Tracking sea trout, cod, wrasse, salmon and sharks around Bergen

Knut Wiik Vollset[1], Saron Behre[1], Anne Christine Knag, Lotte Svengård Dahlmo[1], Robert Lennox[1,3]

[1]NORCE Norwegian Research Centre, Laboratory for Freshwater Ecology and Inland Fisheries, Nygårdsgaten 112, Bergen 5008, Norway
[2] Bergen Kommune, Bymiljøetaten
[3]Norwegian Institute for Nature Research, Høgskoleringen 9, Trondheim 7034, Norway

Acoustic telemetry is a tool that is used to track aquatic animals around the world. It involves physically capturing and operating a battery driven transmitter into the fish, and then tracking its behavior by a network of hydrophones (i.e. receivers) that can decode the information sent from the transmitter. In and around Bergen, our group has established a network of more than 100 receivers where multiple research projects will track salmon, sea trout, cod, wrasse, and sharks over the next decade. The latest addition to this network is a local network around the city centre of Bergen in collaboration with Bergen kommune, where the goal is to track the behavior of cod, wrasse and sea trout during a period of 3 years to study how fish are impacted by the ongoing marine sea floor restoration, river restoration in Møllendal and the sea front restoration in Store Lungegårdsvatn. The goal of this project is to document how these species are impacted before, during, and after the process of restoring the urban fjord areas, and give concrete advice on how to best conserve and further develop the ecosystem services these species provide. This involves taking samples of fish to measure endocrine stress levels and tagging and tracking the three species to inform Bergen kommune about how to minimize impact on fish and their habitat and facilitate the succession of thriving urban ecosystems in the years to come.

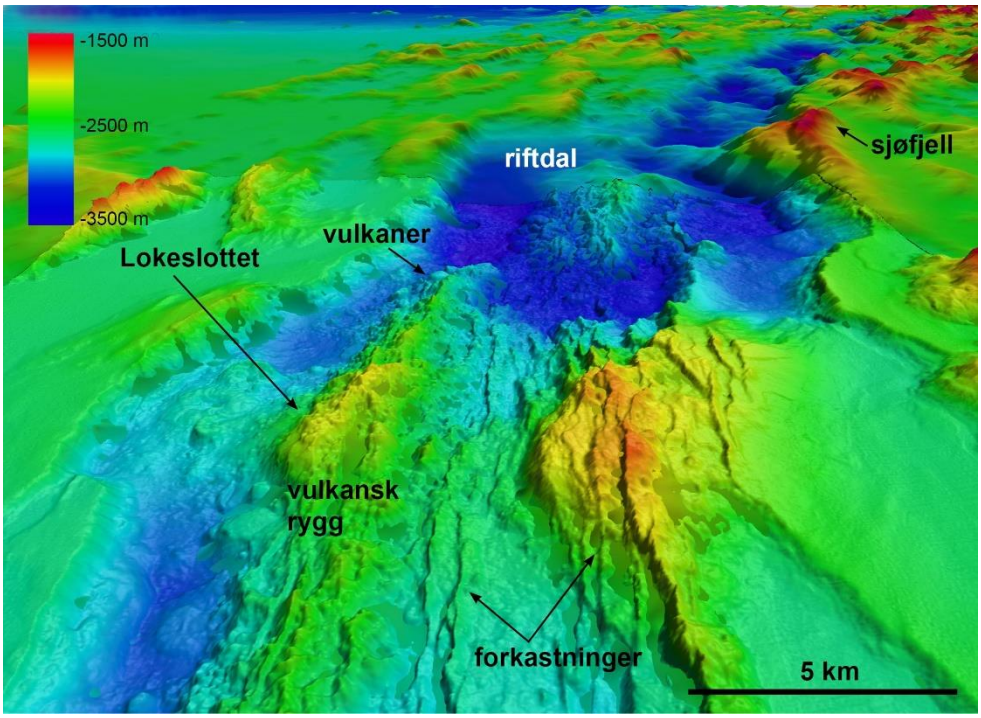
Mareano på store dyp i Norskehavet

Terje Thorsnes[1], Lilja Bjarnadottir[1], Hanne Hodnesdal[2], Frithjof Moy[3]

[1] Norges geologiske undersøkelse, Postboks 6315 Torgarden, 7491 Trondheim
[2] Kartverket Sjødivisjonen, Postboks 60, 4001 Stavanger
[3] Havforskningsinstituttet, Nye Flødevigsveien 20, 4817 His
Kontakt: terje.thorsnes@ngu.no

Mareanoprogrammet har siden 2005 kartlagt miljøforholdene på havbunnen på store deler av kontinentalsokkelen i Norskehavet og Barentshavet. Nå står dyphavet for tur.

Det er forventninger til at det finnes økonomisk utnyttbare forekomster av mineralforekomster i dyphavet. Stort behov for sjeldne metaller til for eksempel vindmøller og solcellepaneler, som skal realisere det grønne skiftet, og usikkerhet omkring fremtidig forsyningssituasjon og behov har aktualisert leting etter havets gull. Virkningen av en potensiell mineralindustri til havs er ukjente, og det er et stort behov kunnskap om miljøet i dyphavet for å fatte kunnskapsbaserte vurderinger. Universitetet i Bergen med professor Rolf Birger Pedersen i spissen har siden tidlig på 2000-tallet studert varme kilder og metallforekomster langs den midt-atlantiske ryggen, og manganskorpeforekomster på bratte fjellsider. Oljedirektoratet har siden 2018 utført flere tokt for å kartlegge geologiske og geofysiske ressurser, og i 2019 trådte et nytt lovverk om havbunnsmineraler i kraft. Gjennom forvaltningsplanarbeidet for Norskehavet har regjeringen påpekt kunnskapshull med hensyn til miljøforholdene i de dype delene av Norskehavet. Dette er bakgrunnen for at Mareano har startet opp en regional kartlegging av havbunnen i dyphavet.



Figur 1 Terrengmodell fra den midt-atlantiske ryggen, med bl.a. mineralforekomsten Lokeslottet.

Quantifying blue carbon beach deposits using high-resolution UAV imagery

Yalei Li[1,2], Kasper Hancke[1]

[1] Adresse: Norwegian Institute for Water Research (NIVA), Oslo, Norway
[2] Adresse: State Key Laboratory of Estuarine and Coastal Research, Institute of Eco-Chongming, East China Normal University, Shanghai, China
Kontakt: Yalei Li, 52173904027@stu.ecnu.edu.cn

Seagrass and macroalgae biomass deposit onshore as 'beach wrack' by tidal waters and episodic events and hereby represent an ocean-to-land transport of carbon and nutrients. On land, beach wrack can be directly consumed by macrofauna, re-mineralized by microorganisms, or washed back to the sea, during which recycling of carbon and nitrogen will affect the biochemical cycles in coastal zones. Manual quantifications of beach wrack are difficult and time-consuming due to the complex topographic conditions and remote locations. Here we presented the development of a novel tool using unmanned aerial vehicles (UAVs) photogrammetry combining *in-situ* sampling for carbon and nitrogen contents of wrack to quantify marine nutrition depositions at beaches. The accuracy of UAVs method for volumetric acquisition was evaluated by comparing the UAVs-based volume estimates with ground measurements of positioned cubes ranging in size from 125 to 88, 218 cm^3, showing a high accuracy of the UAVs method. We also compared the accuracy of UAVs estimates with other conventional methods such as ruler and GNSS-RTK measurements and found that UAVs performed better in measuring the cross-transect area, followed by GNSS-RTK and ruler measurement. The volumetric estimates of beach wrack depositions showed robust results (using Pix4Dmapper for volume calculations) however somewhat lower volume estimates than conventional methods. The lower estimates (38 to 43%) were likely due to differences in algorithms, irregular beach terrain and rough surface of beach wrack, or personal errors derived from manual measurements. This study demonstrates that UAVs method can be regarded as a good choice for volume estimates, especially when the terrain features below the beach wrack was known. Besides, UAVs demonstrate a strong advantage when time and cost were included in the evaluation and even performed best when the automatic-process time was excluded. The advantage would further increase with the rise of project scale, and as such the method has multiple scientific and commercial applications related to environmental monitoring and marine resource exploration, respectively.

Benthic mesocosms, a tool to understand complex ecological processes in the coastal zone

Hartvig Christie[1]

[1] Norsk Institutt for Vannforskning, NIVA. Økernveien 94, 0579 Oslo
Kontakt: hartvig.christie@niva.no

While mapping and monitoring uncover strongly degraded ecosystems in e.g. seaweed or seagrass beds, the understanding of complex processes/drivers/stressors behind the changes are difficult to understand, particularly when more than one factor is responsible. Building up coastal ecosystems in large mesocosms has been a tool to understand such complex interactions. At NIVAs field station Solbergstrand we have during years established highly diverse seaweed ecosystems in 12 large mesocosm, each on 12m^3 of water and 1.5 m deep. They are supplied with ambient seawater, wave generators and 30 cm tidal water level variations. These communities can be manipulated with different physical (e.g. waves), chemical (e.g. eutrophication), and biological stressors (grazing, predation). These factors can be tested alone and in combination (synergism) compared to controls. Some examples will be given on effects of eutrophication, mesopredator release, and grazing. The results can be of importance for restoration actions.

The use of optics and acoustics on gliders and satellites to understand the Lofoten-Vesterålen Marine Ecosystem

Sünnje L. Basedow[1*], Kanchana Bandara[1], Cait McCarry[2], Stig Falk-Petersen[3], Lionel Camus[3], David McKee[2], Huizi Dong[4], Meng Zhou[4,] Emlyn Davies[5], Walker O Smith Jr[4]

[1] UiT The Arctic University of Norway, Tromsø, Norway
[2] Strathclyde University, Glasgow, Scotland
[3] Akvaplan-niva, Tromsø, Norway
[4] Shanghai Jiao Tong University, Shanghai, China
[5] Sintef Ocean, Trondheim, Norway
* Contact: sunnje.basedow@uit.no

In recent years several larger research projects (NRC Sea Patches, NRC-SNCF Stressor, NRC Demo2000 Glider) have focused their attention on one of the designated, especially important and vulnerable ecosystems in Norway, the Lofoten-Vesterålen marine ecosystem. New technology (Sailbuoy, Seaglider, echo sounder EK80) in combination with advances in theoretical development (remote sensing, Lagrangian Coherent Structure modelling) have deepened our understanding of important processes operating in the area. This includes: (i) a strong and stable front between Norwegian Coastal Current and Norwegian Atlantic Current that effectively hinders exchange of plankton across that barrier for 40 days on average each year and can contribute to a spatio-temporal match between cod larvae and their naupliar prey (ii) very high abundances of *Calanus finmarchicu*s, in particular at the shelf break, that can form dense surface swarms, which we might observe by ocean colour remote sensing and which can exert a significant grazing pressure on primary producers, and (iii) new insight into copepod behaviour, with *Calanus* sp. responding flexibly to cloud cover, surface turbulence and predators.

Impacts of airgun blasts used in seismic surveys on mortality and growth in the copepod *Acartia tonsa*

Vereide, Emilie Hernes[1]; Mihaljevic, Marina[2]; Browman, Howard I.[2]; Fields, David M.[3], Agersted, Mette Dalgaard[4]; Titelman, Josefin[5]; de Jong, Karen[1]

[1] Institute of Marine Research, Nykirkekaien 1, NO-5004 Bergen, Norway
[2] Institute of Marine Research, Austevoll Research Station, Sauganeset 16, NO-5392 Storebø, Norway
[3] Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, P.O. Box 380 East Boothbay, ME, USA 04544
[4] Aarhus University, Department of Ecoscience, Frederiksborgvej 399, 4000 Roskilde, Denmark
[5] University of Oslo, Department of biosciences, PO BOX 1066 Blindern, NO-0316 Oslo, Norway
Contact: emilie.hernes.vereide@hi.no

Seismic surveys are conducted worldwide to explore oil and gas deposits and map subsea formations. In the Norwegian Exclusive Economic Zone alone, over 133 000 vessel kilometers per year are covered with seismic blasting. Investigations into the effects of seismic airgun blasts on zooplankton are scarce, and even less is known about the impact on the younger life stages despite their importance in marine ecosystems. The few published studies on zooplankton responses to seismic airgun blasts report results ranging from no effects to substantial mortality. We conducted a field experiment to investigate egg hatching, mortality, and naupliar growth of the calanoid copepod *Acartia tonsa* when exposed to blasts from an airgun array (2 x 40-inch airguns). Eggs and nauplii were put in plastic bags and attached to a line at 6 m depth in the field. The airgun array was pulled along an oval transect with its closest point at 50 m from the bags. Three bags of eggs and three bags of nauplii were exposed for 2.5 h to either the airgun array, a boat control, or a silent control. After exposure, the egg hatching rates, mortality, and naupliar growth were quantified. The data shows less increase in body weight over time and increased mortality after seismic exposure, while egg-hatching rates were unaffected. The immediate mortality in airgun exposed nauplii was higher (~13%) in comparison with silent and boat controls (<5%). The same applied for the longer-term mortality, where the airgun exposed nauplii showed higher mortality in comparison with the control groups, measured up to 6 days after exposure. Over the first four days after exposure, the specific growth rates based on average body weight were 0.04, 0.11, and 0.18 day^{-1} in the airgun exposed and silent and boat controls, respectively. Thus, these experiments indicate that exposure to airgun blasts at close range have some effect on mortality and growth of *Acartia* and suggests that future work should include early stages of zooplankton to determine the full range of effects.

Marine basemaps in the coastal zone – the Fjøløy pilot study of remote sensing-methods for shallow coastal habitat mapping

Jonas Thormar[1]

[1] Havforskningsinstituttet, Forskningsstasjon Flødevigen, 4817 His
Kontakt: Jonas.Thormar@hi.no

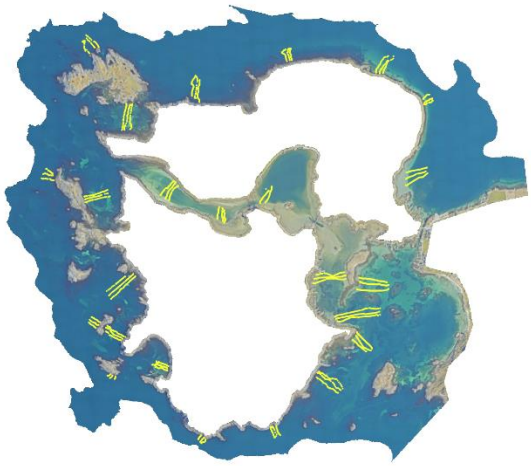
National ambitions of "blue growth", i.e. the sustainable economic growth of the marine and maritime sectors, increases the need and value of marine mapping. Ready access to maps allows for holistic spatial planning with optimal placement of activities and development while at the same time reducing environmental impact, conflicts of interest, case processing time and costs.

"Marine Grunnkart i Kystsonen" is a collaboration between The Norwegian Mapping Authority (KV), Geological Survey of Norway (NGU), and the Institute of Marine Research (IMR) and financed by ministries, municipalities and County Councils. The task is to map three pilot areas and at the same time develop methodology for high quality and efficient processes which is crucial if it is to be scaled to nationwide mapping. The area within 1 nm of the coast is 90.000 km^2 which requires 4500 km^2 to be mapped yearly if to be completed in 20 years.

Within this scope we are testing multiple remote sensing technologies on Fjøløy and Klosterøy in the Stavanger region, covering an area of 5.5 km^2 in the 0-30m depth range. While the focus of IMR and this talk is on biological habitat mapping, the analysis relies on products such as substrates from NGU and depth models from KV which aims at closing the gap towards land where ship-based acoustic methods are inefficient or impossible.

The methods applied span from ground truth and training data collected in the field to remote sensing using acoustics (single beam and multibeam), airborne RGB and hyperspectral imagery, bathymetric LiDAR, and multispectral satellite imagery.

Although data are yet to be analyzed, the methods and perspectives will be discussed. Each technology has strengths and limitations of e.g. coverage, depth, spatial- and classification accuracy. Some may only provide good maps of single vegetation type and a suite of methods needed if quality is the only decisive parameter. But cost-benefit prevails, and identifying the optimal combinations is paramount to deliver end products for the benefit of society.



Autonom optisk kartlegging av havbunn – Erfaringer fra kartlegging av Store Lungegårdsvann

Trygve Olav Fossum[1], Anne Christine Knag[2], Øystein Sture[1], og Petter Norgren[1]

[1] Skarv Technologies AS, Havnegata 9, 7010, Trondheim
[2] Bergen kommune
Kontakt: tof@skarvtech.com

I forbindelse med prosjektet Renere Havn Bergen ble det foretatt optisk havbunnskartlegging av Store Lungegårdsvann. Her ble det brukt autonome undervannsfarkoster (AUV) og overflatefarkoster (ASV) til arbeidet. Det ble innhentet data med stereo- og undervanns hyperspektralt kamera. Det ble også testet nyutviklede undervannslys som reduserer backscatter-effekten under turbide forhold. Hovedformålet med undersøkelsen var å kartlegge forsøpling opp mot planlegging av oppryddingsarbeid, men også granske biologisk mangfold og status. Automatisk deteksjon av objekter gjøres ved bruk av mønstergjenkjenning og maskinlæring, der alle deteksjoner blir nøyaktig georeferert. Prosjektet er et eksempel på hvordan marin robotikk kan brukes til å gjøre mer effektiv og detaljert undervannskartlegging av urbane områder som havnebasseng.

Figur 2. Undervannsfarkostene som ble brukt under undersøkelsen. Farkost SROV (stereokamera [til venstre]) og farkost UROV (undervannsspektralkamera).

Behavioural plasticity offset thermal drivers of spawning phenology in cod

Anders Frugård Opdal[1], Peter Wright[2], Geir Blom[3], Hannes Höffle[4] and Olav S. Kjesbu[4]

[1] Institutt for biovitenskap, Universitetet i Bergen
[2] Marine Scotland Science, Marine Laboratory, Aberdeen
3 Statistikkavdelingen, Fiskeridirektoratet, Bergen
4 Havforskningsinstituttet, Bergen/Tromsø
Kontakt: anders.opdal@uib.no

Increasing sea temperatures are expected to speed up the physiological rates of ectotherms. In fish, ovarian development rates are known to increase with increasing temperatures, predicting earlier spawning in warmer waters. A general expectation is that climate change will lead to a trophic mismatch between spawners and the food for their newly hatched offspring. We used biological data, including body length, otoliths and gonad developmental stages, collected from ~200.000 individual Northeast Arctic cod caught between 62°N and 72 °N in the years 1980 to 2019. Our analysis show that cod has spawned progressively earlier since the 1990s, likely due to ocean warming. More interestingly, we also find that individuals appear to delay or advance spawning time by several weeks, dependent on their choice of spawning location, but independent of their thermal history. The ability to offset thermal drivers, can allow individuals to track local environmental conditions, other than temperature, such as the phytoplankton spring bloom onset, and regulate their spawning time to maximize fitness.

Hva spiser torsken - modellstudier på torskens diett og næringsnettet i Barentshavet

Geir Ottersen[1] og Rebecca Emma Holt[2]

1 Forskningsgruppe Oseanografi og klima, Havforskningsinstituttet
2 Seksjon for akvatisk biologi og toksikologi, Institutt for Biovitenskap, Universitetet i Oslo
Kontakt: geir.ottersen@ibv.uio.no

Vi presenterer her resultater fra prosjektet CoDINA - Cod DIet and food web dyNAmics. CoDINA er et Norsk-Britisk-Russisk samarbeidsprosjekt ledet av Havforskningsinstituttet. Vi har studert sammenhengen mellom Barentshavstorsken (skrei) og dens viktigste byttedyr, altså predator-byttedyr interaksjoner. Lodde, mindre torsk (kannibalisme), andre fiskearter og ulike krepsdyr er de viktigste innslagene på menyen. Et sentralt spørsmål er hvordan dette samspillet påvirkes av størrelsen på torskebestanden, om det er mange store torsk i bestanden, og tilstanden ellers i økosystemet.

Kvaliteten på resultatene fra statistiske analyser og modeller avhenger av dataene som er tilgjengelige. Derfor var tilrettelegging og kvalitetskontroll av data i en norsk-russisk database over innholdet i torskemager en sentral oppgave i første fase av CoDINA. Parallelt ble gjenværende deler av et britisk torskmagedatasett for det vestlige Barentshavet fra 1930 til 1970-tallet digitalisert, kvalitetskontrollert, og tilrettelagt. De to datasettene ble deretter slått sammen og utgjør nå en database med kvantitativ informasjon for mer enn 400 000 torsk. Norske og britiske data er åpent tilgjengelige fra https://doi.org/10.21335/NMDC-2139169383.

Trender i torskens diett med økende alder / størrelse, rovdyr-byttedyr interaksjoner og ulikheter i seleksjon i bytte-størrelse ut fra torskens størrelse har blitt undersøkt. Skifte i kosthold med økende torskestørrelse ble observert, med fisk som gradvis viktigere byttedyr. Kostholdet varierte betydelig mellom årene i løpet av perioden 1984-2016, i samsvar med endringer i mengden av ulike byttedyr.

I løpet av 2000tallet har antallet snøkrabber i Barentshavet økt mye. Vi har funnet at mengden snøkrabbe i magene til litt større torsk også har økt. Dette er et eksempel på at informasjon fra torsken kan, sammen med andre målinger, brukes for å lage indikatorer for økosystemtilstand.

Vi har også sett på hvordan omfanget av kannibalisme hos Barentshavstorsken fluktuerer med størrelsesfordelingen i bestanden og om den blir påvirket av variasjon i mengden av favorittbyttedyret, lodde.

The role of food limitation and increased temperature in the recent recruitment failure of North Sea herring

Marta Moyano[1], Anna Akimova[2], Gregor Börner[3], Cindy van Damme[4], Romain Frelat[5], Myron A. Peck[6]

[1] University of Agder, Universitetsveien 25, 4604 Kristiansand, Norway
[2] Thünen Institute of Sea Fisheries, Herwigstraße 31, Bremerhaven D-27572, Germany
[3] Institute of Marine Ecosystem and Fishery Science, University of Hamburg, Große Elbstraße 133, Hamburg D-22767, Germany
[4] Wageningen Marine Research, Haringkade 1, 1976 CP Ijmuiden, the Netherlands
[5] Wageningen University & Research, 6708 PB Wageningen, the Netherlands
[6] Royal Netherlands Institute for Sea Research (NIOZ), Department of Coastal Systems (COS), PO Box 59, 1790 AB Den Burg (Texel), the Netherlands
Kontakt: marta.moyano@uia.no

Early-life history of marine fishes is believed to be the main driver of the recruitment variability and an important bottleneck in the adaptation of fish populations to changing climate. Starvation is an important cause of larval mortality but many aspects, e.g. the spatiotemporal variability in prey availability, the role of suboptimal feeding or larval behavioral adaptation to unfavorable feeding conditions, are still not well understood. Here we investigate the role of food limitation and increased temperature as drivers of recent recruitment variability of North Sea herring (*Clupea harengus*) by using a combined field and modelling approach. First, we implemented micro- and mesozooplankton sampling (55 – 3000 μm) in a routine fisheries assessment survey (International Herring Larval Survey, 2013-2019) to obtained information on spatiotemporal variability in plankton diversity, biomass, and size-structure in the spawning grounds. Then we used this *in situ* data to explore potential food limitation using an individual-based model of larval herring growth and foraging. Modelled outputs suggest that prey fields could support growth for larvae > 12mm in autumn spawning grounds (Buchan/Banks), but not in December (Downs) when food-limitation seem to impact for most larval sizes (9-20 mm). Model-based estimates of the cumulative starvation mortality were highly sensitive to the choice of the initial length distribution of exogenously feeding larvae. Our results suggest that, during the time period we examined, starvation mortality had an important contribution to overall mortality in December, but that during September other additional processes (e.g. predation on early larvae and/or prey field deficits impacting the survival of later larval or juvenile stages) have likely contributed to larval mortality.

Hot and hungry: a trait-based theoretical approach to the direct and indirect effects of heatwaves on plankton communities.

Maria Grigoratou[1], Camila Serra-Pompei[2], Andrew Pershing[1,3]

[1] Gulf of Maine Research Institute, Maine, USA
[2] Center for Climate Change Science, Massachusetts Institute of Technology, Massachusetts, USA
[3] Climate Central, Princeton, New Jersey, USA
Kontakt: mgrigoratou@gmri.org

Empirical and theoretical approaches have shown strong links between ocean warming and shifts in distribution and community composition. Though as temperature is linked with other environmental conditions, is hard to identify the ecosystem drivers for different trophic levels. Here we extend the Nutrients-Unicellular-Multicellular (NUM) model of the plankton community to account for the traits of size, feeding modes and temperature optima. With the model we explore the effects of heatwaves on community composition at seasonal and annual time scales. Without acclimation or adaptation, the preliminary results show temperature as the main driver of protist distributions, while the distributions of metazoa are driven by trait- and density-mediated indirect interactions caused by temperature. Heatwaves also alter the functional richness and total biomass of the community, but the results depend on the duration of the heatwave and the season it appears. Our study highlights the importance of species traits and interspecies interactions on population dynamics under changing climate conditions.

Parasite disease in coastal zooplankton

Josefin Titelman[1], Lasse Eliassen[1], Even Garvang[1], Tom Andersen[1]

[1] Department of biosciences, University of Oslo, PO BOX 1066 Blindern, 0316 Oslo
Kontakt: josefin.titelman@ibv.uio.no

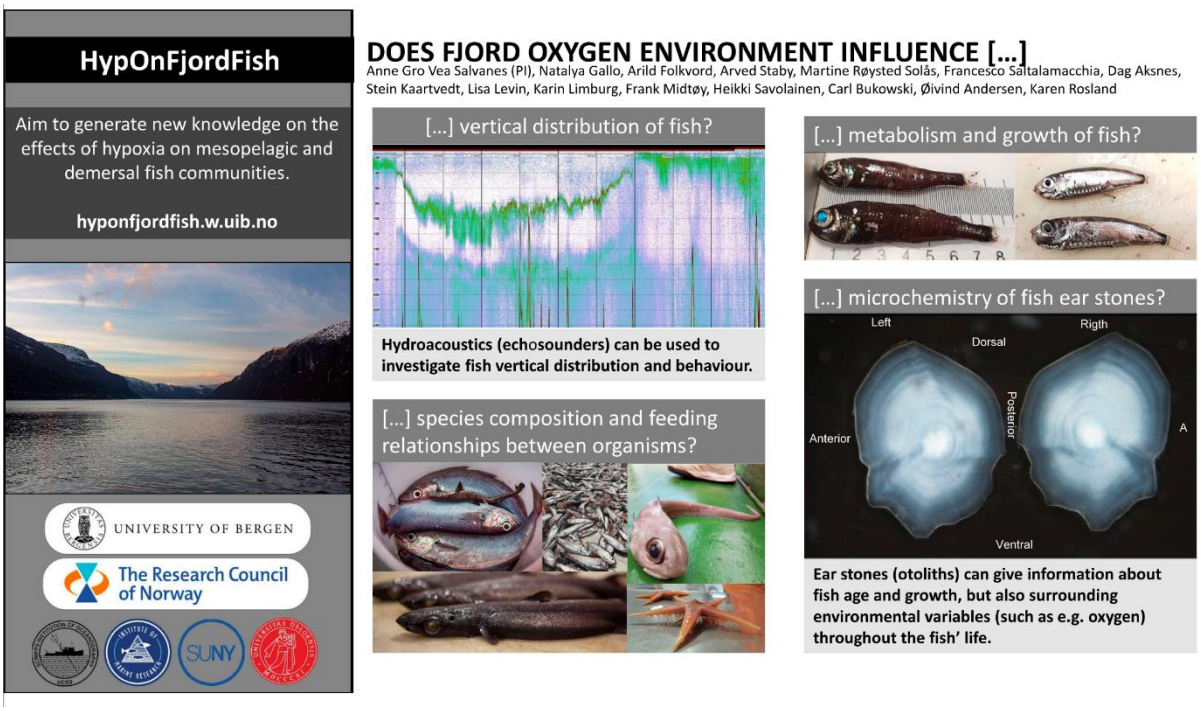
By now, we are all painfully aware of the capacity of disease to alter individual state and behavior, as well as communities, ecosystems, and even the globe. All organisms interact with others on different temporal and spatial scales, and most organisms harbor other organisms, symbionts, within them. Despite the overwhelming theory and knowledge stemming from terrestrial systems, our understanding of how parasites and disease affect common zooplankton and structure pelagic systems is in its infancy. In a recently started project (POICE) we focus on copepods and their parasitic and nonparasitic symbionts to quantify the role and effect of parasites on their hosts and on pelagic ecosystem functioning. We will present some (i) preliminary data of seasonal distribution patterns of parasites in Oslofjorden, as well as (ii) a colorful example of a common, but mysterious parasite that affects the looks, physiology, and vertical behavior of its *Calanus* host. Finally, the POICE team also has a simple request for the audience.

The HypOnFjordFish project - effects of oxygen loss on fish in West Norwegian fjords

Anne Gro Vea Salvanes[1], Natalya Gallo[1], Arild Folkvord[1], Arved Staby[2], Martine Røysted Solås[1], Francesco Saltalamacchia[1], Dag Aksnes[1], Stein Kaartvedt[3], Lisa Levin[4], Karin Limburg[5], Frank Midtøy[1], Heikki Savolainen[1], Carl Bukowski[1,6], Øivind Andersen[1], Karen Rosland[1]

[1] Department of Biological Sciences, University of Bergen
[2] Institute of Marine Research, Bergen
[3] Department of Biology, University of Oslo
[4] Scripps Institution of Oceanography, University of California, San Diego, USA
[5] State University of New York College of Environmental Science and Forestry, USA
[6] Freie University, Berlin
Kontakt: Anne.Salvanes@bio.uib.no

We will provide a poster that present the background for the recently started project *"Hypoxia effect on fjord fish (HypOnFjordFish)"* and what we are planning to do, and perhaps provide some glimpses of preliminary findings. *HypOnFjordFish* is a multidisciplinary research project that uses West Norwegian fjords as natural infrastructure to generate new knowledge on the effects of hypoxia on mesopelagic and demersal fish communities. Such information is needed to sustainably manage marine resources and fjord environments. The project originate from findings on an annual graduate field course in Marine Ecological Field Methods (MAR310….BIO310…and now BIO325 Ocean Science), which takes students on annual research visits to Masfjorden and other neighboring fjords. Repeated visits to Masfjorden led to the serendipitous discovery: the basin water turned hypoxic in 2016! The project aims to generate new knowledge on how fish physiologically and behaviourally respond to hypoxia and how this affects populations, trophic interactions, and production in fjord ecosystems.



Temperature tolerance and distribution of the invasive non-indigenous red algae *Agarophyton vermiculophyllum* in seagrass meadows in Norway

Ingvild Sundal Joys[1,2], Barbro Haugland[2], Vivian Husa[2], Kjersti Sjøtun[1], and Henning Steen[2]

[1] Department of Biological Sciences, University of Bergen, Bergen, Norway
[2] Institute of Marine Research, Bergen, Norway
E-mail: ingvildjoys@gmail.com

Invasive non-indigenous species are considered one of the main threats to the global biodiversity. The marine red alga *Agarophyton vermiculophyllum* originating from the northwest Pacific has been introduced to all the main coast in the northern hemisphere, Norway included and is considered highly invasive. *A. vermiculophyllum* has been shown to negatively affect *Zostera*-species, which form the highly productive and biodiverse habitat of seagrass meadows.

A field study was conducted to assess the abundance of *A. vermiculophyllum* in south-eastern Norway in areas with large seagrass meadows. Abundance data was obtained through a combination of video footage and grapnel samples. Low abundance was detected at the two sites in the outer Oslo fjord, while higher abundance was detected at the sites in inner-Oslo fjord. On the four sites combined *A. vermiculophyllum* was present on more stations outside the seagrass meadows than together with the seagrass *Zostera marina*.

In addition, a temperature experiment imitating Norwegian winter conditions was performed to investigate survival of *A. vermiculophyllum* by ability of regrowth and photosynthetic capacity once returned to favourable conditions. There was found no significant differences in the growth or maximum photosynthetic yield (Fv/Fm) between the groups that had been exposed to water of 0°C, 2°C, 8.4°C or 11.7°C degrees.

Agarophyton vermiculophyllum does not seem to be a threat to the investigated seagrass meadows at this point, but areas where it is present together with the seagrass should be monitored to assess possible future negative impact on this ecosystem. Exposure to low temperatures had no effect on survival, and temperatures down to 0°C hence does not serve as an apparent limitation to further dispersal in Norwegian waters.

ScandiFish: A metabarcoding reference database for Scandinavian fish based on MiFish primers.

Eivind Stensrud[1], Alexander Eiler[1], Mats Töpel[2,3]

[1]Universitetet i Oslo
[2]IVL Svenska Miljöinstitutet AB
[3]Göteborgs universitet
Contact: eivisten@uio.no

Metabarcoding is a powerful tool which has the potential to be a non-invasive analysis for high-resolution assessment of biodiversity. DNA from a sample can be amplified and compared to a reference database to give an indication of what species are present. This method can separate cryptic species and DNA can be extracted from various environmental samples as water, or other samples where morphological identification is impossible (Thomsen & Willerslev, 2015).

To prepare sequencing libraries, DNA in a sample is amplified with a set of primers. These primers attach to the DNA and binds to DNA polymerase which amplify the DNA between the primers as well as add sequencing specific adapters. The choice of primers can influence the resolution of the analysis, as some amplified DNA fragments are better suited to separate species. MiFish is regarded to be the superior for separating fish-species (Zhang, Zhao, & Yao, 2020), and therefore ScandiFish is based on the hypervariable region of 12s rRNA gene which MiFish primers amplify (Miya et al., 2015).

A list of 525 unique fish species were extracted from artsdatabanken.no/se and naturbasen.dk in November 2020. The official Latin names were obtained from the Catalogue of Life database through FishBase. Then the accession numbers and sequences which was assigned to the Scandinavian fishes is downloaded from GenBank. To find sequences matching the MiFish-region, BLAST was used to compare to the reference sequences. If they matched, they were added to the database for further validation.

With this method, sequences are not required to be annotated to the 12s rRNA gene region, which allows for most sequences of interest to be found. This results in a higher coverage of species which decreases false discovery rate and increases the classification sensitivity, which results in a better estimation of biodiversity.

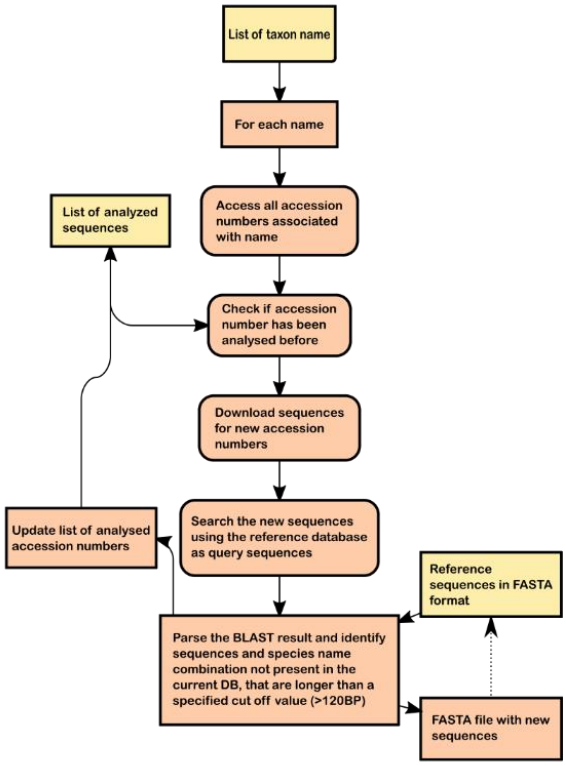


Figure 1: A flowchart display of the workflow for the pipeline used to build ScandiFish. Yellow boxes indicate input files. Brown boxes indicates analytics steps. Squares are steps which are done locally on a computer and boxes with rounded edge are done

In short, ScandiFish has a higher coverage than existing databases for the Scandinavian fish community and compatible to a set of primers with a higher discriminatory power compared to more widely used primers (Collins et al., 2021).

Collins, R. A., Trauzzi, G., Maltby, K. M., Gibson, T. I., Ratcliffe, F. C., Hallam, J., . . . Genner, M. J. (2021). Meta-Fish-Lib: A generalised, dynamic DNA reference library pipeline for metabarcoding of fishes. *J Fish Biol, 99*(4), 1446-1454. doi:10.1111/jfb.14852

Miya, M., Sato, Y., Fukunaga, T., Sado, T., Poulsen, J. Y., Sato, K., . . . Iwasaki, W. (2015). MiFish, a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species. *Royal Society Open Science, 2*(7), 150088. doi:10.1098/rsos.150088

Thomsen, P. F., & Willerslev, E. (2015). Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. *Biological Conservation, 183*, 4-18. doi:https://doi.org/10.1016/j.biocon.2014.11.019

Zhang, S., Zhao, J., & Yao, M. (2020). A comprehensive and comparative evaluation of primers for metabarcoding eDNA from fish. *Methods in Ecology and Evolution, 11*(12), 1609-1625. doi:https://doi.org/10.1111/2041-210X.13485

eDNA as a monitoring tool for the invasive *Neogobius melanostomus.*

Lars Martin Myhre[1], Vivian Husa[2], Rudolf Svensen[2], Thomas Dahlgren[3]

[1] Universitetet i Bergen
[2] Havforskningsinstituttet
[3] Stavanger Museum
[4] NORCE Norwegian Research Centre
Contact: larsmmyhre@gmail.com

The round goby, *Neogobius melanostomus*, is a wide-ranging invasive species that originates from the Black Sea. Through both shipping and natural dispersal, it has spread and established in the Laurentian Great Lakes, the Baltic Sea and European rivers the last decades.

In the Baltic Sea it was first observed in the early 90s along the coast of Gdansk, Poland. Genetic evidence suggest that the species is introduced to the Baltics at multiple, separate occasions. In addition, it has slowly spread through natural dispersal over the years. Despite it being present in Skagerrak since 2010, it is yet to be observed along the Norwegian coast.

This project set out to find the round goby through active fishing, passive fishing and using environmental DNA (eDNA) methods. eDNA from water samples has earlier been proven as a efficient tool to indicate the presence of *Neogobius melanostomus* in both lab-experiments and field-experiments. Through these experiments eDNA testing has shown to improve monitoring. However, the method is still not reliable enough to be implemented as a sole monitoring tool, hence additional methods were used in this project.

Our project investigated Gothenburg, the eastern- and the western side of the Oslo fjord. Each station was selected with regards to environmental factors such as salinity and substrate. Within each station there were taken water samples for eDNA testing. Further, there were placed minnow traps for passive fishing in addition to active fishing. The active fishing was performed with a simple rod and baited hook set-up.

The water samples were filtered with pore-size of 0.45µm. During November and December 2021 DNA will be extracted from these filters and be investigated for genetic material from *N. melanostomus*. It is expected to find a correlation between captures/observations and positive responses from eDNA-testing. As this is still an ongoing project there are little to none results to be presented yet.

Deep-sea community responses to deoxygenation and reoxygenation in a western Norwegian fjord

Natalya D. Gallo[1,2], Martine Røysted Solås[1], Anne Gro Vea Salvanes[1,2]

[1] Department of Biological Sciences, University of Bergen, Bergen, Norway
[2] Bjerknes Centre for Climate Research, Bergen, Norway
Kontakt: natalya.gallo@uib.no

Between 2011 and 2018, the basin water of Masfjord, a western Norwegian fjord, experienced a ~67% decline in dissolved oxygen and rapidly transitioned from a well-oxygenated to a nearly hypoxic, deep-sea system. Following 2018, oxygen levels began to gradually increase, and then the basin water was renewed in the spring or early summer of 2021, returning basin water dissolved oxygen levels to those observed in 2011. Between 2011-2021, the University of Bergen has been conducting annual net-based sampling of mesopelagic and demersal communities in Masfjord through an ocean science course for Master's students. This unique 10-year ecological time series allowed us to examine how deep-sea communities responded to changes in dissolved oxygen conditions in the fjord. Since all aerobic organisms have specific respiratory requirements for dissolved oxygen, decreases in dissolved oxygen can affect organismal physiology and behavior and translate to changes in species distributions, interactions, community diversity, and composition. We will share the preliminary results of the community analysis on how deep-sea community diversity, biomass, and species composition responded to the deoxygenation and reoxygenation events in Masfjord. We will also identify species that showed strong responses across this time series, either in abundance or vertical distribution, which may suggest greater sensitivity to changes in dissolved oxygen. These results will help inform our understanding of deep-sea fjord community vulnerability to future trends in deoxygenation and will contribute to the growing understanding of the ecological impacts of ocean deoxygenation to marine ecosystems around the world.

A potential laboratory approach to expose animals to pressure drops that occur around a seismic airgun.

Karen de Jong[1], Emilie Vereide[1]

[1] Institute of Marine Research, Nykirkekaien 1, NO-5004 Bergen, Norway
Kontakt: karen.de.jong@hi.no

Airguns are used in seismic surveys to map geological structures below the sea floor, for example, in search of oil and gas. This activity exposes animals to impulsive sounds that are created by releasing an air bubble under water that expands explosively. The sounds consist of a loud pulse followed a sharp pressure drop. It has proven difficult to reproduce this sound in the laboratory, because underwater speakers of a size that is manageable in the laboratory are unable to provide enough power in the lower frequencies. Here, we propose a relatively cheap and easy-to-build chamber to expose small animals, such as zooplankton, to pressure drops in the laboratory. We compare the pressure drop to a recorded signal from a seismic airgun and discuss the potential and the limitations of the set-up.

Correlation between underwater light attenuation and dissolved oxygen

Solås Martine Røysted[1], Aksnes Dag Lorents[1]

[1] Department of Biological Sciences, University of Bergen, Bergen, Norway
Contact: martine.solas@uib.no

Many small pelagic fish and invertebrates undertake diel vertical migrations (DVM) in response to the daily variations in sunlight. These organisms appear as acoustically dense layers on an echosounder and are referred to as sound scattering layers (SSL). The daytime depth of the SSL has become an important proxy for active carbon flux by DVM organisms and the associated carbon sequestration. Since the first studies of SSLs in the 1950s, it has been known that the SSL daytime depth relates to epi- and mesopelagic light penetration, i.e., that the daytime depth is shallower in murky water than in clear water. More recent studies have found that shallow SSL daytime depth also concur with hypoxia, which has been interpreted as the SSL organisms avoiding hypoxic water masses. Due to lack of simultaneous in situ light and dissolved oxygen measurements, however, the role of dissolved oxygen versus light is uncertain. Several previous studies have found that hypoxic water tends to have higher light attenuation than well-oxygenated water. Here, we explore this relationship with simultaneous in situ measurements of light and dissolved oxygen in a fjord, Haugsværfjorden, that contains well-oxygenated, hypoxic as well as anoxic water masses. Our results suggest a strong positive correlation between light attenuation and hypoxia, meaning that less light penetrates hypoxic water. If this finding applies to the oceanic oxygen minimum zones, we should expect shallower SSL daytime depth and reduced active carbon flux in these regions due to the elevated light attenuation.

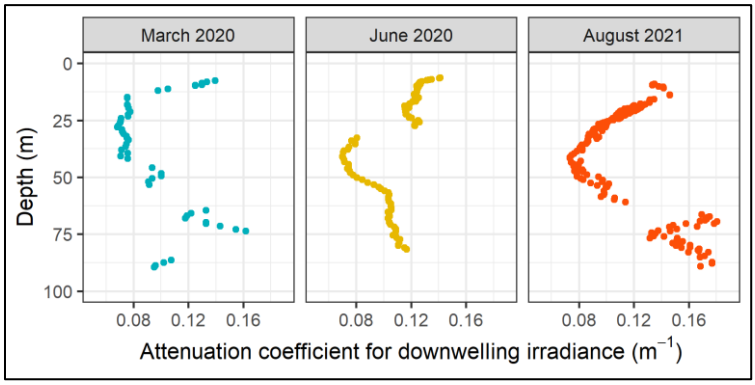


FIGURE 1. Preliminary figure of light attenuation coefficients from *in situ* light measurements for Haugsværfjorden in March 2020, June 2020 and August 2021 (two stations).

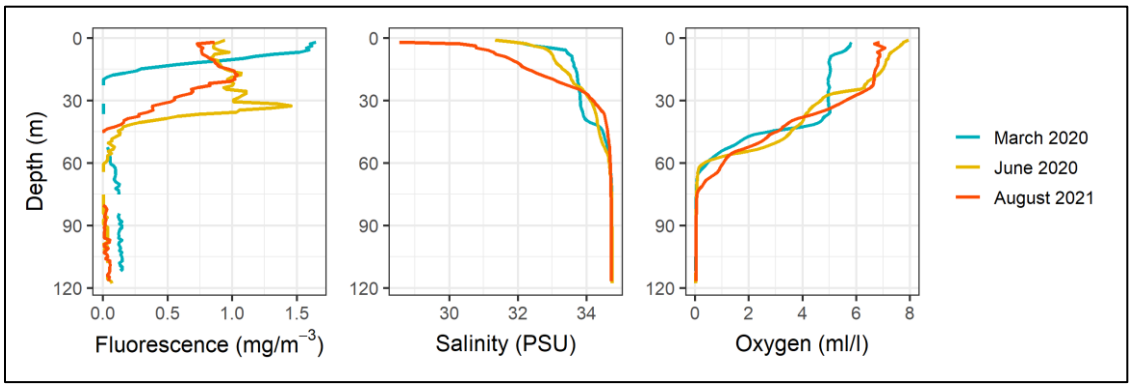


FIGURE 2. Preliminary figure of water characteristics of Haugsværfjorden from CTD casts during the three research cruises: March 2020, June 2020, and August 2021.

Validation of a species-specific eDNA-based test system for detecting non-indigenous American lobster *Homarus americanus*

Maud Ødegaard Sundt[1], Thomas Gunnar Dahlgren[2], Ann-Lisbeth Agnalt[3], Vivian Husa[3], Aud Larsen[4]

[1] Universitetet i Bergen [2] NORCE Norwegian Research Centre [3] Havforskningsinstituttet [4] NORCE Norwegian Research Centre Kontakt: msu031@uib.no

Introduced species have the potential of being a major threat to local biodiversity. Intentionally or unintentionally release of live specimens across physical barriers limiting the natural distribution of species, may lead to the establishment of invasive populations. The potential danger of invasive species calls for effective monitoring methods to detect early establishment of non-indigenous populations. The last decade numbers of studies using environmental DNA (eDNA) for bio monitoring has increased significantly. Organisms release eDNA into the environment which can be detected by analysing environmental samples with species-specific or universal primers. The aim of the present study was to investigate whether eDNA can be used to detect the introduced American lobster (*Homarus americanus*). *Homarus americanus* pose a threat to the Norwegian ecosystem as it may establish and function as a competitor, predator, spreader of pathogens, in addition to producing hybrids with the European lobster (*H. gammarus*). In the present study species specific primes and probes were designed and tested for detecting *H. americanus* and *H. gammarus* eDNA. A lab experiment was also conducted to assess the amount of released *H. americanus* eDNA and its degradation time. In addition, field seawater samples collected from a location with a known *H. gammarus* population and a location where a *H. americanus* female was found with remains of hybrid eggs. The field samples were analysed for both *H. americanus* and *H. gammarus* eDNA. The concentration of *H. americanus* eDNA was low in lab samples, and no eDNA from either *H. americanus* or *H. gammarus* was found in field samples. Further studies should focus on testing release of eDNA under different life stages and in varying environmental conditions, in addition to sampling in different ecological compartments. Results of the present study might however indicate that using eDNA is not a suitable for detection of lobsters as no *H. gammarus* eDNA was detected in area of established population. This result is important for conservation managing, where money and effort is put into researching the use of eDNA in bio monitoring, as it indicates that the method might not be optimal for detecting all species.

dCOD 1.0: decoding Ocean Health through a systems toxicology approach

Anders Goksøyr[1,8], Guttorm Alendal[2], Augustine Arukwe[3], Malin Celander[4], Dorothy J. Dankel[1], Nancy Denslow[5], Marta Eide[1], Siri Øfsthus Goksøyr[1], Bjørn Einar Grøsvik[8], Ketil Hylland[9], Inge Jonassen[6], Jan Ludvig Lyche[10], Mette Bjørge Müller[10], Pål A. Olsvik[8,11], Daniela Pampanin[12], Cinta Porte[13], John Stegeman[7], Fekadu Yadetie[1] & Odd André Karlsen[1]

[1]Dept of Biological Sciences, University of Bergen (UoB), Norway
[2]Dept of Mathematics, UoB, Norway
[3]Dept of Biology, NTNU, Norway
[4]Dept of Biological and Environmental Sciences, U of Gothenburg, Sweden
[5]U of Florida, Gainesville, FL, USA
[6]Computational Biology Unit, Dept of Informatics, UoB, Norway
[7]Woods Hole Oceanographic Institution, MA, USA
[8]Institute of Marine Research, Bergen, Norway
[9]Dept of Biosciences, U of Oslo, Norway
[10]Dept of Food Safety and Infection Biology, NMBU, Norway
[11]Nord University, Bodø, Norway
[12]University of Stavanger, Stavanger, Norway
[13]CSIC, Barcelona, Spain.

The Ocean is a fundamental contributor to human health and well-being. However, the marine ecosystems are under substantial and continual anthropogenic pressure. Direct effects of human activities, such as overfishing, waste disposal, and unsustainable aquaculture, are now coupled with global trends of climate change and ocean acidification. Furthermore, the Ocean serves as a sink for anthropogenic chemicals and microplastics that, in many cases, originate from negative side effects of legal offshore and coastal activities, urban run-offs and agriculture. Many of the contaminants released since the 1930s have later shown to be extremely persistent even after being banned, leaving a legacy of adverse effects on reproduction and growth in wildlife also at remote and pristine areas, such as the Arctic.

The Atlantic cod (Gadus morhua) is an important species in North Atlantic fisheries, as well as coastal and pelagic ecosystems. It is also a widely used indicator species in European monitoring programs. The goal of the dCod 1.0-project has been to integrate competencies in environmental toxicology, biology, bioinformatics and mathematics across the traditional department boundaries and within a Responsible Research and Innovation framework, to create a deeper understanding of the Atlantic cod's adaptations and reactions to stressors in the environment. Building on thorough studies and mapping of the cod genome and long research traditions on the physiology, toxicology and reproduction biology of cod, the dCod 1.0 project will expand our knowledge with genomics-based methods, with studies of how the cod genome responds under different environmental conditions. Through this approach, we hope to be able to develop methods that can be useful in assessing the health of the Ocean in various contexts, e.g. as a tool for environmental monitoring and risk assessment.

In dCod 1.0 we have generated large amounts of experimental samples and data using *in silico (*defensome modelling and metabolic reconstruction*), in vitro* (luciferase reporter assays with cod nuclear receptors and aryl hydrocarbon receptors*), ex vivo* (precision-cut liver slices), and *in vivo* aquaria and field studies, as data sets for bioinformatics analyses and mathematical models that can describe responses based on different scenarios. These can be important tools in search for tipping points and in designing new experiments.

Here we will highlight some results and experiences from the project involving lab and field studies, omics analyses, and transdisciplinary activities. How these results can translate into understanding environmental change and new practices for marine environmental monitoring will be discussed.

The dCod 1.0 project is funded under the Digital Life Norway initiative of the BIOTEK 2021 program, and the iCod 2.0 project under the ECOSYSTEM program of the Research Council of Norway (project no. 248840 & 244564).

"A cleaner break": Genetic divergence between geographic groups and sympatric phenotypes revealed in ballan wrasse (*Labrus bergylta*)

Gaute W. Seljestad[1,2] , María Quintela[2], Ellika Faust[3], Kim T. Halvorsen[4], François Besnier[2], Eeva Jansson[2], Arild Folkvord[1,2] , Kevin A. Glover[1,2]

[1] Department of Biological Sciences, University of Bergen, Bergen, Norway
[2] Institute of Marine Research, Bergen, Norway
[3] Department of Marine Sciences—Tjärnö, University of Gothenburg, Strömstad, Sweden
[4] Institute of Marine Research, Austevoll Research Station, Storebø, Norway
[5] Institute of Marine Research, Flødevigen, Norway
[6] Centre for Coastal Research, University of Agder, Kristiansand, Norway
Kontakt: gaute.seljestad@uib.no

Capture and long-distance translocation of cleaner fish to control lice infestations on marine salmonid farms has the potential to influence wild populations via overexploitation in source regions, and introgression in recipient regions. Knowledge of population genetic structure is therefore required. We studied the genetic structure of ballan wrasse, a phenotypically diverse and extensively used cleaner fish, from 18 locations in Norway and Sweden, and from Galicia, Spain, using 82 SNP markers. We detected two very distinct genetic groups in Scandinavia, northwestern and southeastern. These groups were split by a stretch of sandy beaches in southwest Norway, representing a habitat discontinuity for this rocky shore associated benthic egg-laying species. Wrasse from Galicia were highly differentiated from all Scandinavian locations, but more similar to northwestern than southeastern locations. Distinct genetic differences were observed between sympatric spotty and plain phenotypes in Galicia, but not in Scandinavia. The mechanisms underlying the geographic patterns between phenotypes are discussed, but not identified. We conclude that extensive aquaculture-mediated translocation of ballan wrasse from Sweden and southern Norway to western and middle Norway has the potential to mix genetically distinct populations. These results question the sustainability of the current cleaner fish practice.

Populasjonsdynamikk og livshistorie hos kråkeboller *Strongylocentrotus droebachiensis* i tareskog og nedbeitede områder langs norskekysten og Svalbard

Knut Sivertsen

Institutt for arktisk- og marin biologi, UiT-Norges Arktiske Universitet, Tromsø

Tareskogen ble nedbeitet langs norskekysten fra Nordmøre og nordover av kråkeboller (*S. droebachiensis*) fra begynnelsen av 1970-tallet. De nedbeitede områdene vedvarer fremdeles nord for Bodø. Populasjonsdynamikk til disse kråkebollene ble undersøkt i 21 lokaliteter fra ni områder langs norskekysten fra Stavanger i sør til Svalbard i nord for å finne variasjoner i populasjonene i Nordøst-Atlanteren. Kråkebollene ble aldersbestemt ved å telle ringer i interambulakralplatene. I nedbeitede områder dominerte aldersgruppene 4-10 år, mens de eldste var 16 år gamle. Basert på alder og størrelse (diameter) ble vekst og dødelighet beregnet. Vekst beregnet med Vonbertalanffy vekstfunksjon (VBGF) og dødelighet med z. Både vekst og dødelighet var høyest i sør og avtok nordover og høyere i tareskog enn i nedbeitede områder. Basert på vekst og dødelighet ble det dannet syv ulike demografiske grupper. De fleste kråkebollene blir kjønnsmodne i alderen 4-6 år og 25-33 mm i diameter i Nord-Norge, og det var stor variasjon både innenfor hver populasjon og mellom populasjonene. I livshistoriesammenheng er *S. droebachiensis* K-strateger til tross for å være små. De lever et langt liv, langsom vekst og sein kjønnsmodning. I nedbeitede områder lever de med høye tetthet, i middel 20-40 individer/m2, med lite mat tilgjengelig, og da under intraspesifik konkurranse. Kråkebollene har levd i nedbeitede områder gjennom mange generasjoner, så langt i over 40 år, og de bærer alle kjennetegn på å danne et klimakssamfunn.

The unknown copepod link between kelp forests, the pelagic ecosystem and deep-sea carbon sequestration

Kristina Øie Kvile[1], Kasper Hancke[1], Dag Altin[2], Dorte Krause-Jensen[3], Rolf Erik Olsen[2], Marc Anglès d'Auriac[1]

[1]Norwegian Institute for Water Research, Oslo, Norway
[2]Department of Biology, Norwegian University of Science and Technology, Trondheim, Norway
[3]Arctic Research Centre, Aarhus University, Århus, Denmark.

Kelp forests are highly productive coastal habitats with high turnover in biomass. On average, >80% of annual kelp production is exported as detritus, but the fate of the exported material is a big unknown in global carbon budgets. Lipid-rich pelagic copepods constitute a key link in marine ecosystems by converting energy from primary production to carbon (lipids) available to higher trophic levels. In the Norwegian and Barents Seas, the copepod *Calanus finmarchicus* dominates zooplankton biomass and is the main prey for planktivorous fish such as herring and mackerel and the larvae of cod. Through vertical migrations, copepods transport significant amounts of carbon into the deep sea, a contribution to deep-sea carbon sequestration that has been estimated to be in the same order of magnitude as passive sinking of organic material. It has been shown that fragmented kelp can serve as food for pelagic invertebrate larvae and various benthic invertebrates, but we know close to nothing about the role of fragmented kelp as food for copepods. We ran a feeding experiment to investigate if kelp fragments can be consumed by copepods (*Calanus finmarchicus*) and if a novel genetic marker of kelp DNA can trace the consumption of kelp by copepods. If successful, this method can be used in future research projects to detect kelp fragments consumed by copepods or other filter feeding organisms in pelagic or benthic habitats. In this presentation, will give a summary of the feeding experiment and preliminary results regarding the genetic marker. Further, I will discuss potential future research avenues on the unknown link between kelp and copepods.

Metabarcode data for marine biomonitoring – bridging the gap between science and management

Miriam Brandt[1], Anders Lanzén[2,3], Thomas Dahlgren[1,4], Andrea Bagi[1], Jon Thomassen Hestetun[1]

[1]NORCE Climate & Environment, Bergen, Norway
[2]AZTI Marine Research, Pasaia, Spain
[3]IKERBASQUE Basque Foundation for Science, Bilbao, Spain
[4]Department of Marine Sciences, University of Gothenburg, Sweden
Kontakt: mibr@norceresearch.no, jhes@norceresearch.no

Benthic marine environments are large biodiversity reservoirs that provide important ecosystem services, yet are increasingly impacted by human activities. In Norway, one major source of anthropogenic pressure is the oil and gas extraction industry, which invests considerable resources on ecological monitoring to ensure compliance with environmental regulations. Metabarcoding can provide faster, more comprehensive, and more cost-effective biodiversity assessments, providing an immense potential for environmental management. However, main barriers for integrating DNA-based approaches to marine policies are 1) the need for standardized protocols to guarantee data comparability across spatial and temporal scales, 2) the need for baselines of biodiversity information in understudied ecosystems, and 3) the need for appropriate metrics to infer impact status from metabarcoding data.

Building upon previous work, we introduce MetaBridge, a collaborative project between science, industry, and policy stakeholders, aiming to validate metabarcoding approaches for marine benthic monitoring of oil and gas extraction sites. Using prokaryote (16S V4-V5), micro-eukaryote (18S V4), and metazoan (COI, 18S V1-V2) data, together with matching environmental parameters and morphospecies inventories, collected in a time series from 2018-2022 from 25 extraction platforms across the Norwegian shelf, we aim to identify the most suitable way to infer ecological status from molecular data, while addressing key method gaps and constructing a baseline dataset for benthic biodiversity along the Norwegian margin.

Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate *Mesodinium rubrum*

Andreas Altenburger[1,2]*, Huimin Cai[3]*, Qiye Li[4,5]*, Kirstine Drumm[6], Miran Kim[6,7], Yuanzhen Zhu[4], Lydia Garcia-Cuetos[2], Xiaoyu Zhan[4], Per Juel Hansen[6], Uwe John[8,9], Shuaicheng Li[3¤], Nina Lundholm[2¤]

[1]The Arctic University Museum of Norway, UiT The Arctic University of Norway, 9037 Tromsø, Norway
[2]Natural History Museum of Denmark, University of Copenhagen, 1350 Copenhagen, Denmark
[3]Department of Computer Science, City University of Hong Kong, Hong Kong 999077, China
[4]BGI-Shenzhen, Shenzhen 518083, China
[5]State Key Laboratory of Agricultural Genomics, BGI-Shenzhen, Shenzhen 518083, China
[6]Department of Biology, University of Copenhagen, 3000 Helsingør, Denmark
[7]Research Institute for Basic Sciences, Chonnam National University, Gwangju 61186, Republic of Korea
[8]Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, 27570 Bremerhaven, Germany
[9]Helmholtz Institute for Functional Marine Biodiversity, 23129 Oldenburg, Germany
Kontakt: andreas.altenburger@uit.no

The marine ciliate *Mesodinium rubrum* is famous for its ability to acquire and exploit chloroplasts and other cell organelles from some cryptophyte algal species. We sequenced genomes and transcriptomes of free-swimming *Teleaulax amphioxeia*, as well as well-fed and starved *M. rubrum* in order to understand cellular processes upon sequestration under different prey and light conditions. From its prey, the ciliate acquires the ability to photosynthesize as well as the potential to metabolize several essential compounds including lysine, glycan, and vitamins that elucidate its specific prey dependency. *M. rubrum* does not express photosynthesis related genes itself, but elicits considerable transcriptional control of the acquired cryptophyte organelles. This control is limited as light dependent transcriptional changes found in free-swimming *T. amphioxeia* got lost after sequestration. We found strong transcriptional rewiring of the cryptophyte nucleus upon sequestration, where 35% of the *T. amphioxeia* genes were significantly differentially expressed within well-fed *M. rubrum*. Qualitatively, 68% of all genes expressed within well-fed *M. rubrum* originated from *T. amphioxeia*. Quantitatively, these genes contributed up to 48% to the global transcriptome in well-fed *M. rubrum* and down to 11% in starved *M. rubrum*. This tertiary endosymbiosis system functions for several weeks, when deprived of prey. After this point in time, the ciliate dies if not supplied with fresh prey cells. *M. rubrum* represents one evolutionary way of acquiring photosystems from its algal prey, and might represent a step on the evolutionary way towards a permanent tertiary endosymbiosis.

Effect of sea lice chemotherapeutant hydrogen peroxide on the photosynthetic characteristics and bleaching of the coralline alga *Lithothamnion soriferum*

Erwann Legrand[1], Aoife E. Parsons[1], Rosa Helena Escobar Lux[2], Florian Freytet[2], Ann-Lisbeth Agnalt[1], Ole B. Samuelsen[1], Vivian Husa[1]

1 Institute of Marine Research, Nordnesgaten 50, 5005, Bergen, Norway
2 Institute of Marine Research, Austevoll Research Station, 5392 Storebø, Norway

Proliferation of sea lice (*Lepeophtheirus salmonis*) represents a major challenge for the salmonid aquaculture industry in Norway. Hydrogen peroxide (H_2O_2) is a chemotherapeutant frequently used on Norwegian farms, however, its toxicity to non-target benthic species and habitats remains poorly understood. Maerl beds are constructed by the accumulation of non-geniculate coralline algae and provide important ecological functions. Due to the rapid expansion of aquaculture in Norway and the continued use of H_2O_2 as an anti-sea lice treatment, it is crucial to understand the impact of H_2O_2 on the physiology of maerl-forming species. In the present study, the effects of a 1 h exposure to H_2O_2 on the photophysiology and bleaching of the coralline alga *Lithothamnion soriferum* was examined through a controlled time-course experiment. PAM fluorimetry measurements showed that H_2O_2 concentrations ≥ 200 mg l^{-1} negatively affected photosystem II (PSII) in thalli immediately after exposure, which was observed through a significant decline in maximum photochemical efficiency (F_v/F_m) and relative electron transport rate (rETR). The negative effects on PSII induced by oxidative stress, however, appear to be reversible, and full recovery of photosynthetic characteristics was observed 48 h to 28 days after exposure to 200 mg H_2O_2 l^{-1} and 2000 mg H_2O_2 l^{-1}, respectively. At 28 days after exposure, there was evidence of two- to four-times more bleaching in thalli treated with concentrations ≥ 200 mg H_2O_2 l^{-1} compared to those in the control. This indicates that despite of the recovery of PSII, persistent damages can occur on the structural integrity of thalli, which may considerably increase the vulnerability of coralline algae to further exposure to H_2O_2 and to other chemical effluents from salmonid farms.

Hydrography and circulation in northern Norwegian fjords

Anna Nikolopoulos[1], Jofrid Skarðhamar[1]

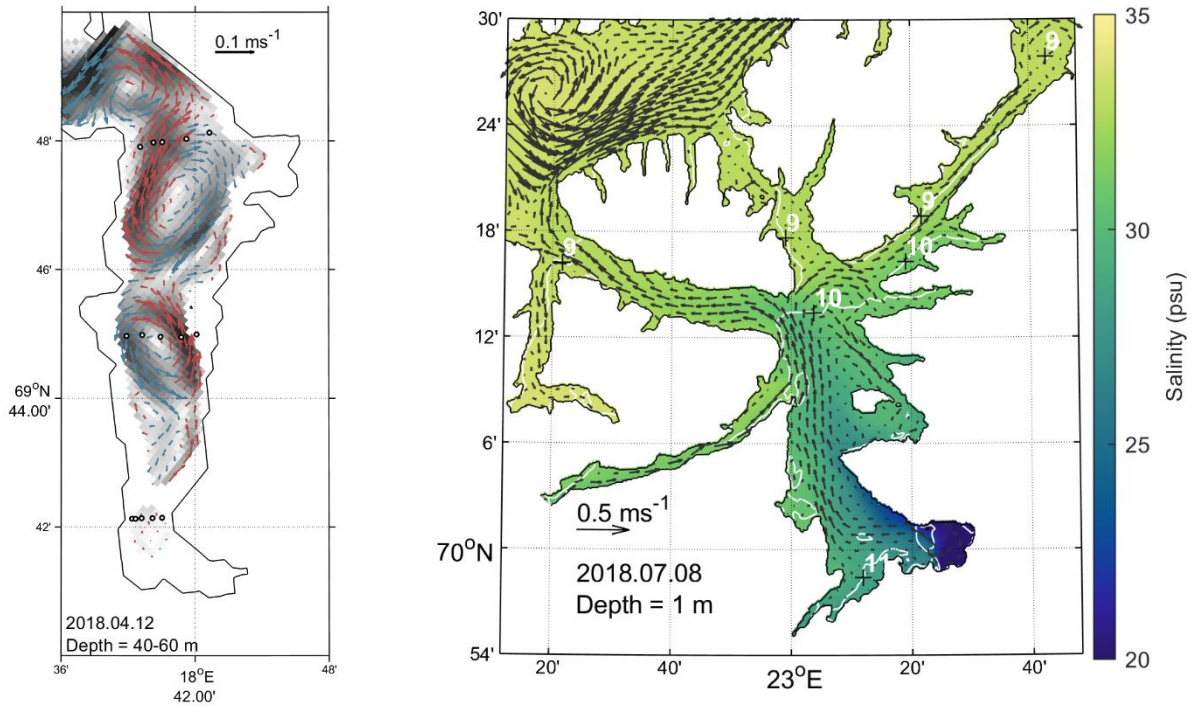
[1] Havforskningsinstituttet, Framsenteret, Tromsø.
Kontakt: anna.nikolopoulos@hi.no

The oceanographic conditions in fjords impact both pelagic and benthic biogeochemical components of its ecosystem. With increased human activity in the fjord environment it is crucial to improve our knowledge on the behaviour of these water bodies.

IMR is monitoring the physical conditions in fjords all along the Norwegian coastline and here we would like to inform the audience about our most recent work on the hydrography and circulation patterns in the northern fjords of Troms and Finnmark.

Our work combines observations from both ships and long-term moored instrumentation and simulations with the numerical NorFjords160m model. The analyses have been carried out with the objective to investigate the fjord dynamics but also for providing environmental parameters to studies of e.g. post smolt migration (Altafjorden system) and pelagic ecosystem dynamics (Kaldfjorden).

The general circulation in the fjords is more complex than classic-notion estuarine fjord circulation, with horizontal gradients and high temporal variability throughout all seasons. The prominent circulation features, and the associated water exchange, are connected to both local and remote winds, as well as to the density-driven communication with the coastal shelf waters, tides and runoff. The size and shape of the fjords, as well as their location with respect to the coastal shelf and major river run-off sources, determines the hydrodynamic response to the driving forces. A combination of extended observations and model simulations is not only preferable but rather necessary for catching the full dynamical functioning of a fjord system.



Examples of the circulation for Kaldfjorden (left; intermediate depths) and Altafjorden (right, near-surface). For Altafjorden we also see the distribution of salinity (colorbar) and temperature (white lines with labels in ºC).

The Arctic melt-down with loss of sea ice-associated species

Haakon Hop

Norwegian Polar Institute, Fram Centre, 9296 Tromsø.
Contact: Haakon.Hop@npolar.no

Large declines in Arctic sea-ice age and extent over the last decades have altered the sympagic, or ice-associated, flora and fauna. The diversity of sympagic unicellular eukaryotes (referred to as sea-ice protists) have changed, as shown by our analyses of composition time series (1980s to 2010s) from the Arctic Ocean. Particularly diatoms shown 39% reduction in species from multiyear to first-year sea ice. Sea ice meiofauna, living inside sea ice, have likely also been reduced in some areas, although long-term analyses of ice cores mainly showed differences among locations related to distance from land. Sea-ice amphipods have declined in abundance from the 1980's to the 2010's, particularly long-lived species such *Gammarus wilkitzkii* that tend to be associated with multiyear sea ice. Some species or populations of marine mammals and seabirds are also negatively affected by reductions in sea ice, particularly ice-dependent species.

Climate model projections indicate that the Arctic sea-ice will continue to decrease through the middle of 21th century with a probability of sea-ice free in September by the end of the century for stabilized global warming of 1.5°C (2°C); IPCC, 2019). However, some models that include the accelerated sea ice losses in 2007 and 2012 have indicated nearly ice-free Arctic in September by 2040. This would result in seasonal loss of ice-associated species to the water column or the benthic environment (or land for upper trophic levels), and their ability to recolonize newly formed ice is questionable – probably low.

Reductions in sympagic flora and fauna will to some extent be outweighed by increased production in the pelagic environment. Because of advection of Atlantic water (i.e. Atlantification) onto the shelves and into basins of the Arctic Ocean, boreal species will continuously spread northwards. If the nutrient availability is enhanced in the Eurasian Basin, as expected, primary production could increase because of the sea ice loss (improved light conditions) and the temperature increase (increase in metabolic rates) in the surface layer associated with the Atlantification. Increases in open water periods will promote northward expansion and intensification of phytoplankton growth, and under-ice blooms will be enhanced due to the thinning ice cover, proliferation of melt ponds, and frequent lead formation. The sea ice loss in the Arctic Ocean also triggers novel autumn phytoplankton blooms with further promotion of primary production.

The zooplankton biomass has increased in Arctic waters, likely because of higher secondary production, but also because of advection of boreal species from the south. In Svalbard fjords and the Arctic Ocean north of Svalbard, many boreal species of zooplankton (e.g. *Calanus glacialis, Themisto abyssorum, Thysanoassa* spp.) have increased in abundance. They are generally smaller and less lipid-rich than Arctic species, but possibly have a faster turnover in warmer water. Changes in structure and function of pelagic communities together with loss of sea ice as habitat for sympagic flora and fauna will have consequences for the marine ecosystem. Even if Arctic marine ecosystems are resilient to environmental and anthropogenic perturbations, we expect to see major changes in the food web with major increases in biomass and production of some species and declines to extinction in others by

the end of this century. Because of such large changes, ecosystems in the new Arctic, with higher temperatures and less sea ice, will be difficult to model and predict.

Setting sail for the future – Statsraad Lehmkuhl's One Ocean Expedition

Katja Enberg[1]

[1] Department of Biological Sciences, University of Bergen
Contact: katja.enberg@uib.no

The pride of Bergen, tall ship Statsraad Lehkuhl, started a 19-month circumnavigation in August 2021. This One Ocean Expedition has as its main goal to «create attention and share knowledge about the crucial role of the ocean for a sustainable development in global perspective». The circumnavigation is part of the UN Decade of Ocean Science for Sustainable Development. In this presentation I will explain the plans the University of Bergen has for the four-month long leg across the Pacific Ocean from Chile to Palau, particularly our interdisciplinary sustainability summer course "Ocean, Climate, Society" where 90 students will, in addition to studying, become crew members as sailing trainees. I will also give examples of data that is being collected during the voyage, and where these data are being made available.