

Building capacities for 'omics' observations in the ocean at high spatiotemporal resolution

FRAM



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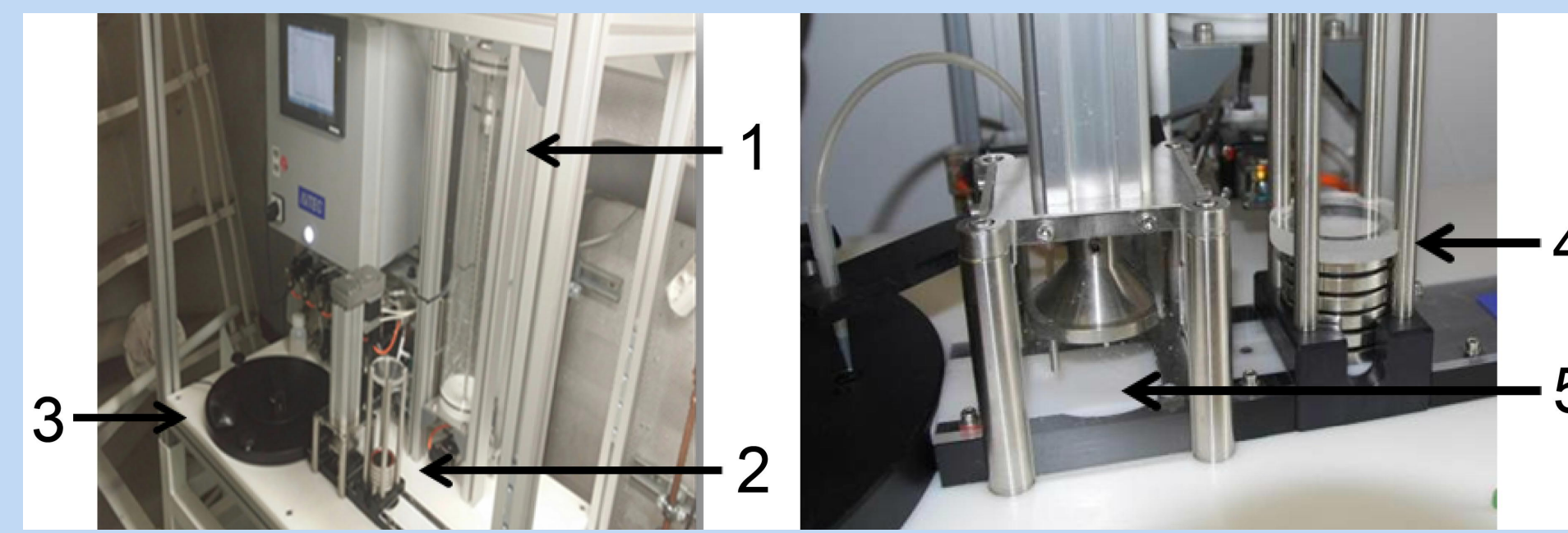
Introduction

Observations of marine unicellular organisms with 'omic' techniques (e.g., (meta-) genomics, metatranscriptomics) improve our understanding of spatiotemporal patterns of eukaryotic microbial and prokaryote community composition. In combination with contextual data, the observations can elucidate biogeochemical functions (e.g., contribution to element cycling) and help to understand and predict responses to natural and anthropogenic pressures. In the framework of EU programs AtlantOS and EnviGuard, capacities were built to facilitate 'omics-based time-series observations of unicellular marine organisms. Focus was on the **development of new samplers (right)** and the **demonstration and validation of relevant methods (below)**.



AUTOFIM underway sampling

The 'AUTOMated Filtration system for marine Microbes (AUTOFIM) performs filtrations of samples taken automatically from the ship's pump systems and – in the future – also on fixed monitoring platforms. Filter wheels currently carry 12 filters each and may easily be changed by lay persons for subsequent molecular analyses of microbial communities.

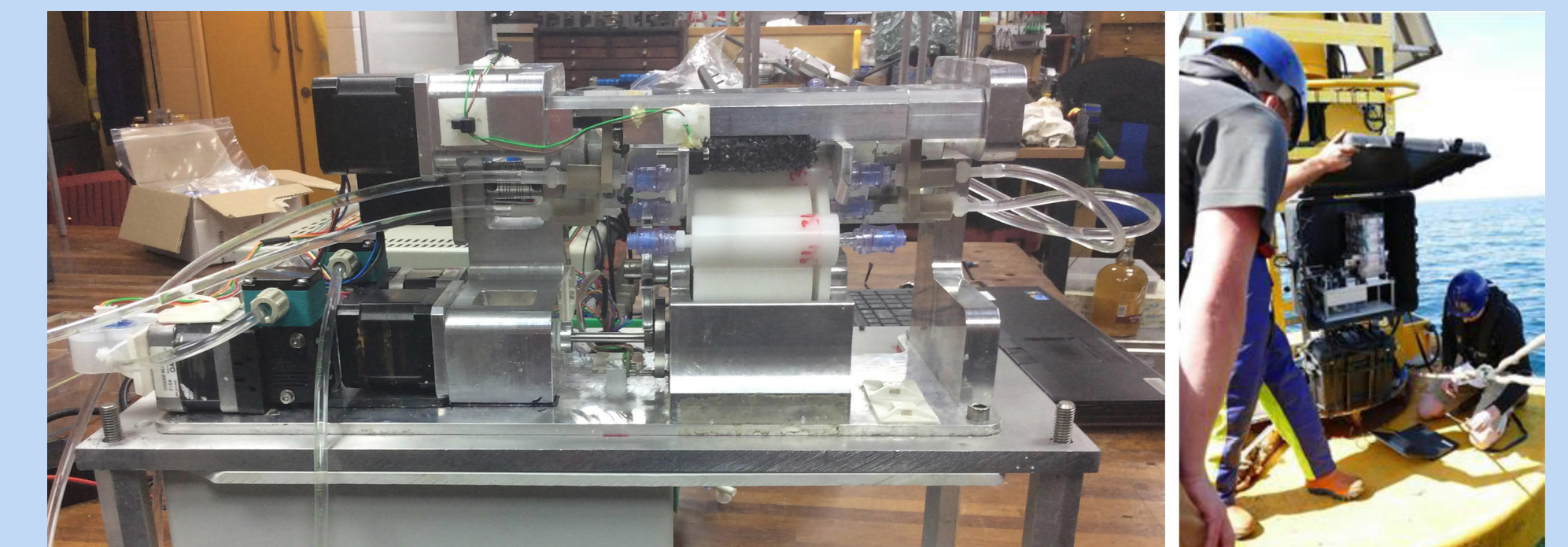


AUTOFIM installed on board RV POLARSTERN with close-up of the filtration-module (right panel). (1) Sample reservoir, (2) filtration-module, (3) archive for preserved filters, (4) filter stack, (5) filtration cap; from Metfies et al. (2016), modified.

AUTOFIM is being integrated into the microbial observatory component of the FRAM observing infrastructure in Fram Strait and greatly enhances the areal coverage of observations during annual expeditions with R/V Polarstern.

MAPS high-resolution sampling

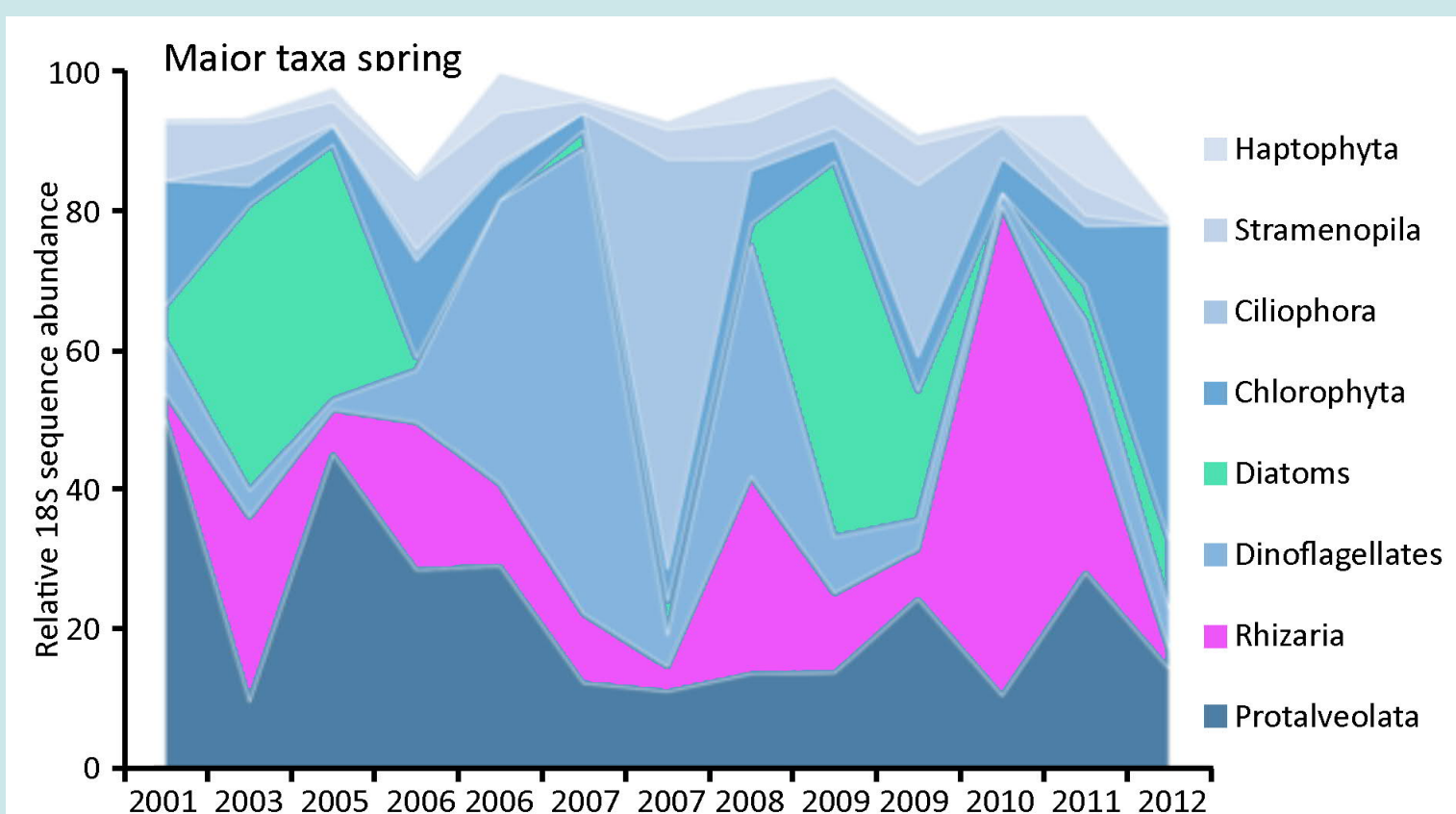
The 'Marine Autonomous Plankton Sampler' (MAPS) hosts magazines with sterile filter units to collect large numbers of samples for genomic analyses of planktonic communities – as well as larger organisms via eDNA. The system is designed for installation on moored or towed platforms and allows to greatly increase sampling frequency as compared to existing instrumentation. MAPS prototypes have been used as part of an underway system during Atlantic explorer cruise AE1714 in the NW Atlantic and successfully deployed at the Station L4 buoy in the Western Channel Observatory.



Left panel: underway observation version of MAPS. Right panel: MAPS mounted on a buoy for unattended long-term deployment.

Time series from legacy samples

Particle trap samples from long-term stations, often kept on the shelf for decades, represent a demanding but highly valuable target for genetic reconstruction of past microalgal communities. 18S genes amplified from DNA obtained from trap samples collected during peak export season in eastern Fram Strait over a period of 10 years were successfully sequenced. Phytoplankton communities show convincing multi-annual patterns that are clearly connected to the strength of the export peak in the respective years. Phylogenetic analyses further revealed the displacement of cold-adapted *Micromonas*-phylogenotypes with warm-adapted phylogenotypes and haptophytes in response to a warming event.



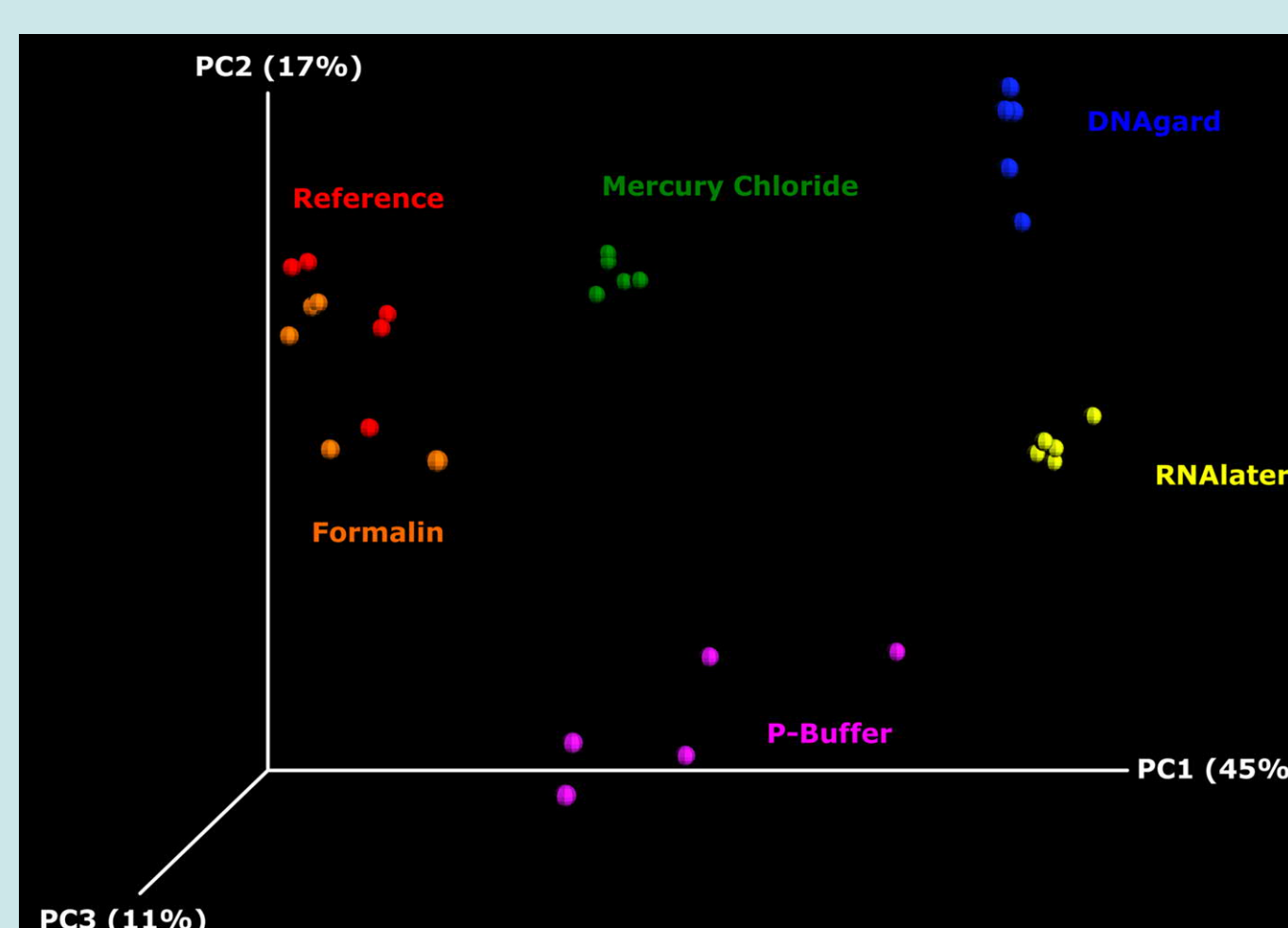
Most abundant eukaryotic microbe taxa as determined by 18S sequencing of DNA extracted from legacy trap samples collected during the spring particle export maxima in the eastern Fram Strait at station HGIV of the Long-term Ecological Research Station HAUSGARTEN

Long term records obtained by omics techniques from legacy samples can serve as baselines to identify nowadays changes and can help to predict microbial community characteristics in the future Arctic under high and low productivity scenarios.

In situ 'sample storage'

Consistent genomic information from samples collected with autonomous systems depends on the proper conservation of DNA during the deployment period of typically one year in open ocean observatories. The performance of five preservatives were compared in a one-year experiment at the temperature typically found at the FRAM microbial observatory in Fram Strait.

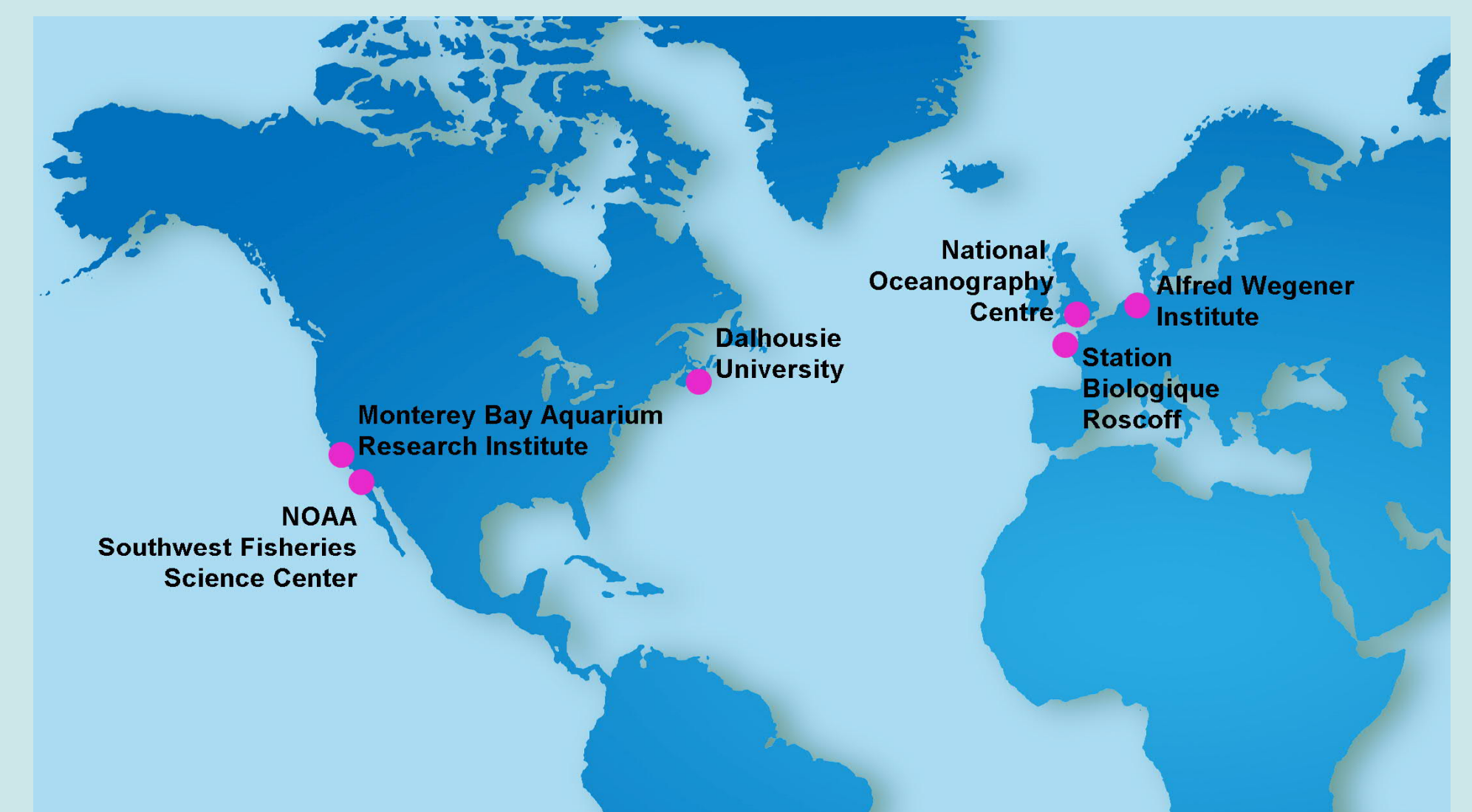
NMDS plot of community compositions from 18S sequencing of environmental samples after 10 weeks storage with different preservatives. Reference communities have been obtained from unpreserved samples at t=0.



Results so far indicate that – at least in cold-water environments – automated sampling over a year allows for studies of seasonal changes in microalgal communities studies without major biases. Surprisingly, sequencing results from samples preserved with standard preservatives deviated less from the reference community than those where specific agents for molecular studies were added.

Validating workflows

As part of the recently-formed Global Omics Observatory Network (GLOMICON), 18S based analyses of surface water samples are currently carried out at different institutions in Europe, the US, and Canada. The inter-comparison addresses the full workflow from DNA extraction to bioinformatics. The study will provide information on the differences introduced by the different methodologies currently in place and will have important implications for the integration and comparison of data from different observatories.



Map with the institutions taking part in the workflow-intercomparison study. Environmental samples are exchanged as well as DNA extracts from mock communities.

Acknowledgements

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