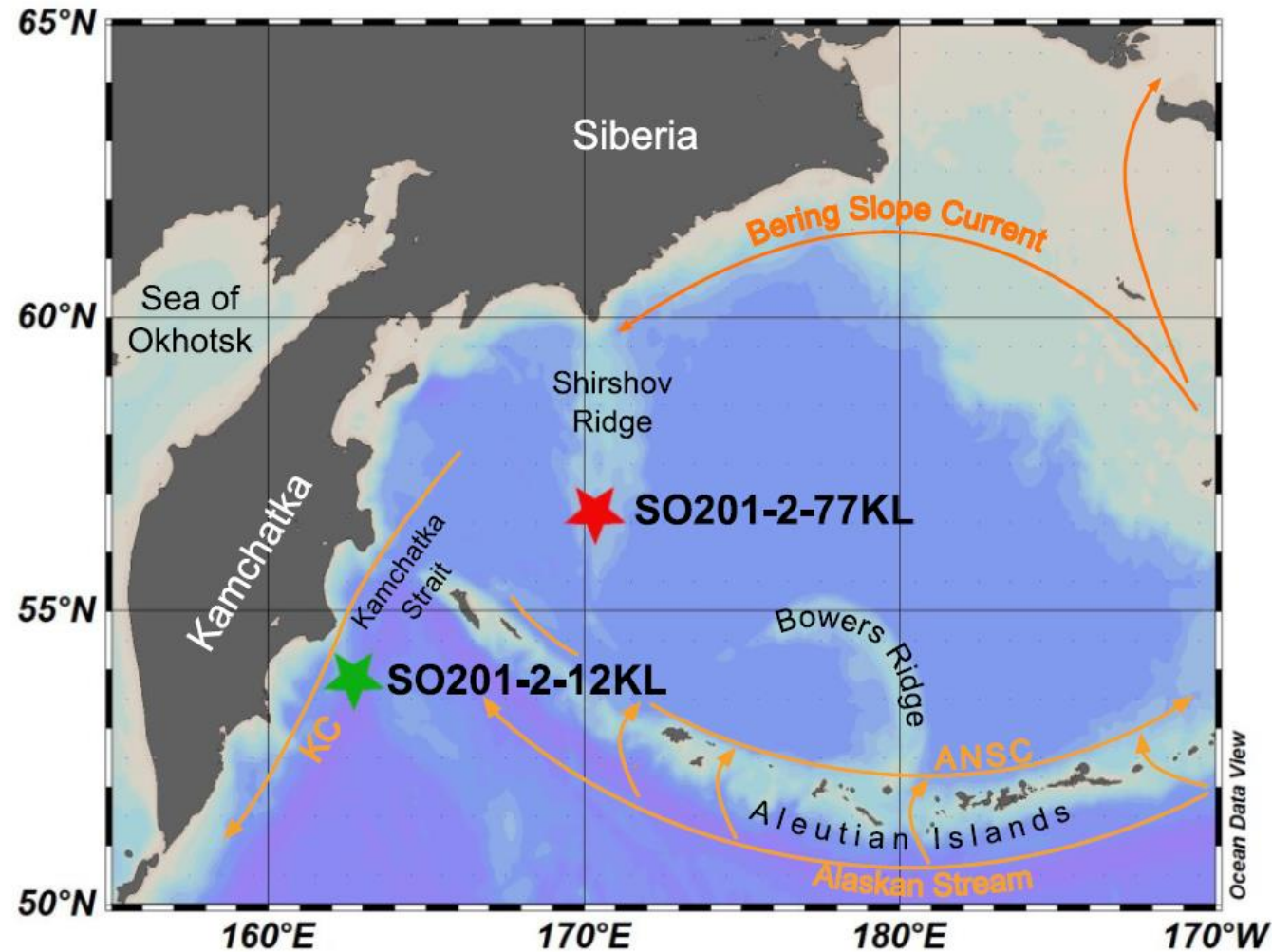
Reconstruct  
**ecological  
communities**

Trace **cascading  
community effects**

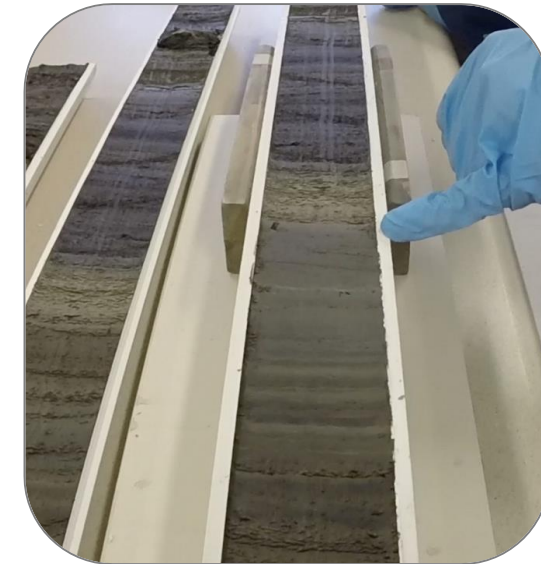


# Background

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Ocean Data View (Schlitzer, 2002) by GEOMAR technician S. Fessler



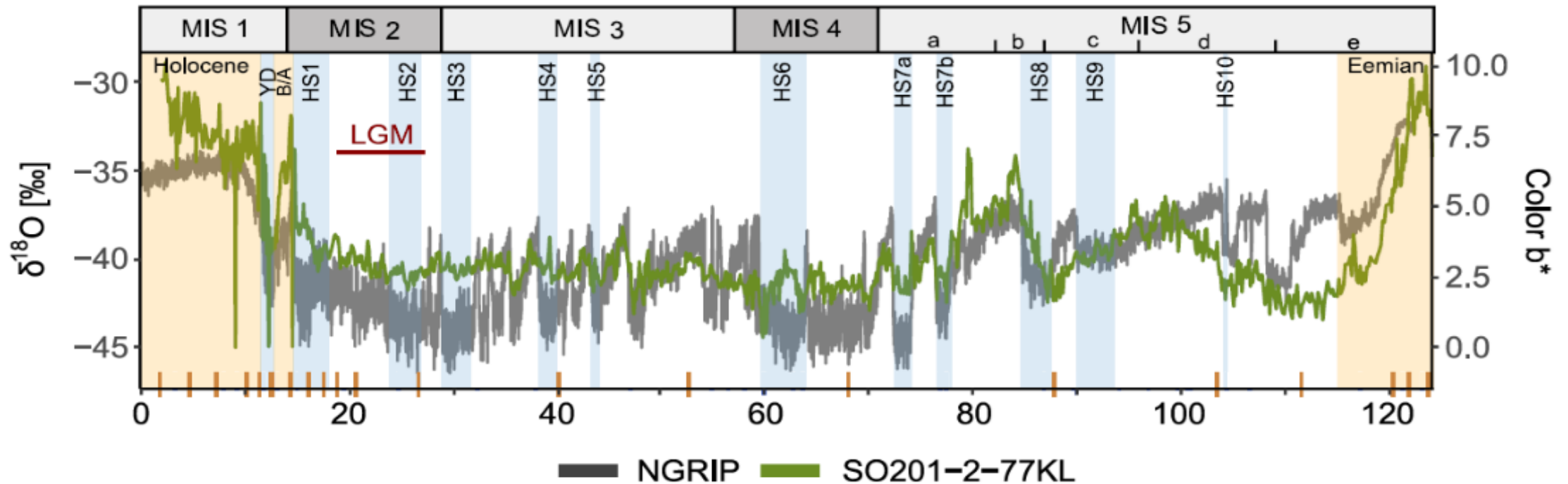
124 kyrs

# Methods

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- 22 samples of sedaDNA
- FastP/FastQ quality control
- Taxonomically classified with Kraken2
- Stratigraphy
- RDA



Age model of sediment core SO201-2-77KL from Max et al. (2012) and Riethdorf et al. (2013b)



# Methods

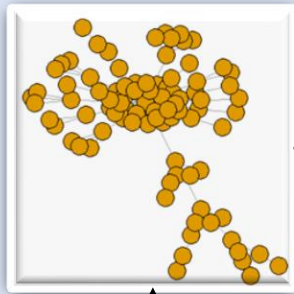
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## Network Analysis

## Experimental method validation

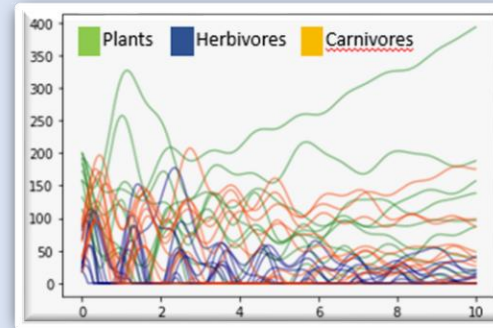
Experiment

### 1. Synthetic network



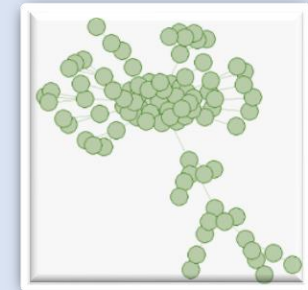
Generate

### 2. Abundance data



Infer

### 3. Association network



Evaluation: compare networks

Configuration

### Network properties

- Topologies (Scale Free, Cluster, ...)
- Date hubs, Party Hubs
- Environmental factors

### Abundance generation

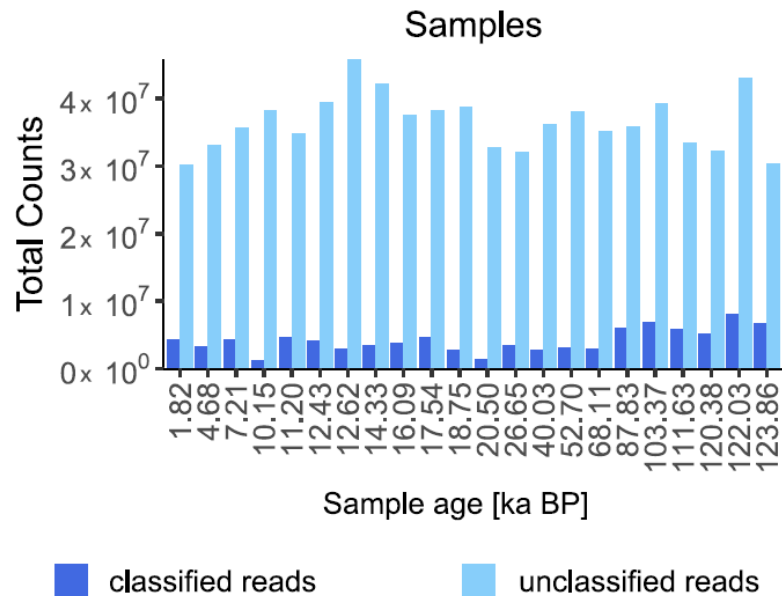
- Model (Predator prey, SPIEC-EASI, presence/absence, ...)
- Model parametrization
- Steady state simulation or sampling of single simulation

### Inference method

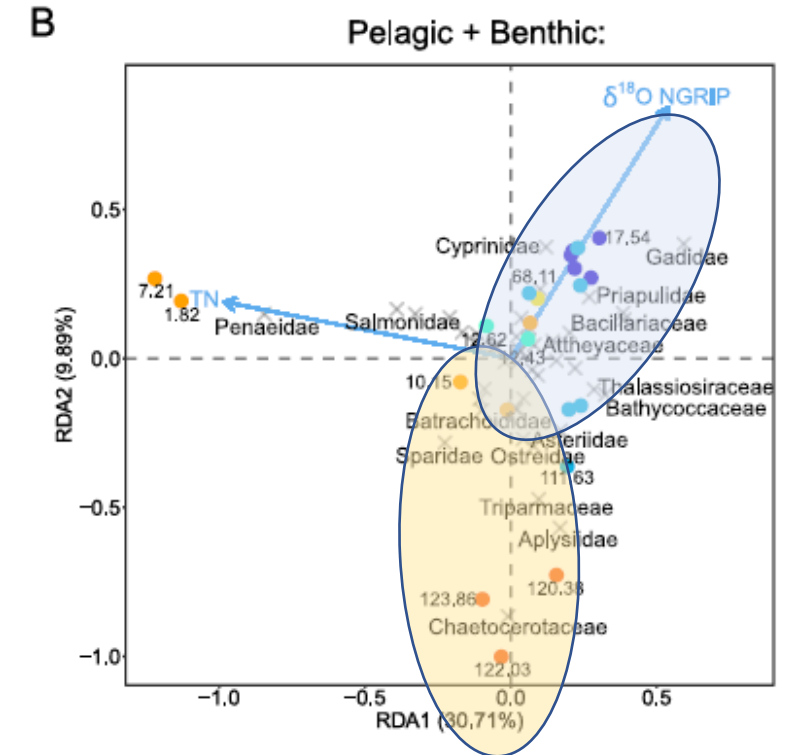
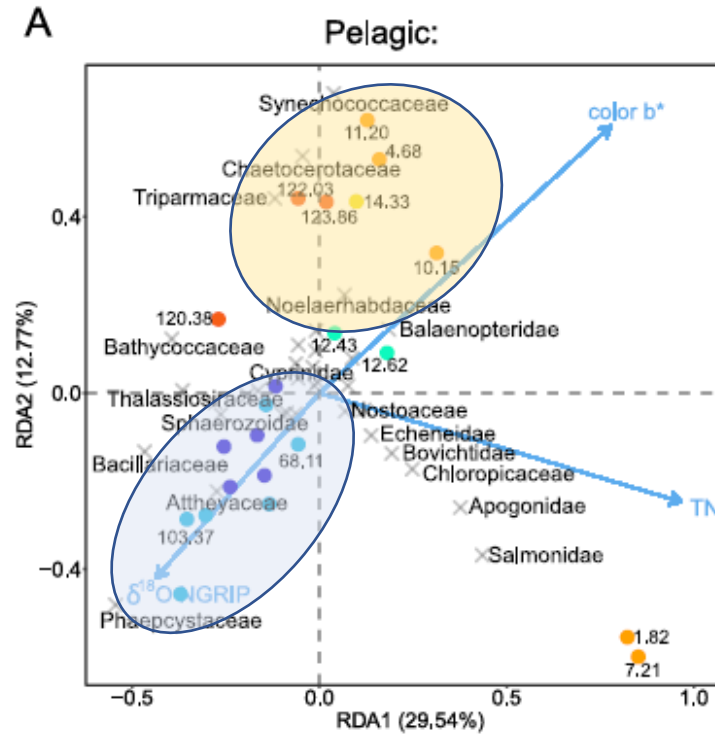
- Spearman, ecoCopula, ESABO, SPIEC-EASI, PC-Cor, SPARCC, ...
- Thresholds & settings
- Random control

# Results: RDA

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Whole Metagenome  
Shotgun Sequencing



warm phases:

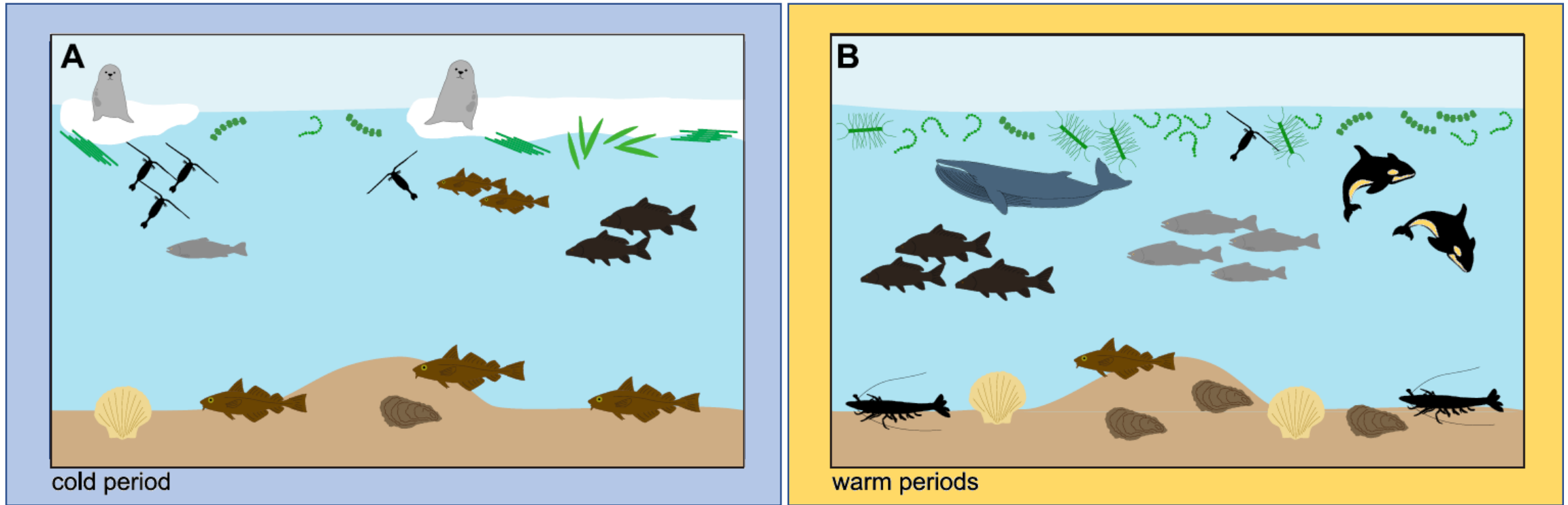
- Holocene
- Bølling-Allerød
- Eemian

cold phases:






- Younger Dryas
- LGM
- Glacial

# Results: Shotgun sequencing



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## Phytoplankton:

-  Synechococcaceae & Nostocaceae
-  *Chaetoceros*
-  *Thalassiosira*
-  *Bacillaria*
-  *Nitzschia*

## Crustaceans:

-  Calanidae
-  Penaeidae




## Mussels:

-  Ostreidae
-  Pectinidae

## Fishes:

-  Cyprinidae
-  Salmonidae
-  Gadidae

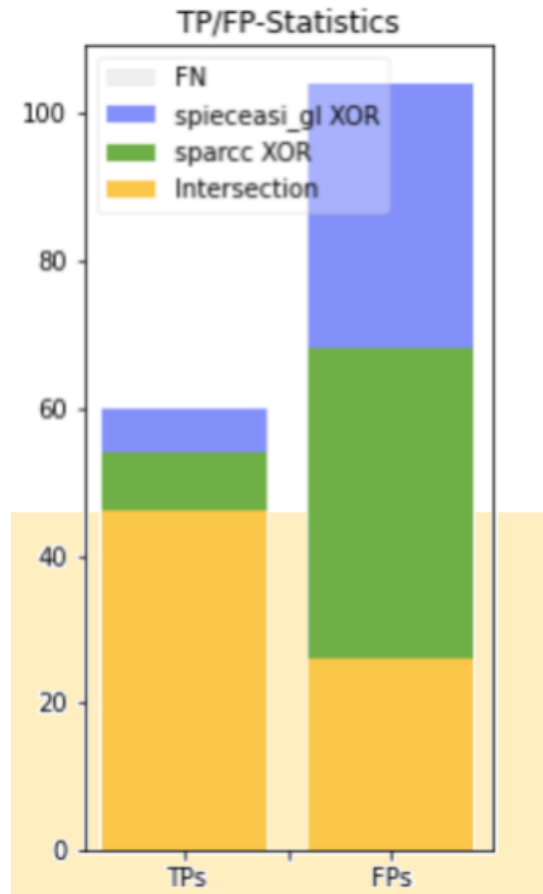
## Marine Mammals:

-  seals
-  Delphinidae
-  Balaenopteridae

# Results: experimental network analysis

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SPIEC-EASI + SPARCC

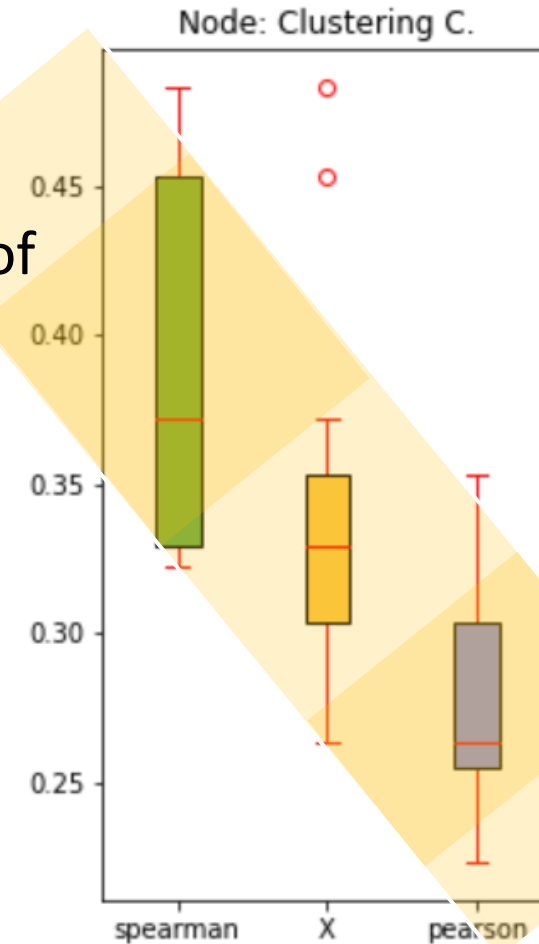


(1) Intersection of results for **fewer false positives**

## Network Analysis

(2) Combination of results increases **variety of „hits“**

PEARSON + SPEARMAN





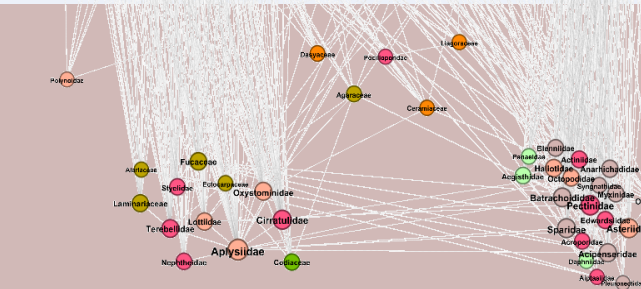
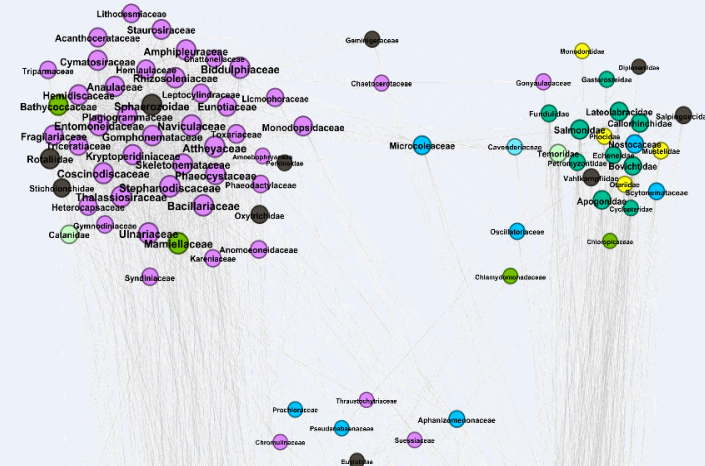
# Results: ecological networks

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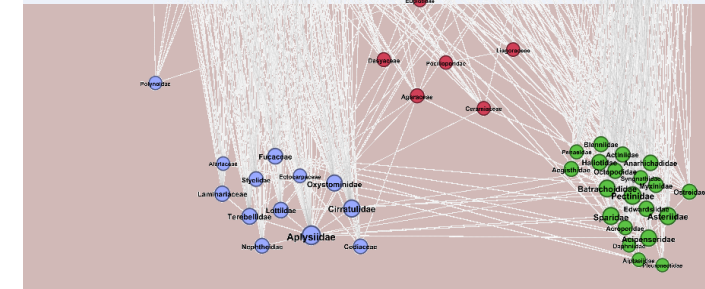
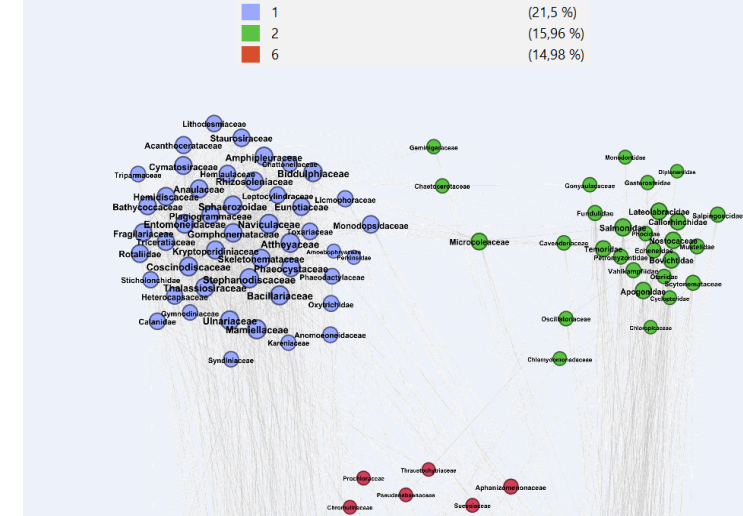
Pelagic

Benthic

phototrophic protists	(18,63 %)
chlorophytes	(11,11 %)
phototrophic bacteria	(9,8 %)
heterotrophic protists	(9,48 %)
red algae	(9,15 %)
sessile/sedimentary benthos	(7,52 %)
fish/nekton	(7,19 %)
demersal fish	(6,21 %)
crustaceans	(3,92 %)
mobile benthos	(3,92 %)
mammals	(3,27 %)
brown algae	(2,94 %)
streptophytes	(2,29 %)
gelatinous zooplankton	(1,96 %)
crustaceous zooplankton	(1,63 %)
slime mold	(0,65 %)
heterotrophic protists	(0,33 %)



1	(21,5 %)
2	(15,96 %)
6	(14,98 %)



*"Ecology is networks... to understand ecosystems will be to understand networks"*  
- Bernard Patten

# Conclusion

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## **I. Output matches documented data**

- ecological community in shotgun sequenced marine sedaDNA ~ recorded community in the modern Bering Sea

## **II. marine sedaDNA opens window to the past 124 kyrs**

- analogues from the past climates can be studied
- estimate the effects of modern global warming

## **III. Inferring ecological networks remains a challenge**

- intersecting results may reduce false positives
- networks are powerful tools → overcoming the challenges greatly improves (II)

# Thank you for your attention!

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## Questions?

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