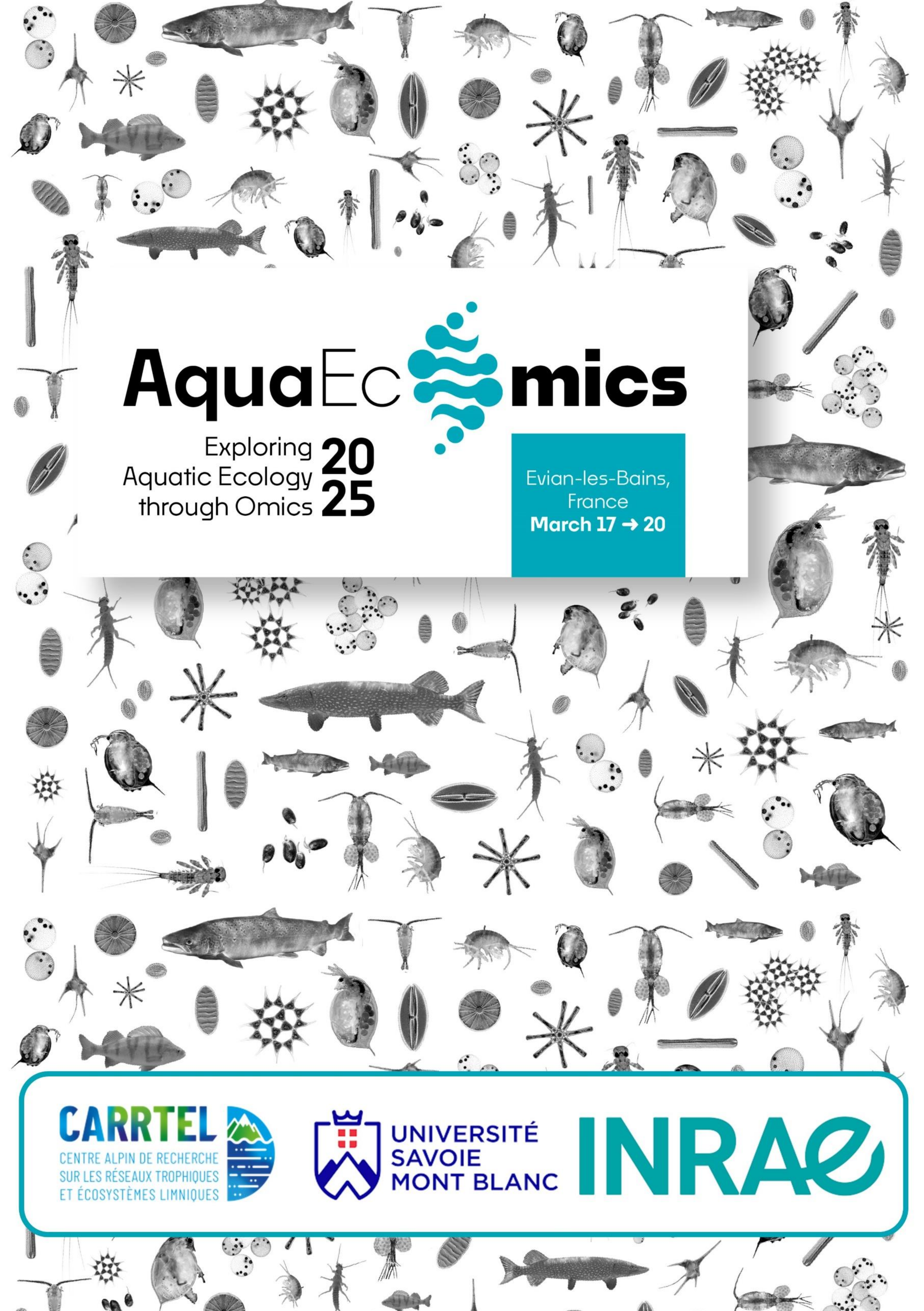


AquaEcomics

Exploring
Aquatic Ecology
through Omics

2025

Evian-les-Bains,
France
March 17 → 20

CARRTEL
CENTRE ALPIN DE RECHERCHE
SUR LES RÉSEAUX TROPHIQUES
ET ÉCOSYSTÈMES LIMNIQUES

UNIVERSITÉ
SAVOIE
MONT BLANC

INRAE

TABLE OF CONTENT

WELCOME WORD

Dear Participants,

Welcome to the AquaEcOmics meeting, a flagship event for the international scientific community dedicated to advancing omics methods in aquatic ecology. Cutting-edge omics approaches continue to revolutionize aquatic sciences and open new avenues in ecological research. Over three conference days, we will explore a diverse array of omics applications through seven thematic sessions, fostering discussions that will shape the future of our field.

We are honored to bring together more than 200 experts, practitioners, and policymakers from more than 25 countries, showcasing the global commitment to integrating omics technologies into aquatic research. Your contributions are essential to the success of AquaEcOmics, and we sincerely thank each of you for your participation—whether in person here in Évian-les-Bains or remotely. Your engagement and enthusiasm for knowledge-sharing will make this event truly impactful.

We hope you will leave this conference enriched with new insights, inspiration, and good memories of your time in Évian-les-Bains.

Welcome, and let’s make this a remarkable event together.

Dr. Isabelle Domaizon, Director of INRAE CARRTEL, Thonon-les-Bains, France

SCIENTIFIC AND LOCAL ORGANIZING COMMITTEE


Luisa Orsini (SC)

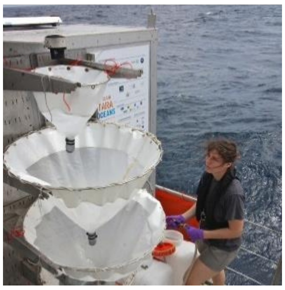

Lois Maignien (SC)


Kristian Meissner (SC)


Bettina Thalinger (SC)


Pedro Beja (SC)


Ramiro Logares (SC)


Lucie Bittner (SC)


Naiara Rodriguez-Ezpeleta (SC)


Florian Leese (SC)

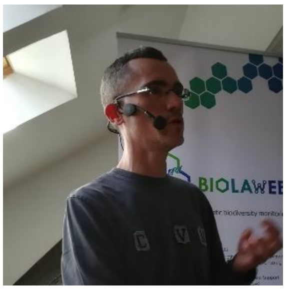

Isabelle Domaizon (LOC)


Frédéric Rimet (LOC)


Jonas Bylemans (LOC)


Nicolas Tromas (LOC)


Clarisse Lemonnier (LOC)


Benjamin Alric (LOC)


Benoit Paix (LOC)


Valentin Vasselon (LOC)

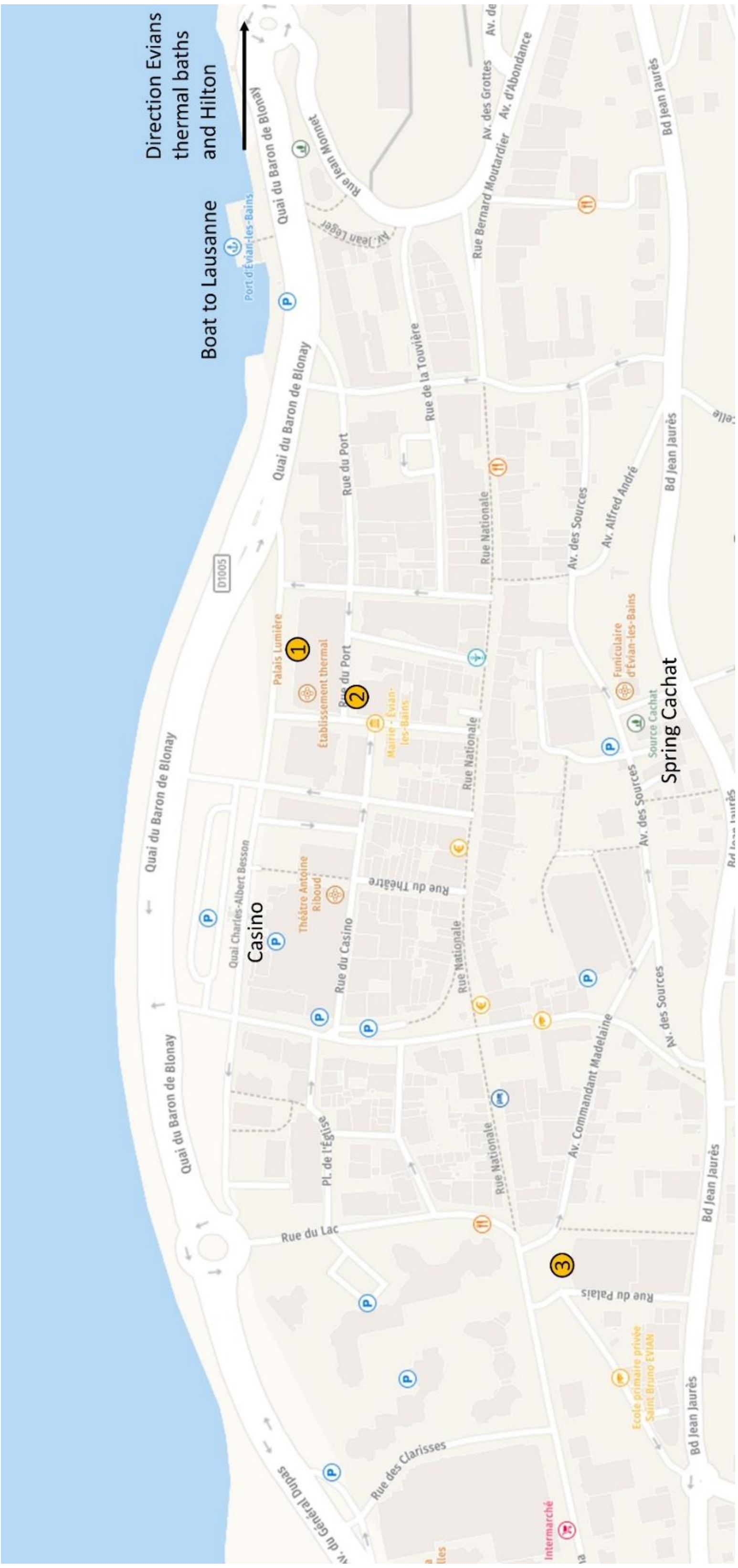
INRAE

UNIVERSITÉ
SAVOIE
MONT BLANC

CARRTEL
CENTRE ALPIN DE RECHERCHE
SUR LES RÉSEAUX TROPHIQUES
ET ÉCOSYSTÈMES LIMNIQUES

SCIMABIO Interface
science management interface for biodiversity conservation

CONFERENCE VENUE



1. Palais Lumière: Main conference venue
2. Espace Brunnarius: Welcome drink & Lunch
3. Palais des festivités: Poster session & Conference dinner

PROGRAM AT A GLANCE

SESSION TOPICS

Session 1	Omics in aquatic ecosystems through participatory science
Session 2	Leveraging omics data to go beyond detections and towards eco-evolutionary insights
Session 3	Understanding Aquatic Ecosystems in an Era of Environmental Change: From Omics Monitoring to Forecasting
Session 4	Knowledge and technological and gaps in omics: what are they and how can they be filled?
Session 5	Biodiversity Monitoring and Reporting: a stakeholders perspective
Session 6	Understanding biotic interactions through the prism of Omics techniques
Session 7	Integrating omics in macroecology to elucidate ecosystem patterns and processes

SCIENTIFIC PROGRAM

Time	Monday 17.03.2025	Tuesday 18.03.2025		Wednesday 19.03.2025		Thursday 20.03.2025		Friday 21.03.2025
		Auditorium	Parallel room	Auditorium	Parallel room	Auditorium	Parallel room	
8:30		Registration		Registration		Registration		
8:45								
9:00		Opening Word		Keynote lecture **Florian Altermatt**		Keynote lecture **Silvia Acinas**		Table Ronde CEN Standardisation Technical Committee meeting
9:15		Presentation of Sponsors						
9:30		Keynote Lecture **Karoline Faust**						
9:45				Coffee Break		Coffee Break		
10:00								Physalia Course
10:15		Coffee Break		Session 7 part 2	Session 3 Validation of Omics Tools	Session 5 Implementation & Standardisation	Session 3 Anthropogenic Impacts part 1	
10:30								
10:45		Session 1	Session 4 Sampling & Analyses					
11:00								
-								
12:30								
12:45		Lunch		Lunch		Lunch		
13:00								
13:15								
13:30								
13:45								
14:00								
14:15		Session 2 Functional Diversity	Session 6 Macro- & Micro-organismal Interactions	Session 3 Bioindicators	Session 2 Quantification & Intraspecific Diversity	Session 3 Anthropogenic Impacts part 2	Session 4 Reference Databases	
-								
16:00								
16:15		Coffee Break						
16:30								
16:45		Session 6 Micro-organismal Networks	Session 7 part 1	Coffee Break		Coffee Break		
17:00	Registration - Palais Lumière							
17:15						Session 4 Technical Advancements	Session 5 Biotic & Abiotic Drivers of Biodiversity	
17:30				Poster Session - Palais des Festivités				
17:45								
18:00		Wine & Cheese - Palais Lumière						
18:15								
18:30	Welcome Drink - Espace Brunnarius							
18:45								
19:00				Conference Dinner - Palais des Festivités				
19:15						Closing Ceremony		
19:30								
19:45								
…								

DETAILED PROGRAM

MONDAY (17.03.2025)

The conference registration desk will open on Monday 17th of March. Participants can register from 17h00 until 19h00 at the main conference venue (Palais Lumière). From 18h30 onwards participants can enjoy a welcome drink and a buffet in Espace Brunnarius located directly behind the main conference venue.

TUESDAY (18.03.2025)

KEYNOTE SPEAKER

Karoline Faust is an Associate Professor at KU Leuven who heads the Lab of Microbial Systems Biology, which focuses on investigating microbial community dynamics in silico and in vitro. In particular, her team is studying interactions between human gut bacteria and the resulting dynamics with synthetic communities in controlled conditions. In addition, the team develops new tools for the analysis of microbiome data, specifically the analysis of microbial networks. The group's work is thus situated at the intersection of bioinformatics, systems biology, and microbial ecology.

Microbetag: a reverse-ecology tool for microbial network interpretation

Ecological interactions are important drivers of microbial community composition and dynamics but are difficult to resolve experimentally. Microbial association networks inferred from abundance data do not predict microbial interactions reliably and are therefore difficult to interpret. In this context, it is helpful to work with genomes that are already known or assembled from metagenomic sequencing data, since they allow applying reverse ecology methods to predict traits and ecological interactions from genes. Here, I will present a new tool, microbetag, that makes use of such methods to help interpret microbial networks.

SCIENTIFIC PROGRAM

Tuesday 18.03.2025		
Time	**Auditorium**	**Parallel room**
8:00	Registration	
8:15		
9:00	**Opening Word**	
9:15	Presentation of Sponsors	
9:30	Keynote Lecture **Karoline Faust**	
9:45		
10:00		
10:15	Coffee Break	
10:30		
	-Session 1- Moderators: Bettina Thalinger & Kristy Deiner	-Session 4- Moderators: Jennifer Harris & François Keck
10:45	**O001. Fidji Sandré** Passive eDNA sampling for enhanced species detection	**O009. Leo Barbut** Using Lagrangian transport model in support of eDNA monitoring in Belgian part of the North Sea
11:00	**O002. Ryo Iwamoto** QuickConc: a novel cationic-assisted eDNA capture method for enhanced biodiversity monitoring	**O010. Vincent Prié** Field sampling of eDNA under complex hydrological conditions
11:15	**O003. Sofie Derycke** eDNA collection by the Belgian fishing fleet: a new gateway towards high resolution marine biodiversity data collection	**O011. Lana Grizancic** Net or Niskin: sampling method most suitable for the northern Adriatic phytoplankton monitoring
11:30	**O004. Lauren Rodriguez** From whale watching to marine biodiversity monitoring: enhancing eDNA sampling with citizen science	**O012. Manuel Lopes-Lima** Unlocking Africa's biodiversity: advancing surveys with cutting-edge eDNA techniques
11:45	**O005. Valérie S. Langlois** Towards revolutionizing conservation efforts in Canada	**O013. Joana Veríssimo** Navigating methodological trade-offs in eDNA biodiversity monitoring: insights from a Mediterranean watershed
12:00	**O006. Bettina Thalinger** Studying bird and fish biodiversity in Canada by engaging local communities in environmental DNA based monitoring	**O014. Philipp M. Rehsen** Improving biomass and abundance assessment of aquatic indicator taxa by combining semi-automated imaging and DNA metabarcoding
12:15	**O007. Yuki Minegishi** ANEMONE Global: establishment of a global network of eDNA-based aquatic biodiversity monitoring.	**O015. Bastien Macé** Finding NeMO: a bayesian adventure in detecting elusive species with environmental DNA
12:30	**O008. Kirsty Deiner** Are lake accumulators of biodiversity information from environmental DNA?	**O016. Gledis Guri** Predicting trawl catches using environmental DNA
12:45	Lunch -Espace Brunnarius-	
-		
14:00		
	-Session 2- Moderators: Silvia Acinas & Nicolas Tromas	-Session 6- Moderators: Fabrice Not & Benjamin Marie
14:15	**O017. Pierre Foucault** Temporal dynamics of microbiomes and life strategies in peri-urban lakes	**O025. Léa Combes** Diversity and long-term temporal dynamics of Microsporidia in Lake Aydat using a paleogenomic approach
14:30	**O018. Arthur Monjot** Metatranscriptomes-based sequence similarity networks uncover genetic signatures within parasitic freshwater microbial eukaryotes	**O026. Kamil Hupalo** Having IMPACT on monitoring aquatic diversity: first experimental results evaluating eDNA as an integrative tool for studying parasites

Tuesday 18.03.2025		
Time	**Auditorium**	**Parallel room**
14:45	**O019. Stéphane Vuilleumier** Bacterial players of the chloromethane cycle in aquatic environments	**O027. Sébastien Duperron** Impact of cyanobacterial blooms on fish gut microbiota: from ecotoxicology to biological invasions?
15:00	**O020. Theodor Sperlea** Detecting semi-annual oscillations in the biotic community of aquatic habitats worldwide using metabarcoding and machine learning	**O028. Benoît Paix** Ecology and evolution of chemical interactions between the brown algae Dictyotales and their epibacterial communities
15:15	**O021. Marlen I. Vasquez** Limiting similarity in temporary streams based on diatom eDNA	**O029. Samuel Orgeas-Gobin** Saving the best for the last: late apoptosis as a mechanism to preserve symbiosis in the thiotrophic bivalve *Lucinoma borealis*?
15:30	**O022. Nathalie Joli** Transcriptomic and epigenomic insights into gene and transposable element regulation in a polar diatom during prolonged darkness and re-illumination	**O030. Erwan Quéméré** Diving deep into kelp forest food webs using dietary DNA
15:45	**O023. Marie-Lee Castonguay** Influence of pollutants, temperature and density on the production and persistence of environmental DNA and RNA (eDNA and eRNA) in aquatic environments	
16:00	**O024. Teun Everts** An omics-based spatial prioritization framework to counter widespread aquatic invaders	
16:15	Coffee Break	
16:30		
	-Session 6- Moderators: Karoline Faust & Ramiro Logares	-Session 7- Moderators: Tristan Cordier & Rosa Trobajo
16:45	**O031. Rafael I. Ponce-Toledo** Modeling the evolution of microbial networks	**O035. Rimet Frédéric** Biogeography of microalgae in freshwaters: new contributions from metabarcoding?
17:00	**O032. Binta Diémé** Cross-feeding interaction within Microcystis phycosphere: new perspectives from the combination of metagenomics and metametabolomics approaches	**O036. Paula Mendoza** Exploring diatom diversity and biogeography in Canary Island watercourses: insights from DNA Metabarcoding
17:15	**O033. Pascal I. Hablützel** Leveraging metagenomics and metatranscriptomics to gain novel insights in the ecological dynamics of microeukaryotic plankton communities	**O037. Briand Jean-françois** Geographic genetic divergence in tychoplanktonic taxa dominating diatom communities in the marine plastisphere
17:30	**O034. Shan Pushpajom Thomas** Co-occurrence networks reveal interactions between aquatic prokaryotes and protists	**O038. Emma Jamon** Divergent Prokaryotic communities across mangrove sediment bioregions: insights from 16S rDNA metabarcoding data
17:45		**O039. Maurine Vilcot** Revealing a diversity continuum in tropical fishes: simultaneous eDNA assessment of populations and communities
18:00	Wine & Cheese -Palais Lumière-	
-		
19:15		

WEDNESDAY (19.03.2025)

KEYNOTE SPEAKER

Prof. Florian Altermatt supervises a team of about 30 people, who address fundamental and applied questions in ecology, with a focus on spatial ecology, biodiversity and ecosystem processes. His work aims to understand how species occur in space and time, how they interact, and how processes such as invasions, dispersal or global change affect natural communities. He uses both experimental and comparative approaches, integrate novel tools such as eDNA, and parallel it with theoretical models. He uses a variety of study systems suited to address broad-ranging questions in ecology. His group is part of the Department of Evolutionary Biology and Environmental Studies at University of Zurich and the Department of Aquatic Ecology at Eawag.

Utilising aquatic environmental DNA to address local to global biodiversity targets

Adequate data on aquatic biodiversity are a necessary prerequisite for biodiversity science. Assessing and attributing the state and change of biodiversity is also essential for bending the curve of biodiversity loss and guiding necessary policy action. Since the mid 2010s, analysis of environmental DNA (eDNA) has become established as a novel and highly powerful approach to assess the state and functioning of aquatic ecosystems and is becoming increasingly implemented by stakeholders, yet its potential is not yet fully tapped. I will present current state in aquatic eDNA research with a particular focus on the policy-relevance of eDNA and its utility in contributing towards the Global Biodiversity Framework (GBF). I will then summarise key technological developments in eDNA science to assess organismal diversity across the full tree of life, to establish ecological indicator analyses in aquatic systems, and its potential for spatial and temporal upscaling as a key reference for local to global biodiversity action. Technological advances in laboratory and sequencing techniques have enabled rapid uptake of the method, yet current challenges remain in the need for adequate reference databases, commonly agreed quality standards (including FAIR principles), and overcoming methodological constraints in retrofitting novel eDNA-based approaches to existing biodiversity monitoring approaches. I will outline the next steps needed to effectively implement eDNA for decision making and addressing global biodiversity targets.

SCIENTIFIC PROGRAM

Wednesday 19.03.2025		
Time	Auditorium	Parallel room
8:00	Registration	
8:15		
9:00	Keynote Lecture **Florian Altermatt**	
9:15		
9:30		
9:45	Coffee Break	
10:00		
	-Session 7- Moderators: Johan Pansu & Cécile Lepère	-Session 3- Moderators: Pedro Beja & Isabelle Domaizon
10:15	**O040. Tristan Cordier** Combining modern surface-to-seafloor eDNA datasets to unlock the potential of sedimentary ancient DNA.	**O050. Coci Manuela** New omics observatory for marine biodiversity in the Adriatic: a case study
10:30	**O041. Benjamin Marie** More than just disorder - metabolite diversity of Microcystis strains shows tight correspondence to genotype and may contribute to ecotype specificities	**O051. Bassam Abubaker** Environmental drivers of diatom diversity: insights from DNA metabarcoding
10:45	**O042. Rosa Trobajo** Diatom metabarcoding for good ecological status assessment and beyond	**O052. Lena Brouwir** Methodology for creating a freshwater bioindicator using periphyton genomics
11:00	**O043. Antonija Kulaš** Diatoms genetic diversity across different climate zones	**O053. Thomas Reinhart** How do eDNA monitoring methods compare to traditional bryophyte surveys in rivers?
11:15	**O044. Anastasija Zaiko** Kelp in the climate equation: leveraging 'omics' approaches to unveil the role of giant kelp habitats as a blue carbon sinks	**O054. Nieves López Rodríguez** From marine to freshwater: using fish eDNA to assess community dynamics across salinity gradients
11:30	**O046. Andrea Burfeid Castellanos** Changed succession patterns in the Arctic Sea observed through metabarcoding	**O055. Pedro Beja** Metabarcoding across the tree of life reveals conservation significance and biodiversity patterns in a tropical river (Corubal, Guinea Bissau)
11:45	**O047. Sergio González-Motos** Gene synchrony and rhythmicity in neighbouring marine microbiomes generates insights on functional redundancy	**O056. Yvonne Schadewell** Harnessing the power of eDNA biodiversity assessment to enhance subsurface water flow pathway reconstruction
12:00	**O048. Ramiro Logares** Integrating short- and long-read metagenomics to reveal local and global macroecological patterns in marine microbial populations	**O057. Hannah Rau** New perspectives on the community composition of groundwater ecosystems using eDNA metabarcoding
12:15	**O049. Mechthild Schmitt-Jansen** A comparative metagenomics approach reveals a common functional potential of plastisphere microbiomes across oceans	
12:30		
12:45	Lunch -Espace Brunnarius-	
-		
14:00		

Wednesday 19.03.2025		
Time	**Auditorium**	**Parallel room**
	-Session 3- Moderators: Luisa Orsini & Raffaele Siano	-Session 2- Moderators: Florian Altermatt & Aurélie Bonin
14:15	**O058. Till-Hendrik Macher** Fit for purpose? Evaluating benthic invertebrate DNA metabarcoding for ecological status class assessment in streams under the Water Framework Directive	**O068. Jonas Bylemans** From anarchy to clarity, data pre-processing and statistical choices influence quantitative environmental DNA (eDNA) analyses.
14:30	**O059. Cristiana Cravo-Laureau** Bioindicators of littoral and retro-littoral wetlands ecosystem functioning	**O069. Mohamed Yosri Zanni** Modeling the interactions between decay and dispersion of eDNA in the Bay of Biscay
14:45	**O060. Jono Warren** Microbial biofilms as indicators of environmental change in English rivers.	**O070. Céline Condachou** Linking metabarcoding quantitative information to fish environmental DNA concentration in Neotropical rivers
15:00	**O061. Sara Beier** Artificial intelligence assisted modelling reveals that species properties rather than species diversity determine community responses to environmental change	**O071. Marie-Pier Brochu** Three-year monitoring of lake sturgeon (*Acipenser fulvescens*) occurrence in a spawning ground using environmental DNA
15:15	**O062. Benjamin Alric** Graph theory at the service of assessing the ecological status of lake ecosystems based on phytoplankton communities	**O072. Micaela Hellström** Reproductive and migratory patterns in fish revealed by MBC analyses of monthly samples.
15:30	**O063. Leire Garate** Sediment microbial communities and their association networks differed depending on their disturbance level	**O073. Emilie A. Didaskalou** Unlocking demography: developing an eDNA-based toolkit to measure sex ratios.
15:45	**O064. Erik Zschaubitz** Machine learning-driven analysis of metabarcoding data to identify anthropogenic trace substances in aquatic ecosystems	**O074. Tamas Malkocs** Species-level detection and population genetic inference of small cetaceans from environmental samples, using mitochondrial and RADseq-derived markers
16:00	**O065. Anders Lanzén** Estuarine microbenthos as ecosystem health indicators, from the Basque estuaries to the whole Bay of Biscay, the world, and beyond	**O075. Marie-Thérése Werner** Population genetic analyses of a key invertebrate species using mitochondrial and nuclear DNA markers
16:15	**O066. Luisa Orsini** Biodiversity time machine: a holistic approach to monitoring and forecasting freshwater ecosystems	**O076. Daniel Zumel** Hybrid horizons: detecting hybridization in natural populations using a novel eDNA toolkit
16:30	**O067. Niamh Eastwood** Exploring the landscape-level drivers of lake biodiversity using data-driven analysis of environmental DNA	**O077. Els De Keyzer** Repeated river–lake introgression in the adaptive radiation of Sailfin silverside fishes in Lake Matano, Sulawesi
16:45	Coffee Break	
17:00		
17:15		
17:30	Poster Session -Palais des Festivités-	
17:45		
-		
18:45		
19:00	Conference Dinner -Palais des Festivités-	
…		

POSTER PRESENTATIONS

No.	Presenter	Poster title
P01	Tristan Lefébure	Monitoring biodiversity of an alpine watershed using eDNA metabarcoding and ecological surveys: a collaborative work between students, scientists and citizens
P02	Vid Švara	ProTecteDNA: portable solutions for eDNA-based biodiversity monitoring in protected areas
P03	Abigaël Chieux	On-site species detection based on eDNA: example of the Natterjack toad (*Epidalea calamita*)
P04	Chiara Mercier	The noose is tightening on parasites: how environmental nucleic acids (RNA/DNA) help us identify the different forms of freshwater parasites
P05	Verena Trenkel	eRNAmaris - the use of environmental RNA to improve fish stock assessments in marine systems
P06	My Dung Jusselme	Wastewater treatment with an oxidizing agent: efficiency on pathogens and antimicrobial resistance
P07	Emilie Delpuech	eDNA as a tool for precision biodiversity reporting: aligning science and stakeholder needs
P08	Jessie-Lee Langel	Can eDNA be a decision support for sea turtle nesting monitoring?
P09	Marine Vautier	Three converging eDNA approaches to track the reproductive dynamics of two invasive dreissenid mussels in lakes
P10	Yeseren Kayacan	Diurnal and intratidal variation in microbial community structure and gene expression in a mudflat biofilm
P11	Sébastien Duperron	The culture collection of cyanobacteria at the MNHN (National Museum of Natural History)
P12	Paula Gauvin	Evaluating littoral zone restoration in lake through a multi-taxa eDNA ecological assessment
P13	Fidji Sandré	Tracking aquatic biodiversity with eDNA: a study in quebec's mining regions
P14	Manon Daudinet	Identifying macrophytes using environmental DNA metabarcoding for biomonitoring and ecosystem management
P15	Clara Dignan	Using OMICS methods to evaluate and monitor marine microbial responses to human in a management perspective - the MICROSURV project
P16	Fanny Charrier	Decyphering the tolerance of leaf litter biofilms to the biofungicide Kasugamycin through the combination of metametabolomics with structural and functional descriptors
P17	Jennifer Harris	Microbial diversity baseline linked to hydrogeological conditions and anthropic pressures in the Beauce Aquifer, France.
P18	Judith Piontek	The potential of eDNA metabarcoding for monitoring demersal fish communities in marine proteced areas of the Baltic Sea
P19	Sulivan Jouanneau	Evolution of genetic and phenotypic diversity in a marine microbial community exposed to pollutants: a microcosm study.
P20	Lin Zi	Developing high throughput metametabolomics in freshwater Periphyton to enhance chemical risk assessment

No.	Presenter	Poster title
P21	Charlotte Van Driessche	Precision in river monitoring: key eDNA sampling sites unlock comprehensive fish biodiversity insights
P22	Lemonnier Clarisse	Comparison of shot-gun sequencing and metabarcoding to assess alpine lakes phytoplankton diversity
P23	Dimitra-Ioli Skouroliakou	Enhancing plankton monitoring: a comparison of short and long-read eDNA metabarcoding for characterizing plankton communities in the Belgian part of the North Sea
P24	Enora Geslain	Refining eDNA taxonomic assignments with a phylogenetic approach
P25	Filipa M.S. Martins	Evaluating the impact of sampling strategies and bioinformatics on ethanol-based DNA metabarcoding
P26	Paul Hamilton	Building the diatom (Heterokontophyta) DNA library with rare species using traditional sequencing
P27	Nika Tivadar	Preliminary comparison of microscopy and molecular methods for determining cyanobacterial composition of a frequently blooming pond
P28	Théo Deremarque	Using environmental DNA to track the spread of invasive host-parasite complexes: a case study of the invasive freshwater fish *Pseudorasbora parva* and the cryptic fungal parasite *Sphaerothecum destruens*
P29	Eloïse Duval	eDNA monitoring at a large scale to spot at-risk salmonid populations regarding an emerging infectious disease
P30	Gael Denys	The eDNA as an interesting tool to protect endangered endemic fish species against restocking: an example with French graylings (Teleostei, Salmonidae)
P31	Laura Jamet	Does the Aquitanian pike (Teleostei, Esocidae) breed during the closed angling season? Elements of answer according to the eDNA approach.
P32	Nieves López Rodríguez	Can eDNA metabarcoding be used to develop a biological quality index for disconnected pools in temporary rivers?
P33	Sébastien Autret	Assessment of the cyanobacteria risk, considering the invasive bryozoan *Pectinatella magnifica*
P34	Martel Alexis	Guilt by association? The role of cyanobacteria-associated bacteria in harmful algal blooms.
P35	Mélissa Eon	Chemical landscape of invasive aquatic plant exometabolomes
P36	Ivaylo Sirakov	How the feeding regimes impact the waste metabolomes in aquaponics
P37	Stéphan Jacquet	Quantifying an example of invasion dynamics and interaction with endemic species: the case of the red blood mysid *Hemimysis anomala* in Lake Geneva
P38	Briand Jean-françois	Relative effect of physico-chemical parameters and contaminants on the diversity of diatom communities along the French Mediterranean coast
P39	Amélie Malherbe	Combination of metabolomics and machine learning to unravel environmental drivers of spatial heterogeneity of microbial metabolome assemblage in aquatic periphyton: The COMBO project

THURSDAY (20.03.2025)

KEYNOTE SPEAKER

Dr. Silvia Acinas is a researcher at the Department of Marine Biology and Oceanography at the ICM (Institut de Ciències del Mar), CSIC in Barcelona. Her research focuses on linking microbial genetic diversity with functional capacities of ecologically relevant marine microbial taxa using metagenomics, metranscriptomics, single cell genomics, and isolation. These approaches are used to gain insights into the evolutionary mechanisms underlying diversification processes. She now focuses on polar marine ecosystems (Arctic and Antarctic), which are threatened by climate change but also blue-biotechnology research.

Unlocking the Ocean Microbiome: From Ecology to Blue Bioprospecting

The planet's greatest diversity lies within the invisible world of planktonic microorganisms. With an estimated 10^{29} prokaryotic cells and at least 10^{11} microbial species (Locey and Lennon, 2016), these organisms harbour immense genetic and metabolic potential and enable the degradation of numerous natural and human-introduced (allochthonous) substances, highlighting their adaptability and potential for innovation. Advances in marine biodiversity research have increasingly revealed microorganisms with molecules and genes of significant commercial and scientific value. Our research group investigates marine microbes' ecology, functional diversity and genetic capacities of marine microbes for Blue Bioprospecting. This presentation highlights several studies based on large-scale metagenomic surveys (Tara Oceans and Malaspina) providing as well examples of blue bioprospecting related to (1) bacteria from the ocean and marine sediments capable of degrading methylmercury, a neurotoxin, and (2) the discovery of novel CRISPR-Cas9 systems from the deep ocean.

SCIENTIFIC PROGRAM

Thursday 20.03.2025		
Time	**Auditorium**	**Parallel room**
8:00	Registration	
8:15		
9:00	Keynote Lecture **Silvia Acinas**	
9:15		
9:30		
9:45	Coffee Break	
10:00		
	-Session 5- Moderators: Kristian Meissner & Florian Leese	-Session 3- Moderators: Anastasija Zaiko & Frederic Rimet
10:15	**O078. Tiina Laamanen** Technology readiness level of biodiversity monitoring with molecular methods - where are we on the road to routine implementation?	**O087. Martijn Callens** Local accumulation of organic matter in marine sand extraction areas drives changes in sediment prokaryotic communities with potential consequences for nitrogen cycling
10:30	**O079. Christina Pavloudi** Preliminary results from the European Marine Omics Biodiversity Observation Network (EMO BON): long-term genomic monitoring and FAIR stakeholder reporting	**O088. Valentin Ambroise** Impact of 10 years of deforestation and population growth on biodiversity seen through the lens of metabarcoding
10:45	**O080. Sandra Garcés-Pastor** Taxonomy-free approach to diatom indicators based on three eukaryotic markers	**O089. Rein Brys** The power, challenges and integration of omics-based ecological insights as a cornerstone for invasive species management in aquatic environments
11:00	**O081. Kálmán Tapolczai** A novel framework for phytoplankton biomonitoring: trait assignment of 23S rRNA sequences	**O090. Ana Baricevic** Omics in the service of characterising the eukaryotic plankton community in the Adriatic Sea
11:15	**O082. Laurine Viollaz** Environmental DNA approach to assess phytoplankton communities in lake environments	**O091. Eeva Eronen-Rasimus** Under-ice methanotrophy may offset Baltic sea ice methane fluxes
11:30	**O083. Jelger Herder** Exploring the potential of eDNA-metabarcoding as an alternative to conventional fish monitoring under the Water Framework Directive	**O092. Anastasija Zaiko** Understanding emerging ecosystems: tracing biodiversity and ecological change in a periglacial Arctic lagoon using eDNA
11:45	**O084. Valentin Vasselon** The fellowship of the ring test confronting a method to rule them all: testing the transferability and comparability of diatom DNA metabarcoding protocols for biomonitoring	**O093. Flora Mottet** Using multi-omics to illuminate responses of sediment microbial communities to hydrological changes in lotic systems and their consequences on carbon cycling
12:00	**O085. Hanneloor Heynderickx** Optimizing MSFD pelagic habitat indicator workflows to accommodate genetic monitoring data	**O094. Kiemel Katrin** Uncovering effects of environmental change through eDNA metabarcoding: a long-term perspective
12:15	**O086. Olivier Monnier** The carbon footprint of diatom molecular research	**O095. Nicolas Tromas** Predicting cyanotoxins concentrations in lakes and reservoirs using microbial community information
12:30		
12:45	Lunch -Espace Brunnarius-	
-		
14:00		

Thursday 20.03.2025		
Time	**Auditorium**	**Parallel room**
	-Session 3- Moderators: Nicolas Creusot & Helène Agogué	-Session 4- Moderators: Karolina Bacela & Till-Hendrik Macher
14:15	**O096. Nicolas Creusot** Multiomics approach to characterize the link between the structural biodiversity and the microbial activity along the natural dynamic of freshwater periphytic biofilms and its response to the chemical stress: main outcomes from the MICROBIOMIQ project	**O106. François Keck** Navigating the seven challenges of taxonomic reference databases
14:30	**O097. Tayebeh Soltanighias** Occurrence of antibiotic-resistant bacteria in household plumbing system	**O107. Arne J. Beermann** dbDNA - A phylogeny- and expert identifier-driven grading system for reliable taxonomic annotation of (meta)barcoding data
14:45	**O098. Chakresh Kumar** Metagenomic insights into the functional microbial diversity of the lower stretch of the river Ganga: mapping antibiotic and metal resistance genes	**O108. Ljubica Vlaović** Challenges in the investigation of the diatom community of saline habitats: a case study of Plava Banja (Serbia)
15:00	**O099. Pedro A. Inostroza** Multi-compartment impact of micropollutants and particularly antibiotics on bacterial communities using environmental DNA at river basin-level	**O109. Kristina Petrović** eDNA-based assessment of phytoplankton community structure and dynamics in a saline lake in Serbia: comparison with microscopy-based method
15:15	**O100. Gaëtan Burgaud** A comprehensive pan-European exploration of fungal plastisphere dynamics along river-to-sea continuums	**O110. Nergiz Dukan** MSFD and impact monitoring with eDNA: Insights from case studies in the Belgian part of the North Sea and Avlékété beach, Benin
15:30	**O101. Nina Röder** Genome-wide responses to chronic Bti and copper exposure in a laboratory culture of *Chironomus riparius*	**O111. Liliana Ballesteros-Mejia** Laying the foundations of a national genetic baseline for species identification in support of biodiversity research and public policies in France.
15:45	**O102. Lise Klunder** Making the invisible visible: molecular methods to trace the success of the restoration of river Emscher	**O112. Vincent Haÿ** A molecular reference database of mitochondrial genomes for freshwater fish in France.
16:00	**O103. Réalis-Doyelle Emilie** From ice to heat: variation in phenotypic and transcriptomic response of Arctic Charr populations from contrasted environments	**O113. David Mann** Metabarcoding "by-catch" is precious
16:15	**O104. Mahshid Oladi** Environmental DNA-based profiling of benthic microbial communities along a crude oil spill gradient in a coral reef in the Persian Gulf	**O114. Daniel Wewer** Overcoming limitations in eDNA metabarcoding with nanopore sequencing of whole mitogenomes
16:30	**O105. Lou-Anne Jannel** Aquatic biodiversity on Reunion Island: responses of biological communities to environmental and anthropogenic pressures using environmental DNA	
16:45	Coffee Break	
17:00		

Thursday 20.03.2025

Time	Auditorium	Parallel room
	-Session 4- Moderators: Mechthild Schmitt-Jansen & Erwan Quéméré	-Session 5- Moderators: Sofie Derycke & Owen Wangensteen
17:15	**O115. Jim Birch** FIDO: a new type of autonomous aquatic sampling instrument for ‘omics studies	**O122. Baudry Thomas** eDNA optimization for regular monitorings of white-clawed crayfish (*Austropotamobius pallipes* species complex): from lab testings to large-scale field validation
17:30	**O116. Armando Espinosa Prieto** Leveraging hybridisation capture for detecting rare events and as a PCR-free metabarcoding approach for vegetation surveys	**O123. Marina Chauvet** Seeking for microbial bioindicators of river run-off inputs: new insights from eDNA data sets
17:45	**O117. Hiroki Yamananaka** Enhancing eDNA metabarcoding accuracy: mitigating PCR bias with droplet PCR	**O124. Haderlé Rachel** Environmental DNA metabarcoding for the assessment of vertebrate biodiversity along the estuarine gradient of the Rance river (Brittany, France)
18:00	**O118. Patrick Łypaczewski** Unrestricted metabarcoding with Nanopore long-read sequencing	**O125. Héloïse Verdier** eDNA outperforms traditional methods for detecting organic pollution in a non-perennial river
18:15	**O119. Fabrice Not** Aquatic diversity of microbial eukaryotes assess by Oxford Nanopore Technology and Illumina sequencing	**O126. Ole Bjørn Brodnicke** Innovating biodiversity monitoring: translating eDNA research and democratizing data to empower stakeholders and the public
18:30	**O120. Alba M. Losa** Addressing workflow challenges of ONT sequencing approaches for riverine microbial communities: long-read vs short-read sequencing	**O127. Daniël van Berkel** eDNA-based assessment of species diversity and its temporal development in a Dutch offshore wind farm
18:45	**O121. Olivier Collard** Nanopore eDNA long-read metagenomics: an holistic window for eDNA analysis	**O128. Auriel Sumner-Hempel** Monitoring Elasmobranch diversity using eDNA in offshore wind farms
19:00		
19:15	**Closing Ceremony** -Auditorium-	
19:30		
19:45		

Sylphium
molecular ecology

e-biom
YOUR PARTNER IN BIOLOGICAL MONITORING

illumina®

INRAE transfert

metaDIA

METYS

DOT
Dartmouth Ocean Technologies Inc

CARNOT
Eau & Environnement

AnaEE
Analysis and Experimentation on Ecosystems
France

ADENEKO
Écologie & Génétique

Argaly

ADN
Agence d'information génétique
Un laboratoire de Qualtech GROUPE

AFEM
Association francophone d'écologie microbienne

Physalia Courses

GREENOMICS
GENOMICS RESEARCH FOR ECO-EVOLUTION AND ENVIRONMENT

MBMG
Metabarcoding & Metagenomics