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Monitoring Marine Biodiversity in Genomic Era

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Abstract

The rapid development of marine industries prompts an urgent need for tools able to accurately and rapidly monitor resulting impacts on marine life. Classical methods of biodiversity monitoring based on morphological species identification are time consuming and require a solid taxonomic expertise that is not readily available. The project Monitoring Marine Biodiversity in the Genomic Era proposes to overcome these limitations by using DNA barcoding and metabarcoding to identify marine species and to monitor biodiversity changes. These DNA-based approaches are highly effective in terms of both cost and time and offer a unique opportunity to include the small-sized organisms (microbes, meiofauna) that play a key role in marine ecosystem functioning but are generally ignored in routine monitoring. The project examines the use of these genetic methods, focusing on marine aquaculture and deep-seabed mining, and provides evidence for their applicability from scientific, economic and legal perspectives. It concludes that emerging DNA-based technologies should be deployed alongside traditional methods to deliver easily-understandable data to environmental managers and authorities, and to ensure the sustainable use of marine resources.

EXECUTIVE SUMMARY

PROBLEM STATEMENT

Marine ecosystems are increasingly threatened by rapidly growing industrial activities. The efficient environmental management tools are necessary to ensure the sustainable development of these activities and to accurately assess their impact on marine biodiversity (Halpern et al. 2012). This project approaches the development of appropriate tools from biological, legal, and economic points of view.

The recent development of DNA barcoding using short fragments of DNA to identify species overcomes some of the limitations of morphological taxonomy (Hebert et al. 2003). The combination of DNA barcoding with high throughput sequencing of environmental DNA (eDNA metabarcoding) represents a new powerful tool for the study of past and present biodiversity (Taberlet et al. 2012, 2018; Pedersen et al. 2015). Several features of eDNA metabarcoding make it suitable technology for conducting Environmental Impact Assessment (EIA) required by national and international regulations. Rapid advances of high-throughput sequencing (HTS) technologies and improved tools for accurate HTS data analysis have the potential to facilitate the use of eDNA for biomonitoring and bioassessment. However, the implementation of eDNA in routine EIA activities involves many challenges and limitations. The project explored ways to integrate eDNA technology into EIA protocols by addressing biological, legal and economic aspects of its use in marine aquaculture and deep-seabed mining.

OBJECTIVES

The aims of this project were to assess specific applications, develop protocols, and formulate strategies for applying new genomic indices of ecological status in marine monitoring. Specific goals included:

- (1) Identifying those aspects of environmental monitoring that can be addressed by eDNA technology
- (2) Defining regulatory requirements that can (or cannot) be met by eDNA technology in the context of coastal aquaculture and deep-seabed mining.
- (3) Developing economic comparisons of traditional and eDNA approaches, including cost-benefit analysis and ecosystem service assessment.
- (4) Formulating recommendations for incorporating eDNA technology into environmental impact assessment and policy.

RESULTS OBTAINED AND THEIR ANALYSIS

ECOGENOMIC INDICES (UNIGE)

The project focused on the development of genomic indices of ecological status (ecogenomics) to assess the impact of anthropogenic activities, specifically marine aquaculture and deep-sea mining.

Regarding marine aquaculture, we established collaborations with salmon farmers in Norway, Scotland, New Zealand and Canada, who provided sediment DNA samples that we could analyse and compare with conventional methods of benthic monitoring. Our objective was to demonstrate that the DNA approach can be as valuable as traditional methods based on sorting and morphological identification of benthic macrofaunal species. We targeted various groups of organisms, including metazoan meiofauna, foraminifera, other protists, and bacteria, which are usually not studied because of their small size and difficult identification.

We collected DNA sequence data from over 20 salmon farms from all over the world and analysed them using our in-house developed bioinformatic pipeline. Our results show that organisms identified by DNA are as good as indicators of organic enrichment associated with marine aquaculture, as traditionally used for macrofauna. We have published several papers testing our method in the case of foraminifera (Pawlowski et al. 2016), metazoan meiofauna (Lejzerowicz et al. 2015), ciliates (Stoeck et al. 2018), and bacteria (Stoeck et al. 2018). The main innovation of our research was to introduce a supervised machine-learning (SML) approach to predict the biotic indices from metabarcoding data (Cordier et al. 2017). The SML approach improved considerably the correlation between biotic indices inferred from eDNA and macrofaunal data. Its wider adoption in routine biomonitoring will release the huge potential of small-sized, morphologically inconspicuous taxa as bioindicators (Cordier et al. 2018, Cordier et al. in prep.)

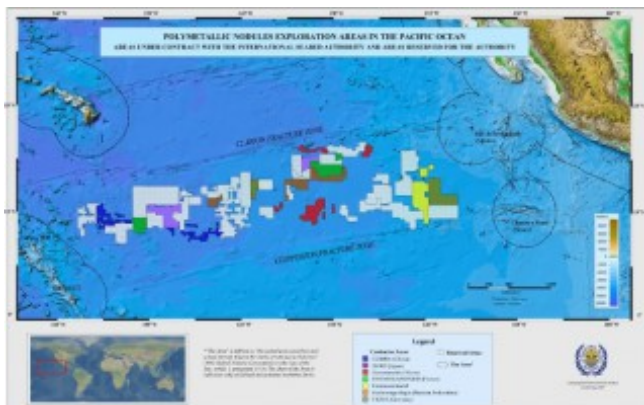


Fig. 2. Clarion-Clipperton Zone in Pacific Ocean

In the case of deep-seabed mining, we explored the diversity of deep-sea organisms using eDNA metabarcoding. We focused on the Clarion-Clipperton Zone (CCZ), an area of the Pacific where future polymetallic-nodule mining may present challenges for the sustainable exploitation of the deep seafloor. We undertook a large sequencing effort targeting four gene markers for both DNA and RNA molecules, analyzing 316 samples from the CCZ as well as sites in the NW Pacific, Atlantic and Southern Ocean (Lejzerowicz et al. in prep).

Our data revealed very different assemblages of foraminifera and other eukaryotes in different ocean basins, suggesting global-scale patterns in distribution of small-sized organisms, with high local variability in some regions, such as CCZ.

COST-EFFECTIVENESS AND ECOSYSTEM SERVICES (UCSD)

This part of the project examines the economic and social benefits of using molecular techniques, such as eDNA metabarcoding, for deep-sea impact assessment by evaluating their (i) cost-effectiveness and (ii) potential as indicators of ecosystem services (ES). These factors may influence the adoption of eDNA technology for environmental assessments and monitoring, especially as high-throughput sequencing (HTS) costs decrease and its capacity to provide novel information about ecosystem function and service is developed. Morphology-based taxonomy (MBT) is used as a comparison because it has traditionally been employed to evaluate biodiversity in environmental assessments and monitoring. One goal is to guide the nascent development of environmental guidelines for deep-seabed mining (DSM).

(i) *Cost-effectiveness*: From an economic standpoint, there are direct (e.g. consumables, sequencing) and indirect (e.g. time, expertise) costs associated with each approach (i.e. eDNA and MBT). There are also scientific tradeoffs between the two because they yield different types of information. Each approach can be incorporated into a network of decisions that influence the economic and scientific outcomes and these decisions are contingent on scientific objectives and monetary constraints. Throughout the eDNA metabarcoding workflow, critical decisions include which markers, tags, primers, adapters, and sequencing platforms to use. Processing sediment samples for MBT is further constrained by taxonomic expertise, which drives many of the decisions in the MBT workflow, such as the number of vertical sections, size-fractions, target taxa, and level of identification. As a result, there may be scenarios in which one approach is more appropriate than the other. However, in general, the approaches can be seen as complementary.

In terms of direct costs for expendables, MBT is approximately half the price of eDNA metabarcoding, given standard laboratory supplies (e.g. microscopes). The cost of the molecular approach is driven largely by the kits and chemicals that are necessary to preserve and extract samples. However, the required time and expertise to process and analyze MBT samples may make eDNA a cheaper option overall. The amount of time it takes to process samples via MBT depends on taxa considered, level of identification, size fractionation, and level of expertise. It can take several years of training to become accurate and efficient at identifying individuals to the species level.

In addition to differences in economic costs, there are also scientific tradeoffs that must be considered while comparing eDNA and MBT. These tradeoffs have significant effects on what data are generated and how to interpret them. MBT cannot be used to assess microbial communities but it can generate data on eukaryote population demographics (e.g. biomass, density, morphological features). In contrast, eDNA metabarcoding can characterize microbial community composition (e.g. using 16S rRNA), and may be more suited for small or cryptic micro- and meiofaunal taxa that are hard to identify morphologically. Because many deep-sea organisms fall into this latter category (i.e. small or cryptic), eDNA approaches may be favored. However, the deep sea is severely undersampled (Ramirez-Llodra et al., 2010; Sinniger et al., 2016) and, therefore, molecular databases (e.g. GenBank, Barcode of Life) required for assigning taxonomy to sequences can be lacking. Consequently, it can be difficult to translate a loss of sequences (i.e. due to DSM) into which species and functions are lost.

(ii) *Potential indicators of ecosystem services*: Ecosystem services (ES) represent the benefits that society receives from ecosystems, establishing a direct link between the human and natural systems (Millennium Assessment, 2005). More recent frameworks for environmental assessment and monitoring incorporate human systems and their dependence on natural systems (e.g. TEEB, 2010; Halpern et al., 2012), highlighting the importance of ES. Practical indicators

of ES must be developed in order to incorporate these benefits, and potential losses, into environmental decision-making.

ES are supported by structures and functions that must be protected in order to continue the flow of benefits. eDNA contains a wealth of information about the species inhabiting ecosystems (i.e. structure). Metabarcoding approaches have been used to detect endangered, invasive, and indicator species (e.g. Ficetola et al., 2008; Jerde et al., 2013). They have also been used to assess overall biodiversity, which is often used as a metric of ecosystem health because it can reflect human impact (Elahi et al., 2015; Pecl et al., 2017), and has been linked to deep-sea functioning and ES (e.g. Danovaro et al., 2008; Loreau, 2008; Pusceddu et al., 2014; Gamfeldt et al., 2015; Le et al., 2017). Currently, metabarcoding approaches may be most suitable for describing microbial communities that mediate key transformations of nutrients and metals that are associated with regulating ES (e.g. Blothe et al., 2014).

The parallel use of other genomics techniques can provide additional information on ES. Metagenomics can reveal, not only which organisms (or sequences) are present, but also the potential functions of the community if genes have been previously identified and annotated (Zehr & McReynolds, 1989; Simon & Daniels, 2011). In the deep sea, metatranscriptomics has identified novel microbial communities in Guaymas Basin that contribute to carbon and nitrogen cycling (Baker et al., 2013). Similarly, metaproteomics has identified key players in nutrient cycling (Schneider et al., 2012), and potential bioindicators of sediment contamination (Floch et al., 2011).

There are many challenges to developing molecular indicators for ES. Deep-sea biodiversity is poorly catalogued (Leray & Knowlton, 2016; Sinniger et al., 2016) and sequence databases are therefore incomplete. The inability to assign taxonomy to sequences makes it difficult to infer function and interpret changes in eDNA following impact. Research needed to apply eDNA to impact monitoring includes improved understanding of how ecosystem structure translates into functions and services, identifying active processes contributing to ES, and the rates at which these processes are operating.

LEGAL FRAMEWORK (ELI)

The research team evaluated existing requirements and standards for environmental impact assessment and monitoring that are relevant to the use of eDNA to determine legal and institutional constraints and opportunities for such approaches.

The implementation of eDNA as a tool for Environmental Impact Assessment (EIA) does not trigger constitutional issues at the domestic level or conflict with relevant international legal instruments. Most legal instruments analysed present similar, broad definitions of the conditions for environmental compliance on seabed mining and marine aquaculture. When setting the requirements for conducting EIAs on ocean activities, statutes tend to use undefined legal concepts like “the best available science,” “recognized methodology,” or “recognized scientific methods.” This approach enables management agencies to design subordinate legislation or implementing regulations that establish more specific requirements for EIA. Consequently, a key element in the regulatory implementation of eDNA lies in how agencies interpret the concept of “best available science” and similar undefined legal concepts, and then echo that interpretation in policies, guidance documents, and operating procedures.

Regulatory analysis shows that there is no standardized procedure to decide the preferred scientific method for EIAs on seabed mining or aquaculture. The complexity of human

interactions with the marine environment often leads to a case-by-case analysis by management agencies. According to some statutes, this approach also involves the selection of the scientific method to be used to assess the environmental impact of a specific development or project, although this is usually left at the discretion of the management agency. This wide regulatory discretion within the relevant legal frameworks allows for the use of eDNA approaches. In a few cases though, (e.g. aquaculture monitoring in Chile), agency documents require a specific methodology for conducting monitoring activities. These guidance documents would need to be updated to facilitate the implementation of eDNA. On the other hand, some domestic-level statutes and policy documents incentivise scientific innovation to improve the understanding of the environmental impact of human activities at sea, thus constituting specific opportunities for the implementation of eDNA in policymaking. (e.g. Scotland Strategic Framework – adaptive management). Similarly, some legal frameworks accept “international standards” as a way of introducing alternative assessment methods (e.g. Norway Environmental Impact Assessment Regulations).

Most regulations for EIAs require developers to conduct studies to provide baseline information on the characteristics of the marine ecosystem likely to be impacted by a proposed development. Some features of the eDNA assessment method (e.g. reliability, cost-efficiency) suggest that it could be particularly suitable for providing this scientific information, e.g. the presence of endangered species at a proposed seabed mining site. The same can be said regarding the regulatory requirements for monitoring the environmental impact of aquaculture facilities.

SUMMARY INDICATING WHETHER THE RESULTS OBTAINED CORRESPOND TO THOSE EXPECTED

ECOGENOMICS (UNIGE)

The eDNA analyses generally yielded results that were congruent with those expected at the beginning of the project. We knew from pilot studies that the biotic indices inferred from eDNA data provided a similar assessment of ecological status as morphological surveys. This was confirmed in the case of aquaculture studies conducted within this project. We also significantly improved the congruence between conventional and molecular assessments of aquaculture impacts by using machine-learning methods to predict biotic indices. In the case of the deep-seabed mining area, the results were less conclusive than anticipated. The large heterogeneity of eDNA data confirmed the immense diversity of deep-sea fauna shown in previous studies. Yet this heterogeneity made it difficult to find reliable bioindicator species and develop a biotic index specific to deep-sea environments. The task was additionally hampered by the lack of eDNA data for impacted areas that could be used to establish the categories of ecological status for use in monitoring deep-seabed mining.

COST-EFFECTIVENESS AND ECOSYSTEM SERVICES (UCSD)

Many of the results obtained for the cost-effectiveness portion of the project were expected. In comparing eDNA metabarcoding and morphology-based taxonomy of meiofauna (MBT), the cost of labor to process MBT samples far outweighs the cost to process sequencing samples. However, the total costs of either of these methods depend on decisions within each workflow that are constrained by monetary budget, scientific objectives, and time. The results regarding ecosystem services were also expected. There are many knowledge gaps in using eDNA to

inform deep-sea ecosystem services, such as unknown taxonomy and function. Additional molecular tools (e.g. metagenomics, metatranscriptomics, metabolomics) promise to be helpful in addressing these challenges, such as for microbial communities.

LEGAL FRAMEWORK (ELI)

The results of the legal analysis were, in general terms, consistent with what was anticipated. As expected, the legal framework concerning the installation and operation of aquaculture facilities is significantly more developed than that on seabed mining. In some case studies it was difficult to identify relevant sources for the management of seabed mining. This is consistent with project expectations and consonant with the approach adopted. Additionally, the in-depth interviews with ocean resources managers and agency practitioners demonstrated a higher than expected lack of knowledge about the eDNA technology and the potential advantages of its implementation for regulatory decision making.

INFORMATION REGARDING THE PRACTICAL APPLICATION OF RESULTS

AQUACULTURE

The application of eDNA tools to monitoring aquaculture was facilitated by collaboration with industry and stakeholders, including environmental agencies and consulting offices. The level of application of eDNA methods differs depending on the countries.

- **At the international level:** the Aquaculture Stewardship Council (ASC) accepted the variance request to use eDNA tests for benthic monitoring of salmon farms in Norway; from 2017 the salmon farms all over the world can apply for ASC certificate based on eDNA data analysis.
- **Norway:** an ongoing research project supported by the Norwegian Seafood Research Fund (FHF) in close collaboration with industry promotes the development of eDNA-based technology and its implementation for benthic monitoring of salmon farms in Norway.
- **Scotland:** a project examining various aspects of eDNA benthic monitoring applied to salmon farming has been initiated by SEPA (Scottish Environmental Protection Agency), in collaboration with Scottish Association of Marine Sciences (SAMS) and industry.
- **Canada:** preliminary study aiming at development of eDNA benthic monitoring for salmon farms in British Columbia has been conducted by the Department of Fisheries and Oceanography (DFO), and independently in collaboration with industry
- **Chile:** collaboration with Fisheries Development Institute was established in order to propose management strategy and administrative measures to the Under secretariat of Fisheries and Aquaculture (SUBPESCA).

Generally, the eDNA approach can be implemented in marine aquaculture, and as a tool for project developers to use, inter alia, in conducting 1) baseline environmental studies; 2) full EIAs; 3) continuous monitoring of human environmental impacts at sea; 4) random inspections. More specifically, following the work conducted in this project, eDNA was accepted by Aquaculture Stewardship Council as an alternative tool for benthic monitoring of salmon farms. eDNA is also in a good position to be proposed as a baseline method for “adaptive management”

of ocean resources. This approach can provide a common information standard for ocean management agencies to incorporate into current Marine Spatial Planning processes.

DEEP-SEA

For the deep sea, a variety of stakeholders developing policy, environmental regulations, research plans and observing networks should be receptive to information about the application of environmental DNA for baseline study and impact assessment. We prioritize the International Seabed Authority, as eDNA can provide useful tools in environmental management for seabed mining, including in regional spatial planning (assessing how representative Areas of Particular Environmental Interest (APEI) are, baseline characterization, impact assessment and monitoring etc). We intend to work with the ISA Legal and Technical Commission and the Deep-Ocean Stewardship Initiative (DOSI) to discuss and advance the project ideas. eDNA also promises to enhance environmental assessment for new international fisheries (FAO-RFMOs), for the new Biodiversity Beyond National Jurisdiction (BBNJ) treaty, and for advancing Sustainable Development Goal 14 on the oceans. A new challenge that promotes the application of eDNA to anthropogenic impacts in the ocean will be proposed to the UN Decade of Ocean Science for Sustainable Development as a major theme for 2020-2030.

QUESTIONS THAT MERIT FURTHER EXPLORATION

The project raised several questions that would need further exploration at biological, legal and socioeconomic levels.

MOLECULAR METHODS

The biological part opened doors for much more extensive exploration of various new “omics” approaches that could be used for eDNA study

- Whether the metabarcoding would be outperformed by metagenomics, metatranscriptomics, metabolomics?
- What kinds of molecular markers most accurately characterize environmental changes due to industrial impacts and document recovery?
- Should we use genomic information to analyse biodiversity changes or instead target functional changes related to ecosystem services?

LEGAL AND SOCIO-ECONOMIC QUESTIONS

- What other anthropogenic impacts (e.g. microplastics, windmills, climate change) could be measured using genomic tools?
- How can we overcome legal uncertainty associated with the existence of several key undetermined legal concepts; especially regarding the definition of “best science” (best for what) and “significant harm” (how harmful is too harmful)?
- What regulatory and institutional options can best improve cooperation between regulatory agencies and the scientific community to define these vague legal concepts?

PRACTICAL AND POLICY RECOMMENDATIONS THAT FOLLOW FROM THE RESULTS OBTAINED

The UN Convention on the Law of the Sea (UNCLOS), adopted in 1982, requires parties (art 145) to adopt measures necessary to ensure effective protection of the marine environment from the harmful effects of seabed mining activities. In December 2017 the UN General Assembly reached agreement to develop the new treaty on marine biodiversity in areas beyond national jurisdiction (BBNJ process). With that decision, the international discussion has entered a new phase. Marine biodiversity is poorly known, the eDNA technology can provide a more comprehensive picture of existing diversity and potential impacts. Its use should therefore be required in new regulations regarding environmental impact assessment. The group is planning to submit a simplified version of the working paper to the International Seabed Authority meetings and to UN BBNJ meetings. The policy recommendations are the subject of the Working Paper.

INFORMATION REGARDING PAST AND EXPECTED PUBLICATIONS AND OUTREACH

PUBLICATIONS RELATED TO THE PROJECT

- Cordier T., Forster, D., Dufresne Y., Martins, C.I.M., Stoeck, T., Pawlowski, J., Pawlowski J. (2018) Supervised machine learning outperforms taxonomy-based environmental DNA metabarcoding applied to biomonitoring. In review
- Cordier T, Pawlowski J. (2018) BBI: and R package for the computation of Benthic Biotic Indices from composition data. In review
- Cordier T, Esling P, Lejzerowicz F, Visco J, Ouadahi A, Martins C, Cedhagen T, Pawlowski J. (2017) Predicting the Ecological Quality Status of Marine Environments from eDNA Metabarcoding Data Using Supervised Machine Learning. *Environ Sci Technol.* 51(16):9118-9126.
- Le JT, Levin LA, Carson RT. 2017. Incorporating ecosystem services into environmental management of deep-seabed mining. *Deep-Sea Research II*. DOI: 10.1016/j.dsr2.2016.08.007

IN PREPARATION:

- Hare-Grogg J, Recio-Bianco X, Seeking the “best” science: strengthening deep seabed legal protection through next generation sequencing of environmental DNA (eDNA). *The Arctic Review on Law and Politics*.
- Le JT, Levin LA, Lejzerowicz F, Cordier T, Pawlowski J. Tradeoffs between metabarcoding and morphology-based taxonomy for deep-sea environmental assessment and monitoring
- Lejzerowicz F et al. Eukaryotic diversity and biogeography at local to global scales in the abyssal deep sea eDNA survey

TRANSMISSION OF RESULTS TO:

- International Seabed Authority: Legal and Technical Commission, working group on Guidelines for exploration/exploitation and EIA
- Deep Ocean Stewardship Initiative: working groups on Minerals mining, UN BBNJ process, Ocean genetic resources, Decade for Ocean Sciences
- Deep Ocean Observing Strategy: Essential Ocean Variables Biology and Ecosystems task team; Demonstration projects
- FAO and Regional Fisheries Management Organisations

PHD THESIS IN PREPARATION:**Jennifer Le, Scripps Institution of Oceanography, USA**

As human impact increases in coastal and marine ecosystems, environmental management and regulation have struggled to keep up with industry. The concept of ecosystem services can provide a useful tool in coastal and marine environmental decision-making, especially as some policy and regulation is currently in development, e.g. deep-seabed mining. Ecosystem services concern the benefits of ecosystems to society and provide a direct link between natural and human systems. In considering ecosystem services, one must also consider the structures that allow for their provision. These include biodiversity and ecological function.

This PhD thesis explores how ecosystem services manifest and can be applied in managing two representative ecosystems subject to human perturbation: deep-sea habitats and coastal urban areas. These two systems, which exhibit contrasting characteristics (e.g. human impact, knowledge base, ease of access), are used to explore different approaches and tools in order to determine those most applicable. This research employs an interdisciplinary approach, heavily influenced by concepts from ecology and economics, to examine the linkages between ecosystem structures, ecological functions, and ecosystem services in order to translate these concepts into environmental management and policy. Chapters include: (1) an examination of how ecosystem services can be incorporated into deep-seabed mining regulation, (2) an investigation of the use of eDNA data as an indicator of ecosystem services within a regulatory framework, (3) an analysis of remotely-operated vehicle video data to characterize biological communities and their associated ecosystem services in different habitats on the continental margin of southern California, and (4) the development of an ecosystem services-assessment tool using a low-impact development in Los Angeles as a case study.

Carlos Arias, Universidad Austral, Chile

In Chile, salmon farming takes place in coastal areas that offer multiple ecosystem services for local communities. Here, the salmon industry is developed close to artisanal fishing, mussel farming, areas of management and exploitation of benthic resources, marine coastal areas of indigenous peoples, priority sites for the conservation of biodiversity and areas of tourist interest. Normally the environmental impact monitoring is restricted to the installation site and does not consider the complex relationships with and between the different activities that take place around it. Including these considerations could be relevant for adequate planning and effective environmental management in the long term of areas with a high concentration of human uses and activities.

This PhD thesis investigates the use of eDNA to monitor the impact of salmon farms on sediments in ecosystems with different complexity of human uses and activities. Functionally,

salmon farming is considered as a point source of nutrient, whose isotopic characteristics ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) can be traced spatially and temporally in sediments. Spatially, its functional relationship is analyzed with other activities that concentrate and restrict the dispersion of nutrients in the ecosystem (e.g., mussel farms). We seek to identify potential ecogenomic markers of environmental conditions, from eDNA sequences representing benthic foraminifera. These sequences will be related to geochemical characteristics of recent and past sediments, using variables that allow establishing their trophic state and interpreting the origin of the deposited material. The area where the research is developed has been defined by state agencies as a intensive production zone of salmonids and there is currently a planning and environmental management participatory process for the use of the coastal zone. Therefore, in addition, the possibility that eDNA metabarcoding tools can be incorporated in this type of processes at local and / or national scale will be evaluated.

CURRENT RESEARCH TOPICS:

Dr Tristan Cordier, Post-doctoral fellow, University of Geneva

More than 50% of eDNA sequences cannot be used to infer the ecological quality status of a marine sediment sample, because the sequences remain taxonomically unassigned, or belong to a taxon for which the ecology is unknown. As the pace of the development of sequencing technologies is much faster than our capacity to describe and classify the living species, new methodologies for assessing the environmental quality are required. The post-doctoral work focuses on the development of taxonomy-free approaches for the monitoring of marine environments. The objective is to build robust predictive biomonitoring models, using supervised machine learning, from eDNA metabarcoding data. The approach focused initially on a well-described biological model (salmon farming), where it proved both efficient and better able to accurately predict ecological quality status than the current methodology. Future efforts will investigate whether the methodology can be applied to a different human marine impact, and whether a trained predictive model can be used in a remote geographical area.

CONFERENCES, WORKSHOPS, WEBINARS

UNIGE team

- Deep Ocean Stewardship Initiative Workshop, Information and planning for the future, Aveiro, 30 August 2015
- ISBA taxonomic standardization workshop, Ghent, 14-17 December 2015
- Workshop on application of genomic tools for benthic monitoring of marine environment: from technology to legal and socio-economic context, Geneva, 4-5 April 2016
Interviews with project leaders: www.youtube.com/watch?v=3PrmpQxI41Y
- International Barcoding of Life Conference, (IBOL2017) Ecobarcoding: taxonomy-free approach for high-throughput environmental DNA-based biomonitoring. Kruger Parc, South Africa, 20-24 November 2017
- Biomonitoring marine biodiversity in the genomic era – Partners' workshop, SIO/UCSD, San Diego, 05-06 March 2018

UCSD team

- UN Conference on Climate Change, COP 21, Paris, Ocean and Climate Forum, Science session. 3 Dec 2015
- Participation in the 22 Session of the International Seabed Authority. July 2016.
- EREGS Workshop: incorporation of molecular methods and ecosystem services into goals and objectives proposed to the International Seabed Authority. February 2017.
- Participation and side event at the Twenty-third Session of the International Seabed Authority. July 2017.
- Input to the Legal & Technical Commission of the International Seabed Authority on environmental regulation (transmitted to G. Patterson).
- Le JT, et al. Ecosystem services associated with methane seeps on the California continental margin. Oral presentation at Sixth International Symposium on Chemosynthesis-Based Ecosystems, 28 August 2017.
- Participation and input to the second Benthic Invertebrate Taxonomy and Bioinformatics workshop. January 2018.
- Le, JT. Lecture for international course (US, Sweden) on ecosystem services. 19 February 2018.

ELI team

- Presentation during the workshop “Natural Marine Resource Management in a Changing Climate.” Tromsø, Norway 13 – 14 June 2017. Presentation title: “Strengthening deep seabed legal protections.
- Outreach activities: ELI will organize a webinar to present the results of the project as part of its ELI-Ocean Seminar Series in September 2018.