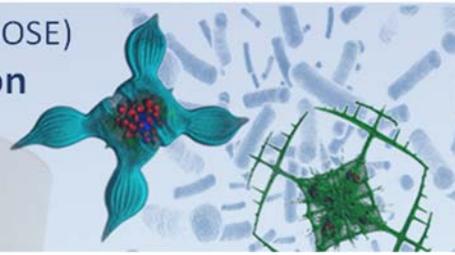


EuroMarine Open Science Exploration (EMOSE) Inter-comparison of Marine Plankton Metagenomic Methods

11-15 September 2017, Porto, Portugal



The 2017 edition of EMOSE will be held in Porto at the Interdisciplinary Centre of Marine and Environmental Research (CIIMAR, University of Porto).

HOW TO APPLY: apply [online](#) before 5 May 2017

OUTCOME: all applicants will be informed by email on 31 May 2017

COURSE FEE: 200€

ACCOMMODATION & MEALS: EuroMarine sponsors the costs for all participants.

TRAVEL: EuroMarine sponsors a maximum of 400€ per participant.

MORE DETAILS: [online](#)

CONTACT: Stéphane PESANT (spesant@marum.de)

PARTICIPANTS: 12 early-career-scientist will be selected based on their experience with marine microbiome analysis and current research activities. They should be postdocs or recently appointed researchers from as many different institutions/countries as possible. Gender balance will also be considered. Participation is restricted to EM full and invited members in order to stress the benefits of being part of the EM network ([see list here](#)). Special care will be taken to include participants with experience with protocols from Tara Oceans, Malaspina, Ocean Sampling Day and the Earth Microbiome project. Participants will be listed in alphabetical order as co-authors of the resulting methodological paper.

The concept of EMOSE is simple and community oriented. We propose to explore open science resources and practices with a small group of early career scientists that conduct a well-defined study. Together with the participants, the EMOSE team will use/explore existing open science resources such as open lab-books, open protocols, and virtual laboratory platforms. Open science is expected to improve access to all intermediate (even unsuccessful) research steps/outputs of the study, and is expected to speed-up the entire life-cycle of the study, i.e. from design to dissemination of research outputs.

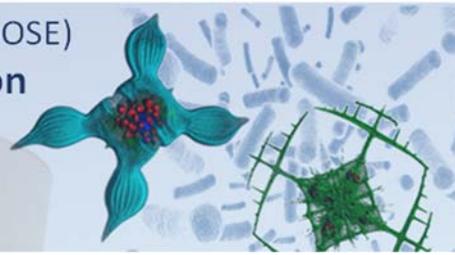
The scientific objective of the first Edition (2017) of EMOSE is to review methods in marine plankton metagenomic analysis, essentially comparing the different filtration volumes and size-fractions used by recent initiatives, i.e. Tara Oceans, Malaspina and the Ocean Sampling Day. Already published data from these projects will be complemented by a new set of data obtained from a comparative experiment of protocols used in the three initiatives. The bulk of the analyses will be done during a 5-day hands-on session in Porto, and a virtual research environment will be used to plan the analysis and to work-up a review paper.

Key invited participants were selected outside the EuroMarine community, but have worked closely with the EM marine microbiome community in various initiatives. They are highly proficient scientists/practitioners from the field of marine microbiology (Fuhrman, USC), sequencing methodology (Poulain, Genoscope), and bioinformatics (Mitchell, EMBL-EBI). Their role is to (1) contribute to the design of the inter-comparison study during virtual meetings; (2) participate in the 5-day hands-on session; and (3) contribute to the analysis, follow-up virtual meetings, and to the resulting methodological paper. The key invited participants will be last authors on the paper.



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Short biography of the organisers and key invited participants:

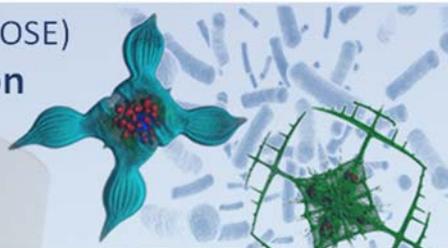
Dr Stéphane Pesant - Biological oceanographer. PhD at Laval University, Québec (1999); Scientific advisor at Fisheries & Oceans Canada, Ottawa (2000-01); Postdoc at the University of Western Australia, Perth (2002-04), leading primary production and carbon flux components of national and international programmes; assistant to the Scientific Director of FP6 Network of Excellence EUR-OCEANS, Villefranche/Mer (2005-09); Since 2009 at PANGAEA (University of Bremen), leading Open Science and data publishing for several European and international projects, including EuroMarine, EURO-BASIN, MicroB3, ATLAS, Oceanomics, Tara Oceans and Tara Pacific; Since 2016, editor-in-chief of the Aquatic Data journal with Elsevier. Early instigator of EuroMarine and member of the steering committee.

Dr Ivo Grigorov - PhD in Marine Science and currently research administrator responsible for fundraising and proposal formulation at the National Institute of Aquatic Resources, DTU-Aqua. IG has been an advocate for Open Science since 2006, and authored Eur-OCEANS' NoE "Cost-benefit analysis of publishing MARINE ECOSYSTEM RESEARCH output through Open Access Self-Archiving". As member of FP7 FOSTER, IG has trained graduate students, librarians and research funding agency staff in strategic benefits of Open Science. IG is a consultant on the design of EC's Open Science Monitor in support of the Open Science Policy Platform, and currently applies the synergies between Open Science and Open Innovation towards more competitive grant proposals and optimising societal impact of research. Full member of EuroMarine.

Dr Tim Deprez - background in marine taxonomy, specializing in taxonomic databases. Since 2008 he has been largely involved in organizational aspects of higher education, and developed the EConsort software for managing educational programmes. He teaches several Masters courses at Ghent University and is a guest lecturer at 2 other European universities. Tim is the executive coordinator of the MSc in Marine Biodiversity and Conservation EMBC/EMBC+. From 2011-2016 he coordinated the Erasmus Mundus MARES Doctoral Programme. From 2012 onwards, he was involved in major European marine training initiatives which led to the development of the European Marine Training platform. Since 2015 he has also been strongly involved in the Belgian pillar of EMBC. His topics of scientific expertise deal mainly with marine biological data management, open training resources, international marine training and education. Full member of EuroMarine.

Dr Francesca Malfatti - PhD in Marine Biology, is a marine microbial ecologist. She received the IRPE Prize (Germany) in 2010. Her major research focus is on the role of marine microbes in global ocean carbon cycle. Her approach is based on the recognition that the metabolic activities of marine bacteria and their adaptive strategies shape the huge ocean ecosystems at the microscale. High-resolution tools (such as AFM, LSCM and NanoSIMS) coupled with small-scale incubation experiments and NGS (from single cell –MDA to meta-data) is a powerful approach to investigate ocean scale consequences of bacterial action on marine organic matter. Current projects span from black carbon effect on the marine microbial loop to bacteria ecology in freshly generated sea-spray aerosol. Furthermore, Dr. Malfatti is serving the European Marine Board on Citizen Science and promotes scientific outreach in Italy. Full member of EuroMarine.





Dr Alessandro Vezzi - PhD in Biotechnology, Dr Vezzi has always focused his scientific interest in genome sequencing and analysis of both prokaryotic and eukaryotic organisms. In fact, he was actively involved in the sequencing of the first ever sequenced plant, *Arabidopsis thaliana*, in the sequencing of a bacterial genome that represents the first work on a complete genomic sequence accomplished entirely in Italy, and lately in the sequencing of agronomical or biotechnological relevant species. His research activities are nowadays mainly focused in NGS data production and analysis, with a particular emphasis in the assembly and fully exploitation of the produced short reads both in genomic and metagenomic projects. Full member of EuroMarine.

Dr Catarina Magalhães - PhD in Marine Sciences, is a researcher of (CIIMAR) and member of the coordination committee of Portuguese Polar Program (PROPOLAR). Her previous investigations resulted in important contributions to understand microbial derived N machineries interactions and to identify the mechanisms regulating their operation. She focuses her research on N-biogeochemical pathways in extreme environments (Arctic and Antarctica). In the context of her research topics the methodologies she use are mainly biogeochemical measurements, microbiome sample processing and genomic and metagenomic NGS work flow analysis. Full member of EuroMarine.

Dr Jed Fuhrman - Biological oceanography PhD (1981), endowed chair University of Southern California. Received the G.E. Hutchinson medal from ASLO (2006); Fellow of AAAS, American Academy of Microbiology, ASLO, and American Academy of Arts and Sciences. His work includes development of the thymidine incorporation method to measure in situ bacterial growth rates which helped demonstrate the significance of the microbial loop; his lab also reported the significance of viral infection of marine bacteria and cyanobacteria, and discovered the highly abundant marine thaumarchaea. In recent years his lab has focused on using molecular genetic techniques to investigate diversity patterns in marine microbial communities (viruses, bacteria, archaea, and protists), such as repeating seasonal patterns and unexpectedly rapid changes in the communities following spring blooms, with an emphasis on using microbial association network analysis to examine community interactions and relationships.

Dr Julie Poulain - Engineer at the CNS (Genoscope-CEA, France) for 15 years. After 10 years of management of the technical teams of the sequencing laboratory, she has been in charge of the follow-up of samples treatment from Tara Oceans project, for meta-omics studies. Today, She is involved in the TaraPacific project and takes part of the scientific logistics and the coordination of meta-omics tasks.

Dr Alex Mitchell - Is content coordinator for the InterPro and EBI Metagenomics databases at EMBL-EBI. He is responsible for the day-to-day running of the metagenomic analysis pipeline, which has processed over 300 billion nucleotide sequences to date. He also oversees benchmarking of new analysis algorithms for potential inclusion in the pipeline. He obtained his DPhil in pharmacology from the University of Oxford, and was previously employed as a molecular biologist at the Institute of Psychiatry in London, before moving to the University of Manchester to work on protein family databases. He joined EMBL-EBI in 2011.

