MOOSE: réseau d’observation en Méditerranée nord-occidentale

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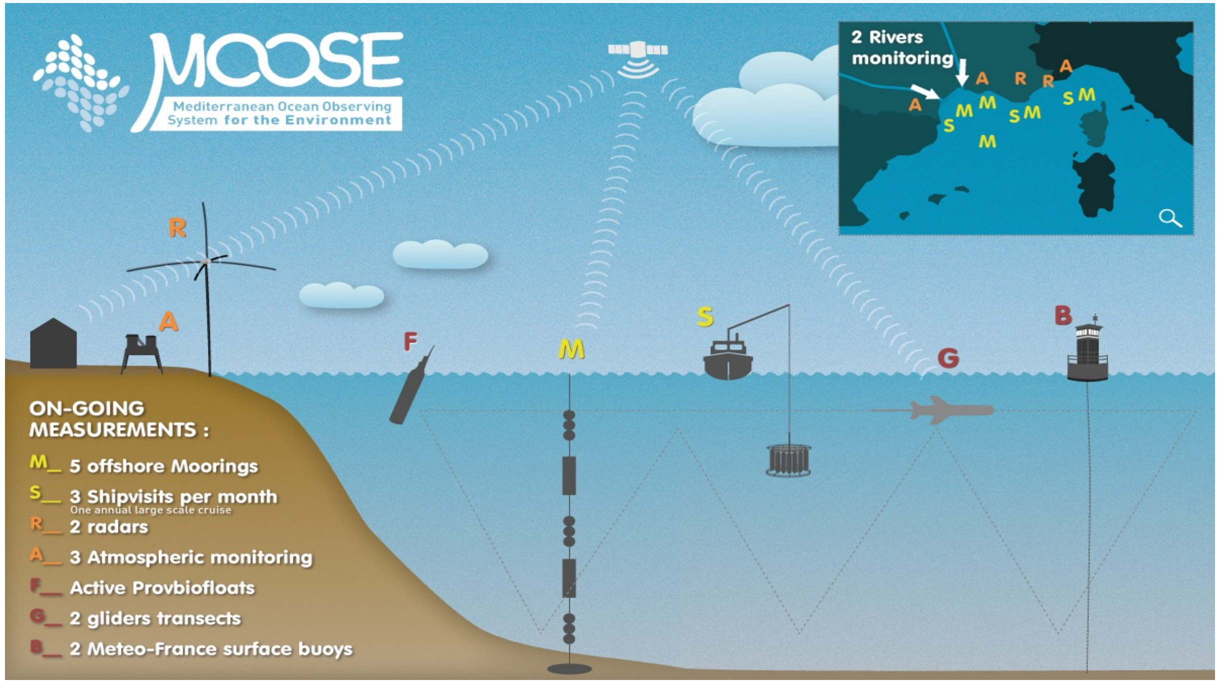
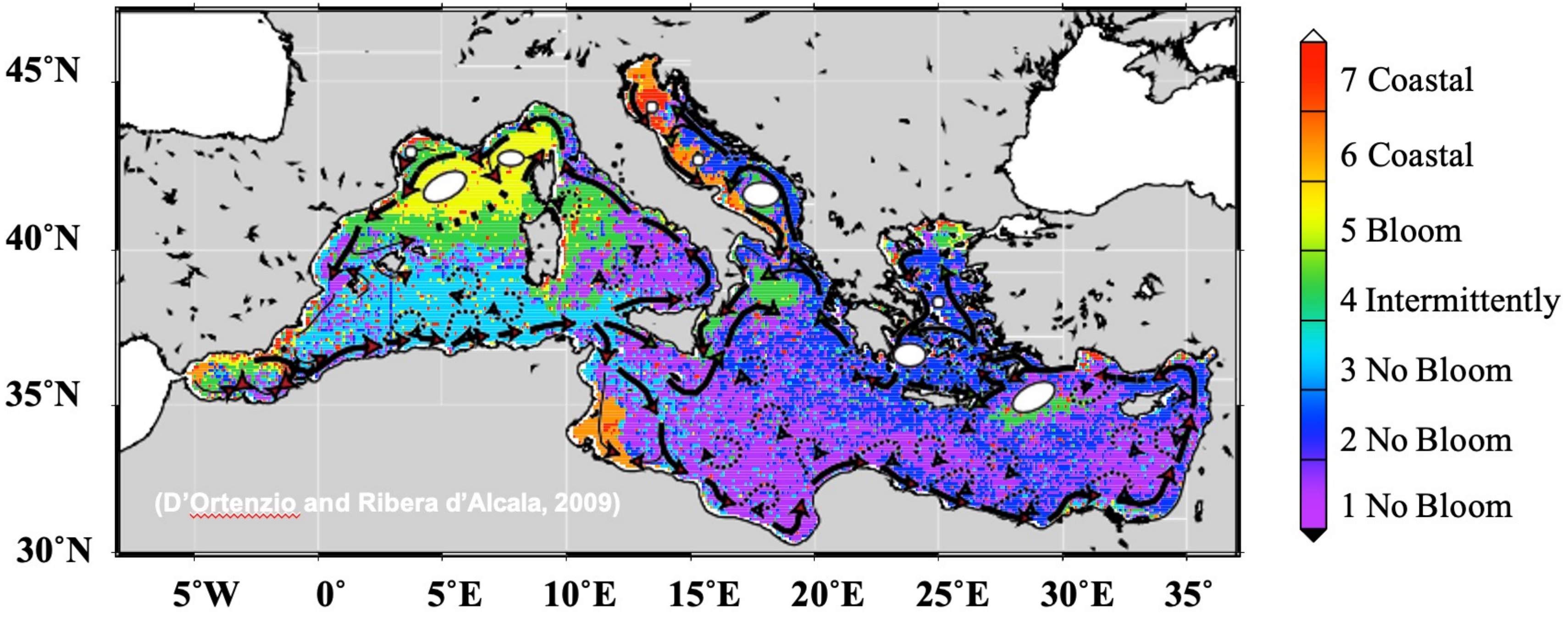
Et les responsables WP/sites: A.Bosse, P.Testor, T.Wagener, D.Lefevre, P.Conan, B.Zakardjan, D.Aubert, C.Migon, W.Ludwig, P.Raimbault, F.Carlotti, L.Guidi, R.Vuillemin, P.Bretel, E.Riquier



CNRS INSU Observer & comprendre · ILICO Infrastructure de recherche littorale & côtière · Ifremer · METEO FRANCE Toujours un temps d’avance

Le système méditerranéen

Bio-regions vue de l'espace



- Mer marginale semi-fermée de grande biodiversité : > 17k d'espèces marines *[Coll et al. (2010)]*
- Forte pression anthropique : 30% du trafic maritime mondial et du tourisme.
- Flux entrant/sortant de ~1 Sv à Gibraltar → impacts méditerranéens dans l'Atlantique
- Écosystème fortement façonné par la physique de l'océan (horizontalement : courants, tourbillons, ...; verticalement : convection profonde (Golfe du Lion, Mer Adriatique, Mer d'Egée, ...)

Phases de la convection profonde :

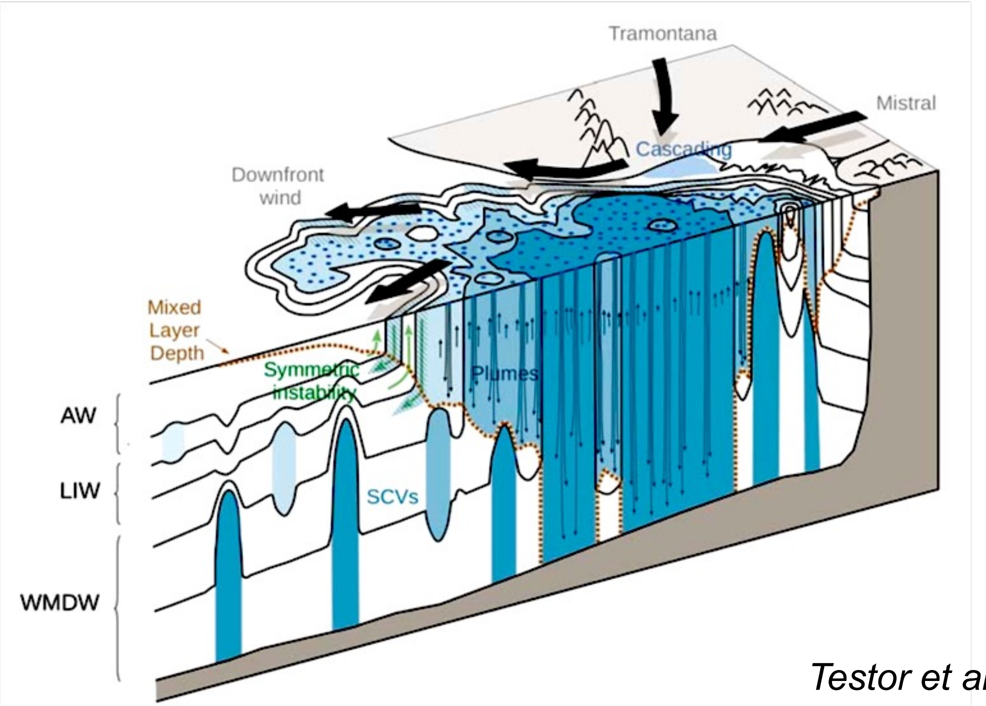
- Préconditionnement : circulation cyclonique
- Phase de mélange :

Perte thermique air-mer intense, mélange profond

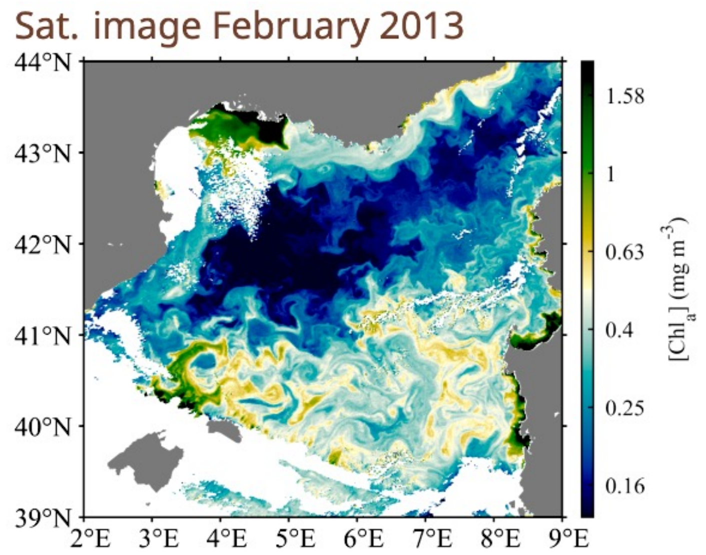
⇒ apports des éléments nutritifs, ventilation des masses d'eau

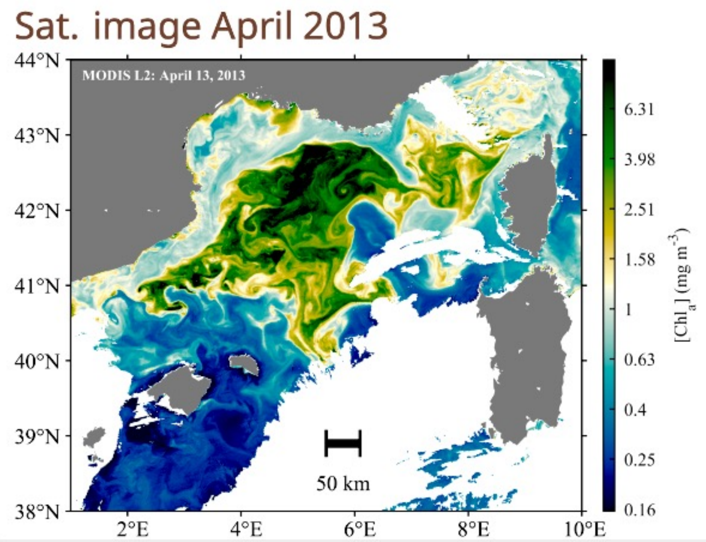
- Phase de restratification

dispersion des eaux profondes ⇒ floraison printanière



Testor et al., 2018





⇒ Nécessité d'un système d'observation de cette zone clé de la Méditerranée résolvant une large gamme d'échelles avec couplage physique-chimie-biologie

MOOSE: historique

2008-2010

Brain-storming
Workshops 2008-2009
Science plan
Implementation plan

2011-2013

Implémentation
Campagne annuelle
Fleuves/Atmosphère
Planeurs sous-marin (DT)
Radars HF
Label SOERE 2011

2014-2015

Activité biologique
Filets zooplancton
Canaux données (QC)
Valorisation DEWEX/MOOSE

2016

Intégration
Label INSU 2016-2020
IR ILICO en 2016

2017

Innovation
Outils génomiques
EMSO ERIC

2019

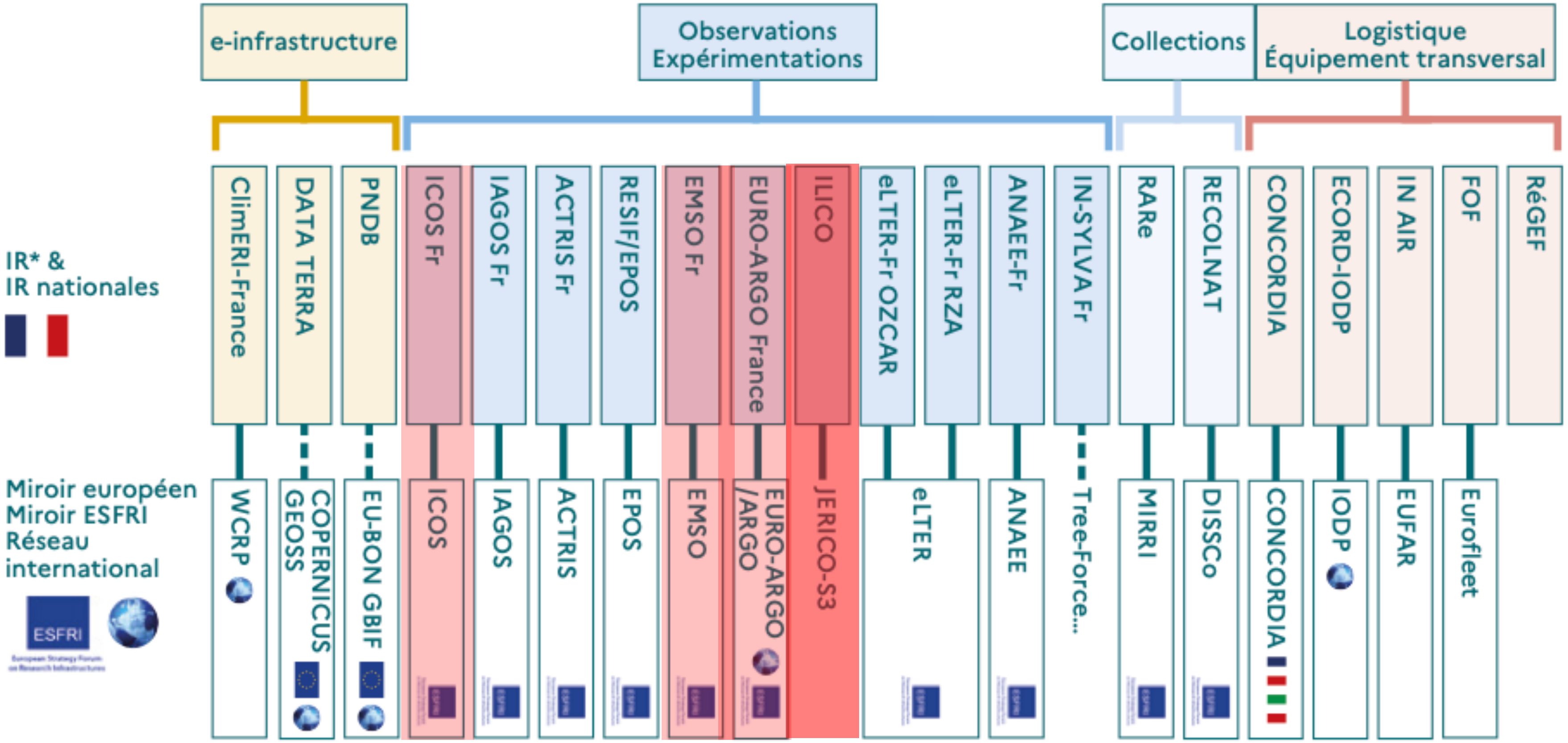
Nouvelle coordination
Label INSU 2020-2024
Arrivée d'un second CNAP

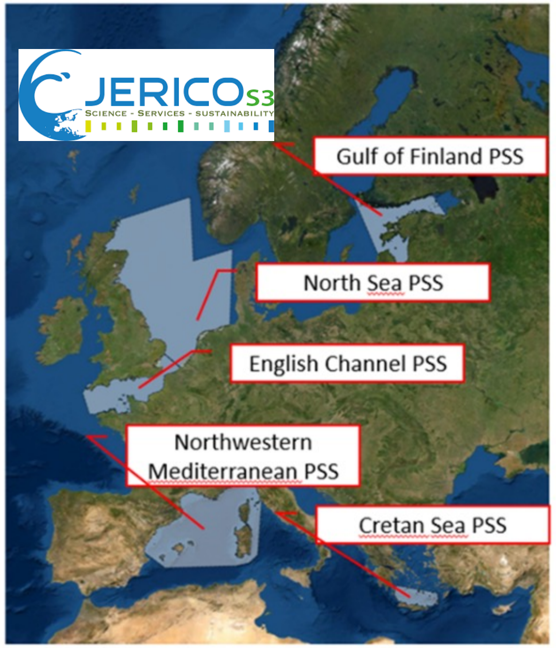
2022

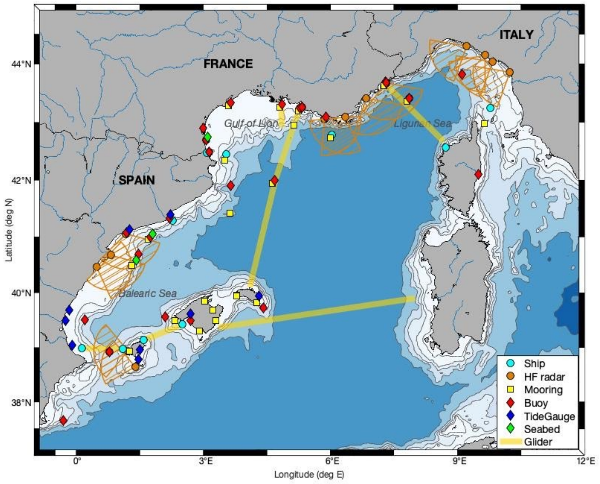
Bilan 2010-2022
Workshop VLFR

Budget maintenance: 180 k€/an (INSU, IR ILICO). Total 2.5 M€/an
Personnel : 52 personnes (eq. 100 HM/an) avec 2 CNAP
Laboratoires: M.I.O., OSU STAMAR, CEFREM, LOCEAN
Instituts: INSU, Universités (SU, AMU, Perpignan), IFREMER, METEO France

MOOSE: intégration dans le paysage des IR/ERIC

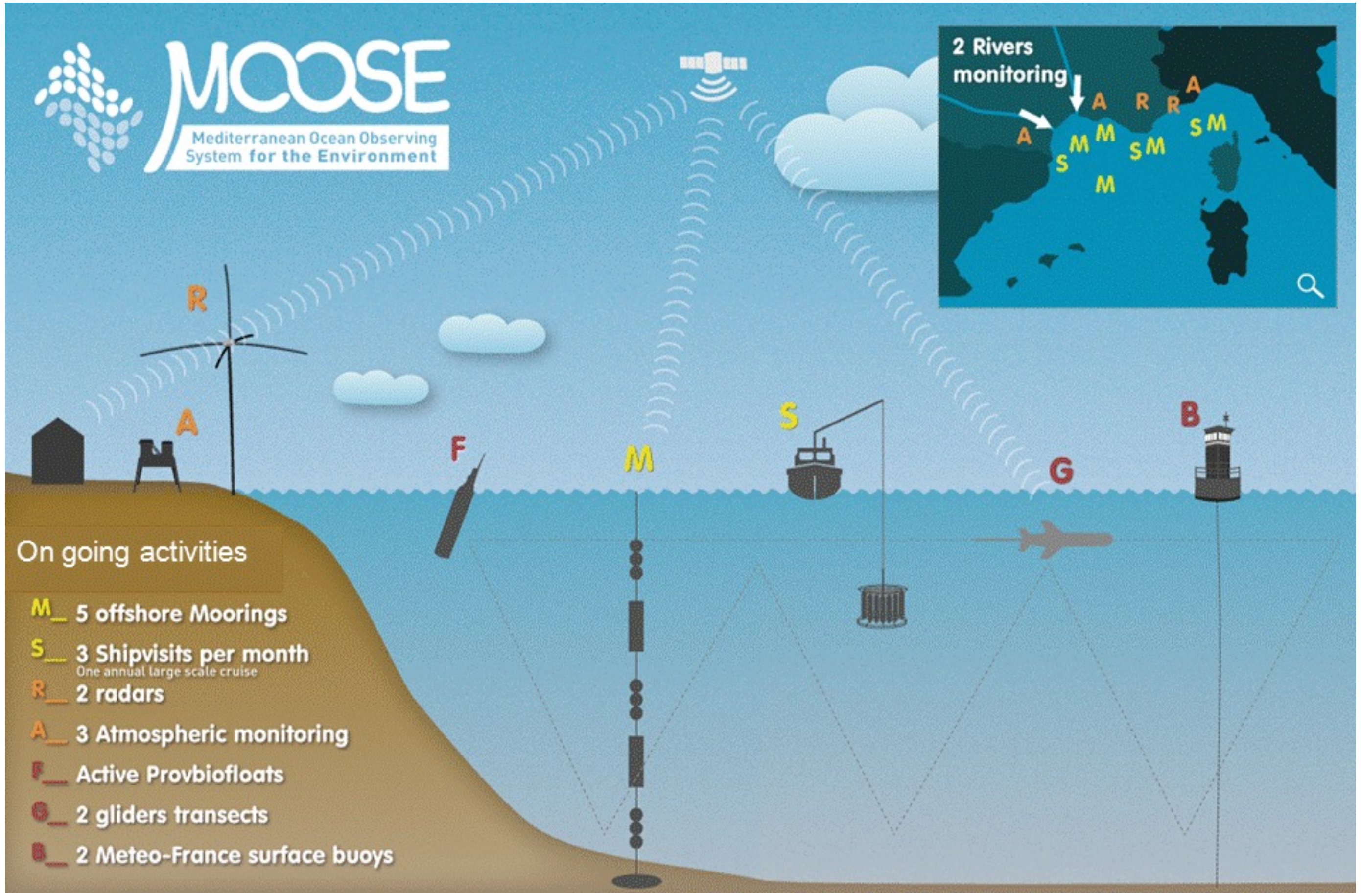






+ implication structures EU: JERICO-RI, EUROGOOS, MONGOOS, JPI Oceans…
+ volet international important: OceanSites, OceanGliders, Argo, GO-SHIP, Ocean time series…

MOOSE: réseau d'observation labellisé CNRS et MESR depuis 2010



Structure « bottom-up »

WP1 : Physique (courants, convection profonde, réchauffement)

WP2 : Biogéochimie (acidification, ventilation, floraison printanière, nutriments)

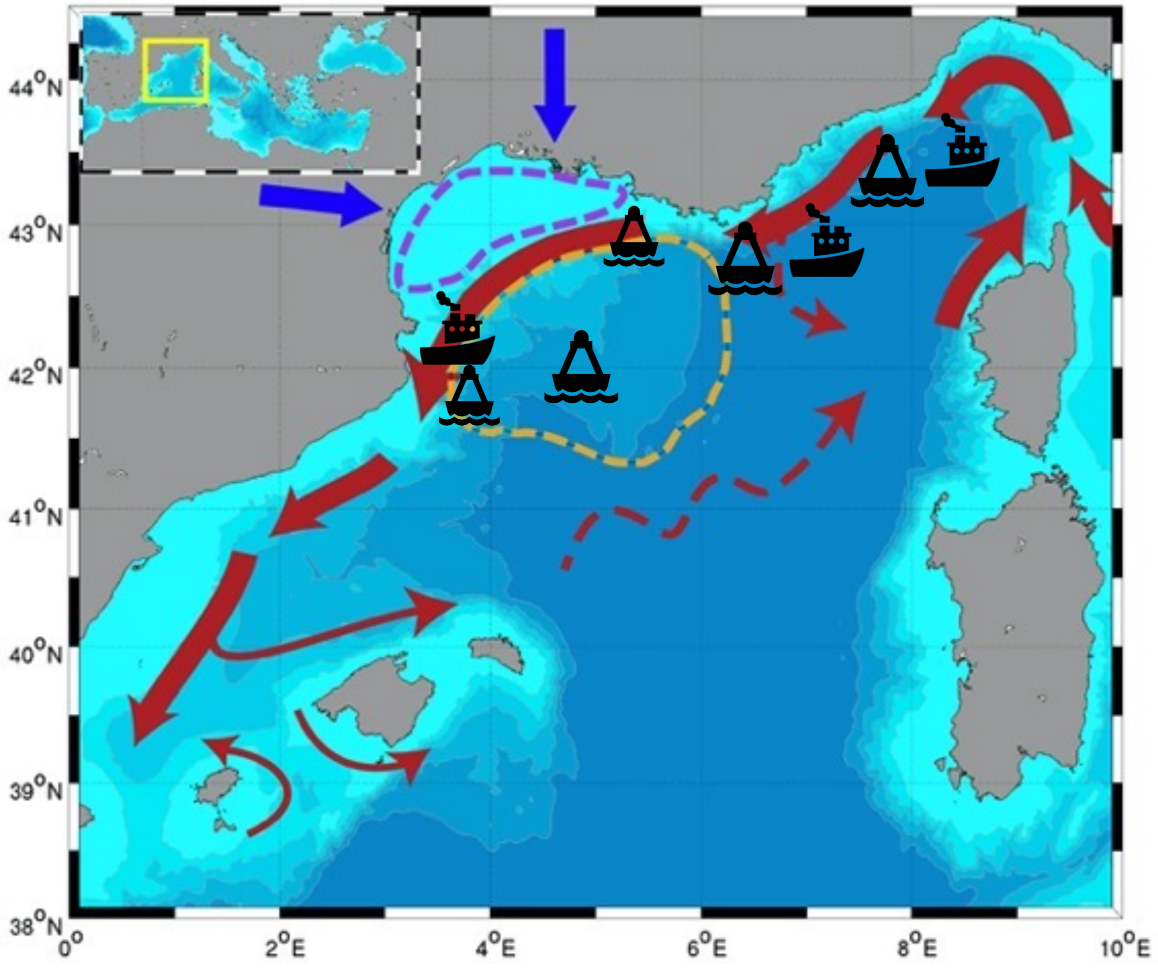
WP3 : Biologie (diversité du phyto/zooplancton)

WP4 : Apports fluviaux (particules, matière organique, métaux)

WP5 : Dépôts atmosphériques (nutriments, métaux)

Labellisation nationale en tant que Service National d'Observation (CNRS-INSU) et intégré dans deux Infrastructures de Recherche ILICO et EMSO (MESR)

MOOSE: approche eulérienne



Mouillage

Navire

Mouillages dans les canyons
LACAZE, PLANIER : 2 mouillages en place depuis 1993 (1000m)

Mouillages profonds
LION, DYFAMED, ALBATROSS/ANTARES: 3 mouillages profonds (2400m)

emso ERIC EUROPEAN RESEARCH INFRASTRUCTURE CONSORTIUM

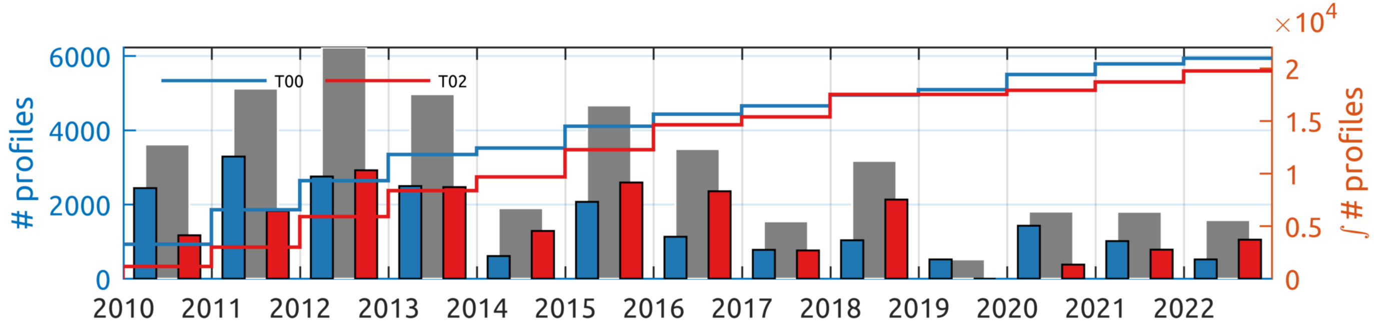
OceanSITES Taking the pulse of the global ocean

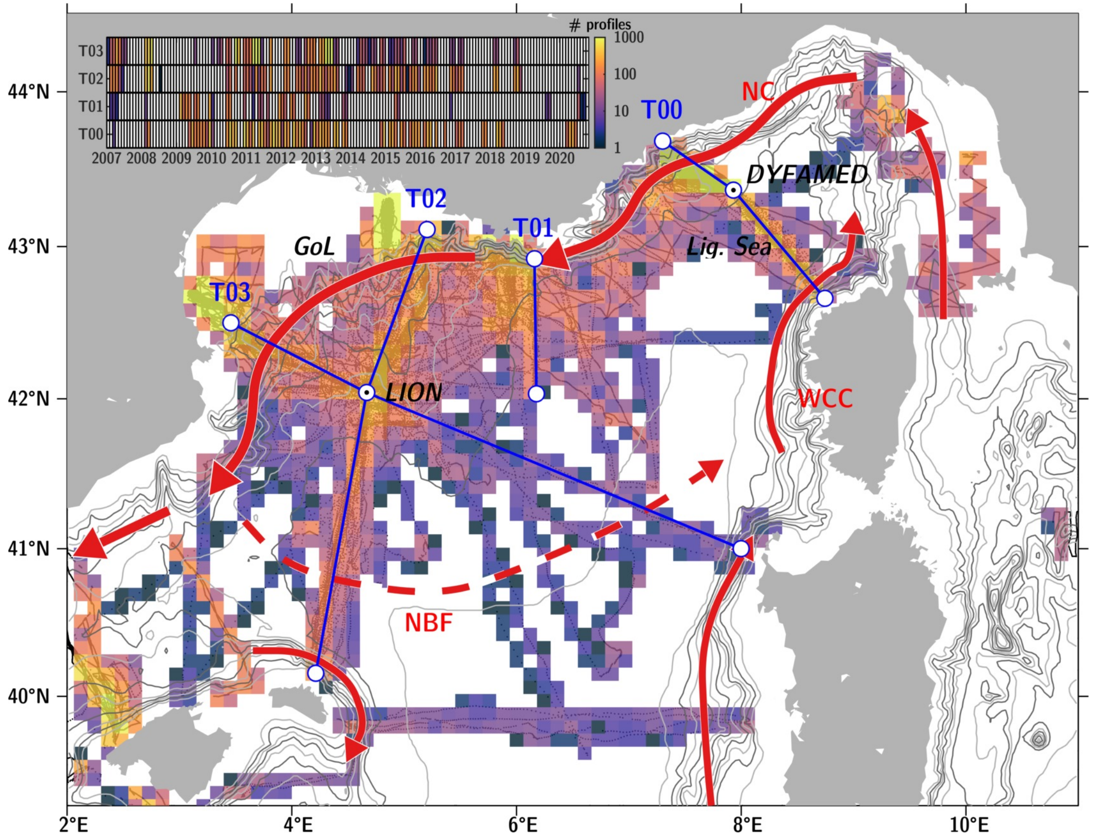
Visites mensuelles par navire de façade sur 3 sites:

MOLA, ANTARES, DYFAMED (CTD, nutriments, carbone-pH, cytométrie, zooplancton)

Longues séries temporelles (plus de 30 ans pour DYFAMED)

MOOSE: approche lagrangienne



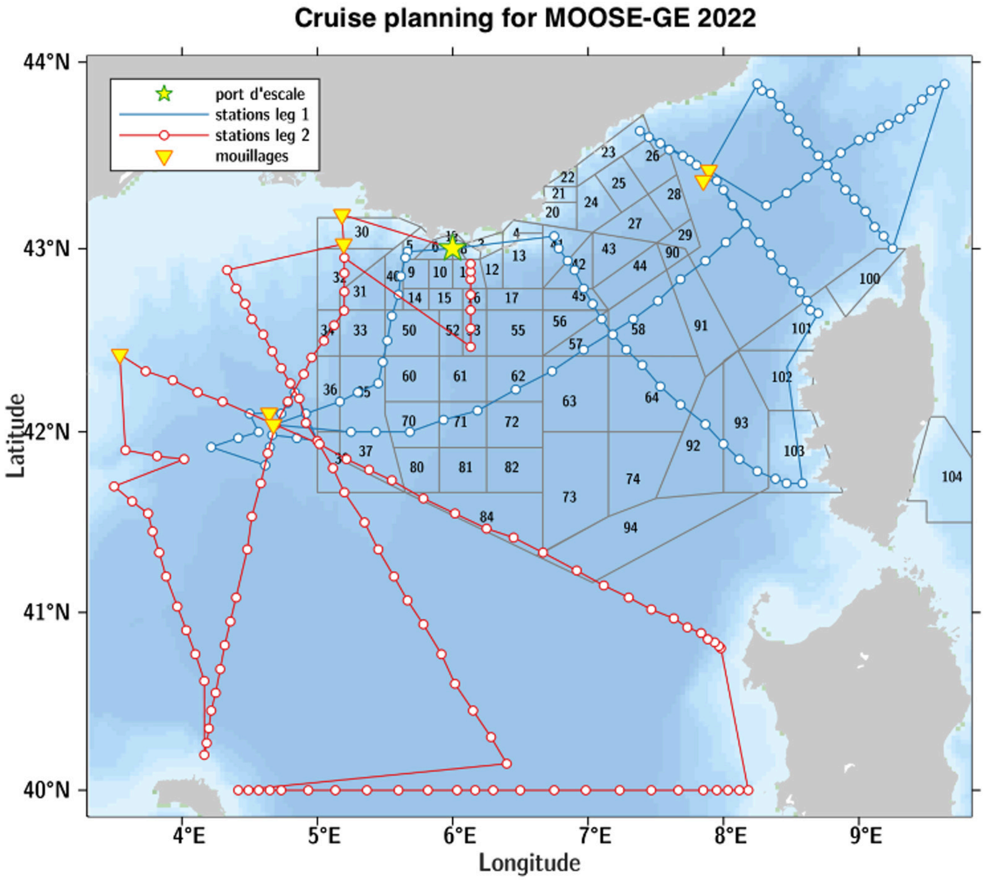


- **Gliders** : deux sections nord-sud (2 x 4.5 mois): T00: Nice-Corse, T02: Marseille-Minorque
- Depuis 2010, **90 déploiements** (T00: 44 depl., T02: 36 depl., 41759 profils)
- 4-6 mois de déploiements pour observer la convection, bloom et les échanges côte-large

- Déploiement/récupération **flotteurs Argo (5-6 tous les 2 ans)**
- Observation: convection, bloom, minimum O2

Contribution à **EURO-Argo, OceanGliders**

MOOSE-GE: la campagne annuelle à grande échelle



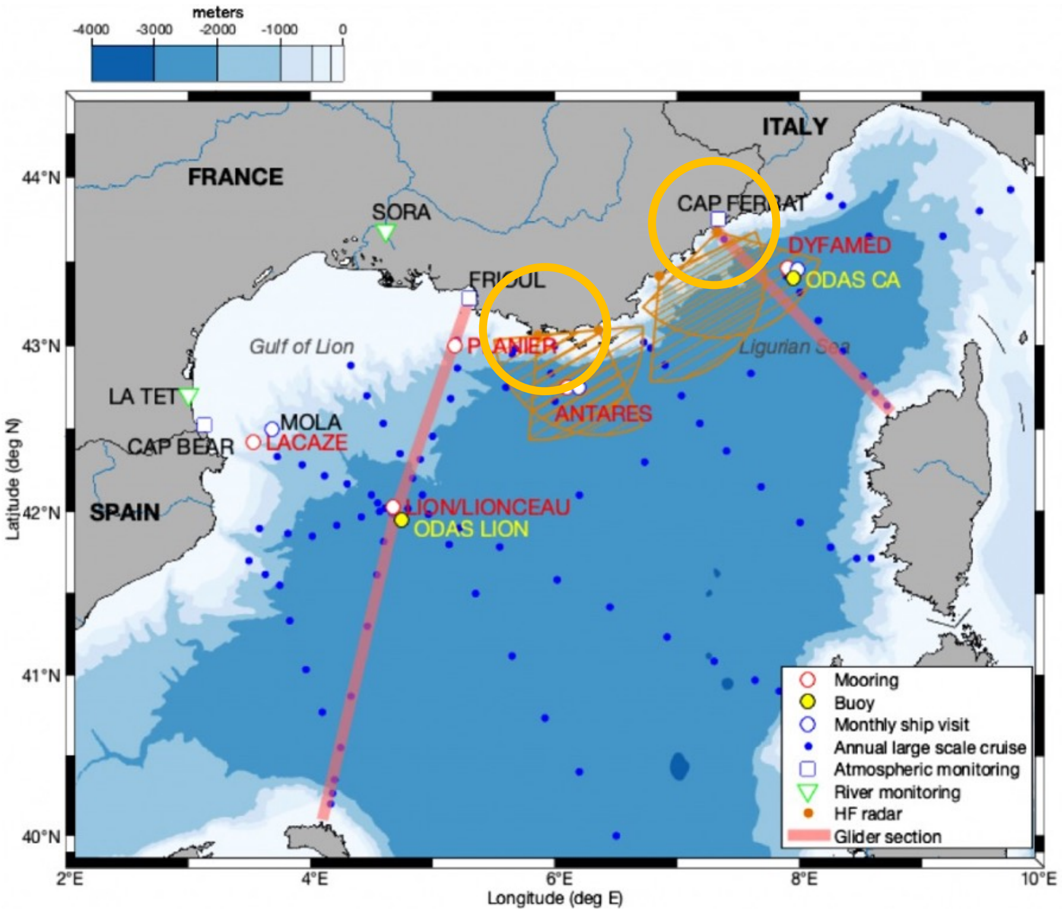
- De la méso-échelle à la petite échelle (stations CTD-LADCP, oxygène, nutriment, carbone, zooplancton)
- Mutualisation de plusieurs activités IR (mouillages, hydrologie/biogéochimie/biologie…)
- Formation des étudiants M2/ENSTA (Institut de l'Océan)
- Descripteurs mammifères/oiseaux (DSCMM)
- Support projets de recherche
- Associé au programme **GO-SHIP** (campagnes TALPRO)

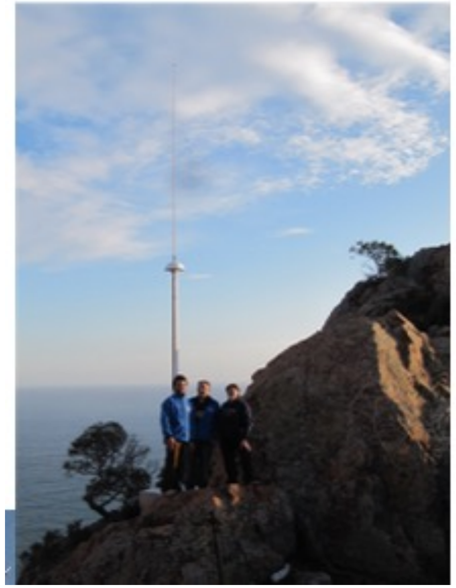
24 jours de temps bateau
ZEE France, Espagne, Italie
130 stations (dont 15 dédiées à la biologie)
24 scientifiques à bord

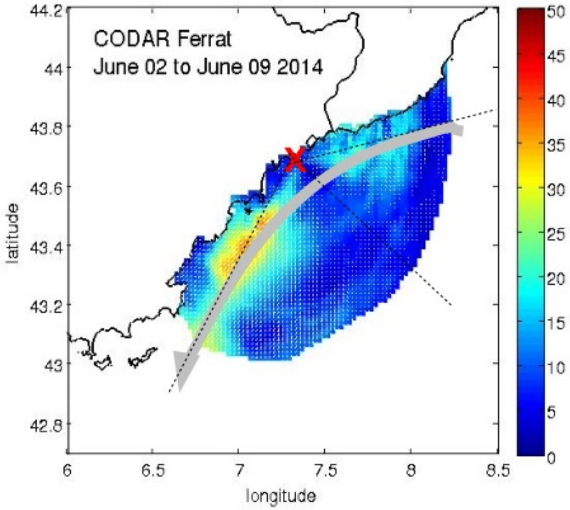
MOOSE: activités des radars HF

2 sites (Toulon, Nice) depuis 2010

Equipements WERA & CODAR







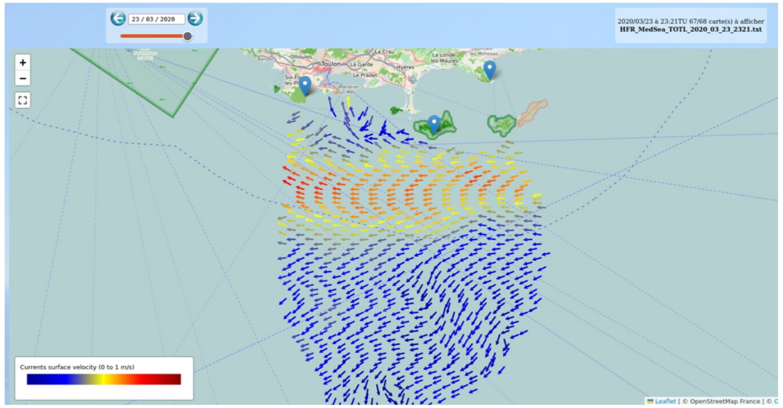


Fig. 1. Exemple de carte de courant horaire le 23 mars 2020 extraite du site hfradar.univ-tln.fr .

http://hfradar.univ-tln.fr

MOOSE: suivi des fleuves et des dépôts atmosphériques

Cap Ferrat (2007)
43°41 N – 7°19 E alt : 130 m
Site de la Marine Nationale

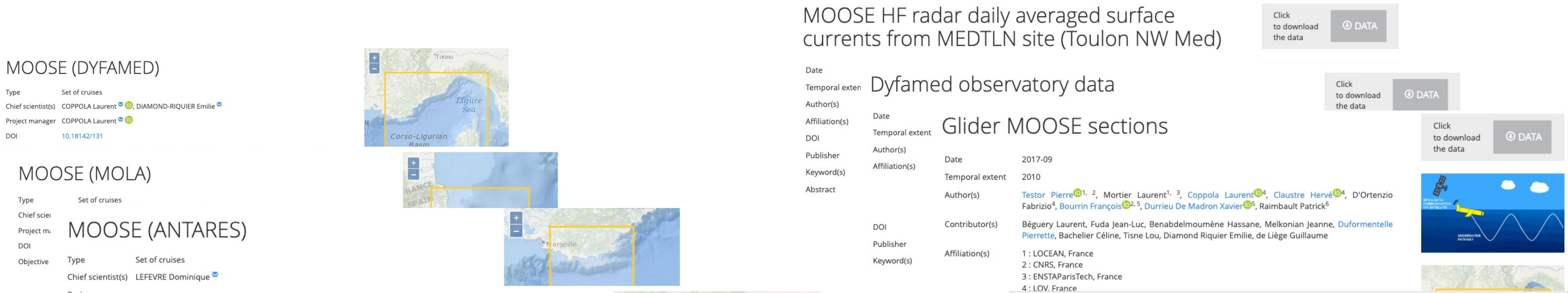
Marseille Frioul (2007)
43°16 N – 5°17 E alt : 40 m

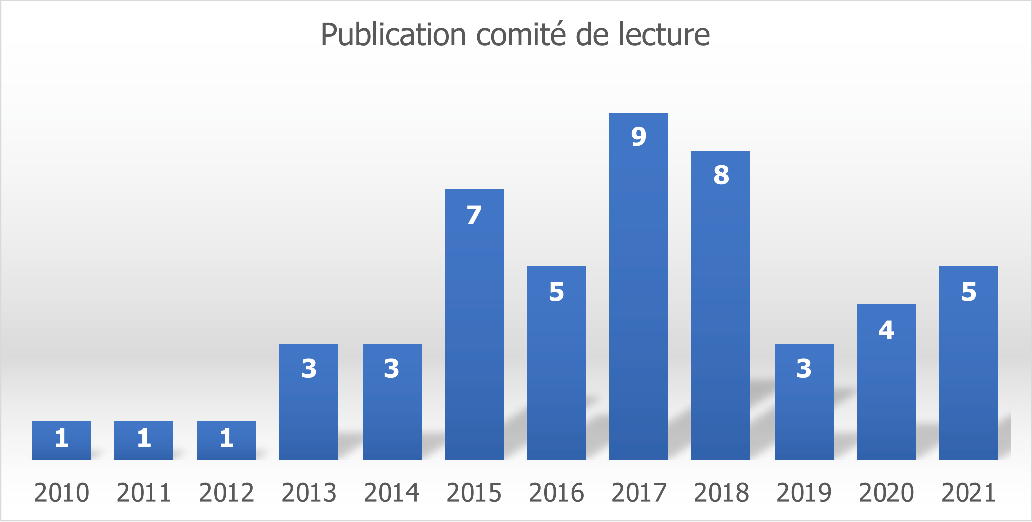
Cap Béar (2011)
42°52 N – 3°13 E alt : 158 m
Site militaire de Fort Béar

Rhône et Têt: apports MES, analyses nutriments et métaux
Systèmes automatisés et prélèvements manuels

Collecte chaque 2 semaines pour les dépôts secs
Collecte des évènements significatifs de pluie
Analyses: nutriments et métaux (particulaire et soluble)

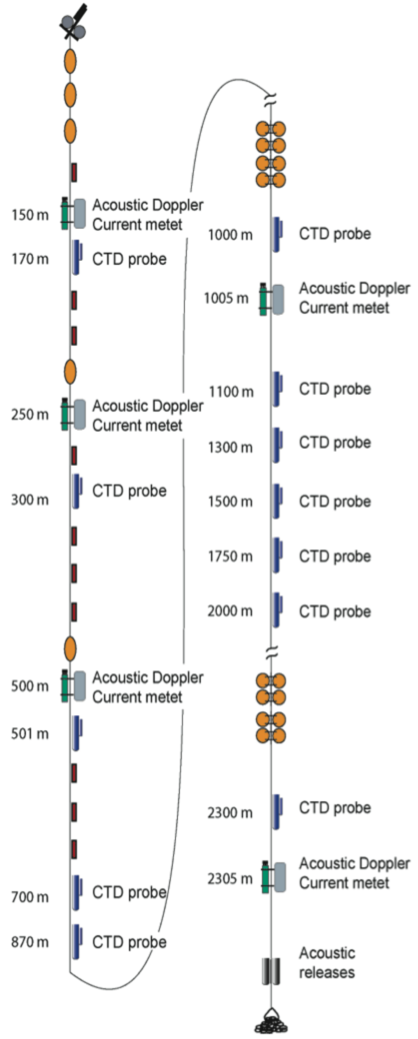
MOOSE: un engagement vers les données FAIR



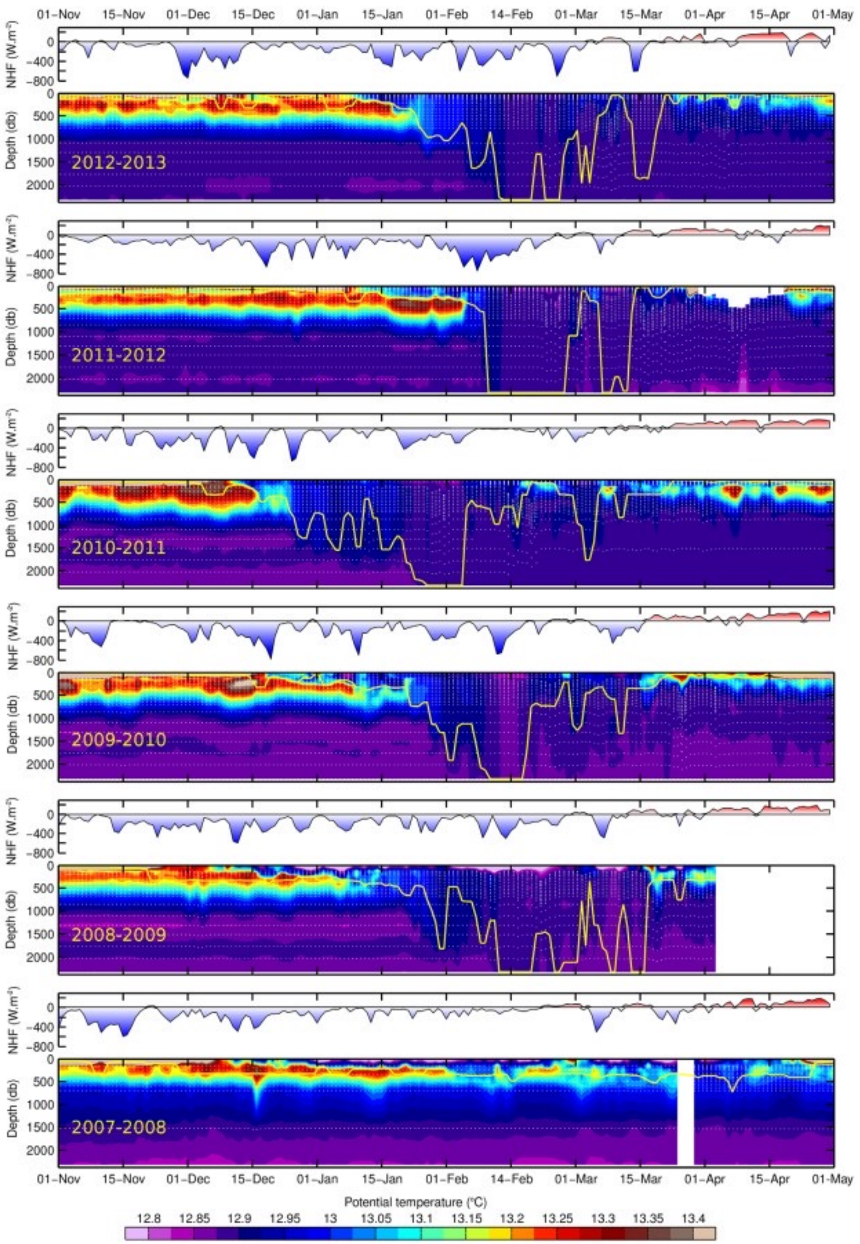


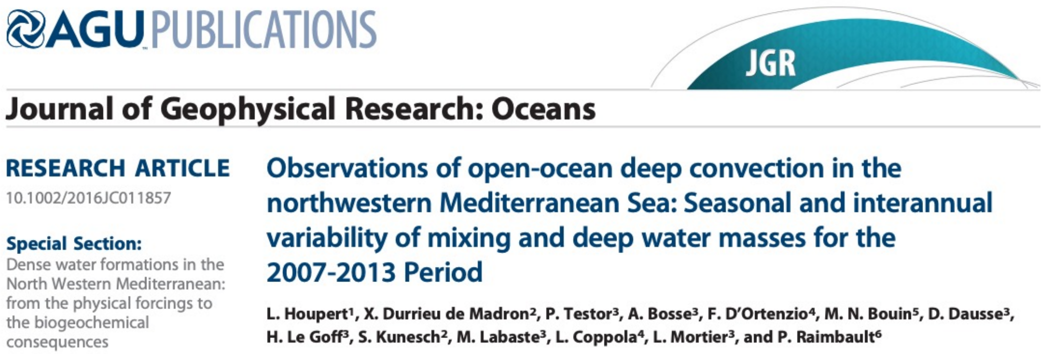
- Données multiples : temps réel et temps différé
- Archivage à CORIOLIS GDAC (planeur, mouillages), SISMER (navire)
- Accès sur SEANOE & SISMER avec DOI et liste des publications (par plateformes et sites)
- Différents formats : ASCII, netCDF
- Diffusion au niveau EU : SeaDataNet, EDMONET
- **Forts liens avec ODATIS (CES O2 et CO2)**
- **2010-2021: 50 papiers ACL**

Exemple d'observations HF



Mouillage LION (100-2400m)





AGU PUBLICATIONS

JGR

Journal of Geophysical Research: Oceans

RESEARCH ARTICLE

10.1002/2016JC011857

Special Section:
Dense water formations in the North Western Mediterranean: from the physical forcings to the biogeochemical consequences

Observations of open-ocean deep convection in the northwestern Mediterranean Sea: Seasonal and interannual variability of mixing and deep water masses for the 2007-2013 Period

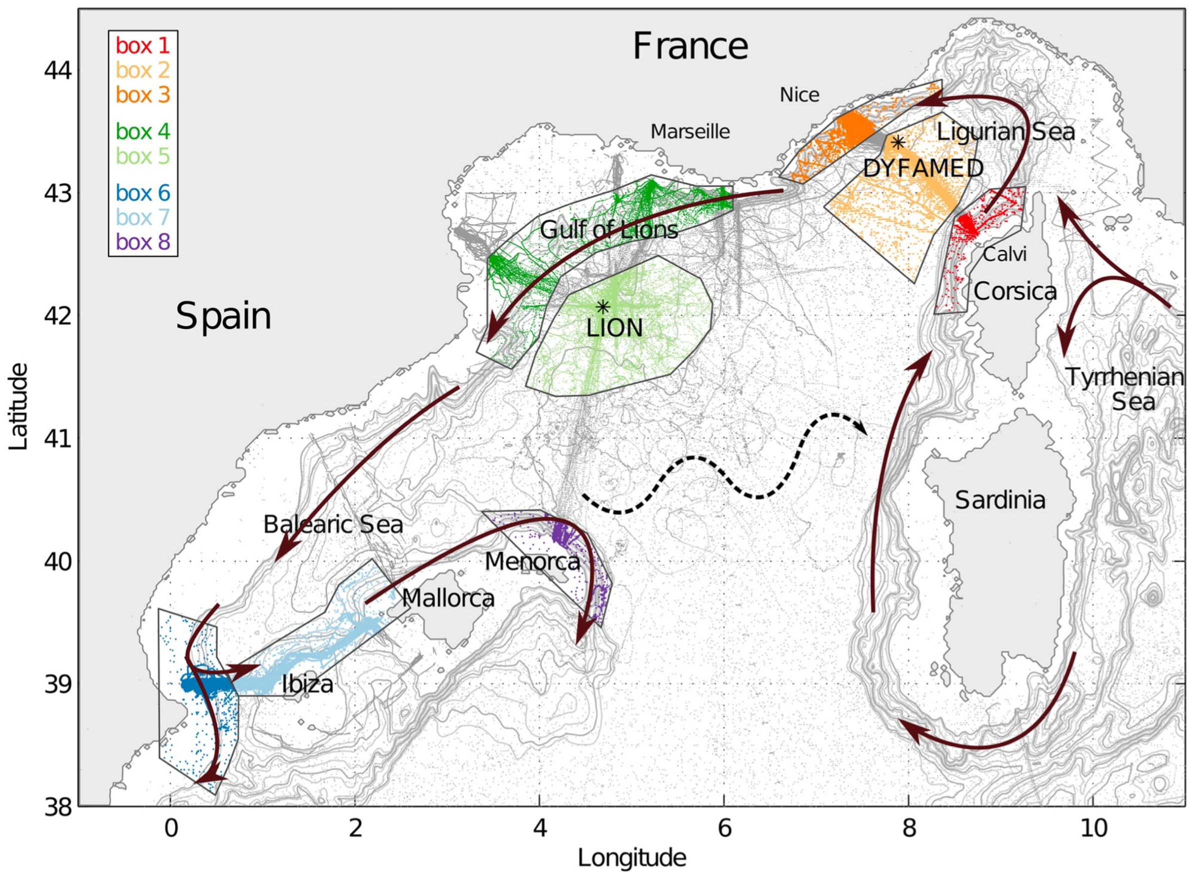
L. Houpert[1], X. Durrieu de Madron[2], P. Testor[3], A. Bosse[3], F. D'Ortenzio[4], M. N. Bouin[5], D. Dausse[3], H. Le Goff[3], S. Kunesch[2], M. Labaste[3], L. Coppola[4], L. Mortier[3], and P. Raimbault[6]

Observations haute fréquence T/S sur toute la colonne d'eau

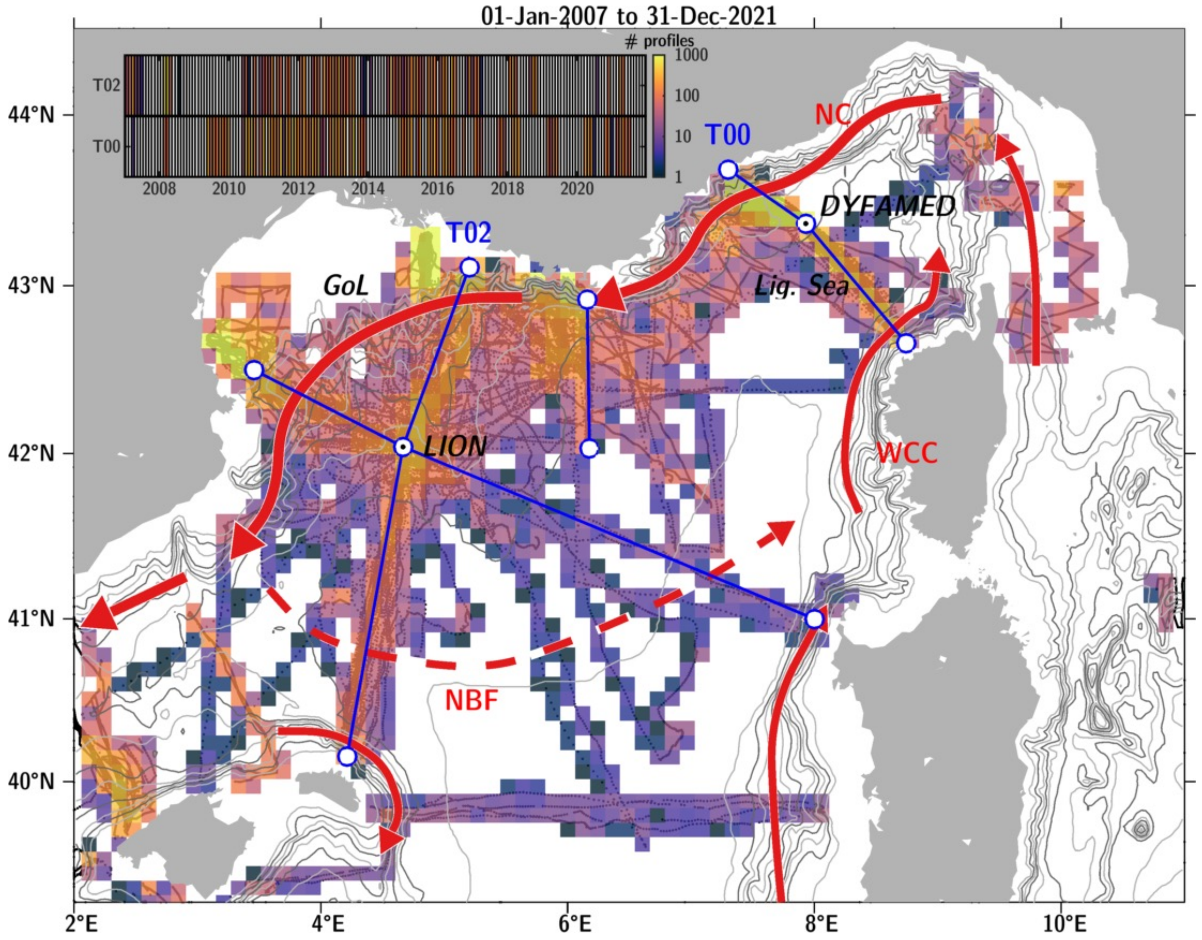
2009-2013 : 5 ans de convection intense jusqu'au fond à 2400m

Observation de convection secondaire après le premier mélange intense

MOOSE: approche intégrée et multidisciplinaire



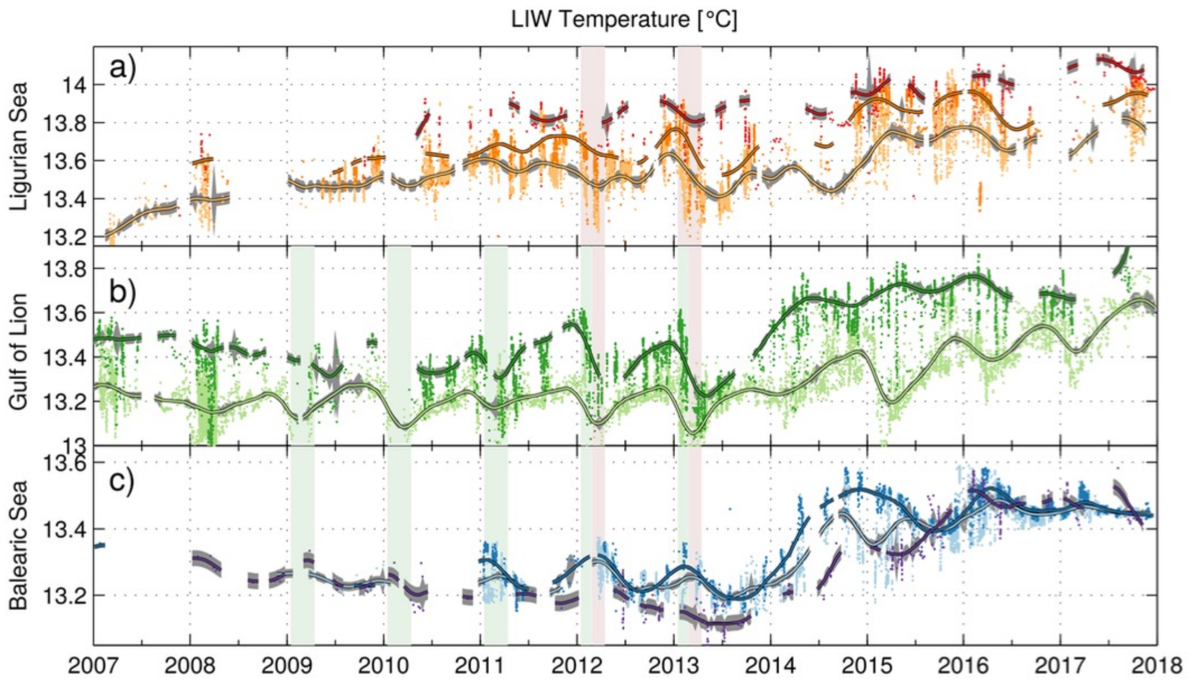
Profils TS de 2007 à 2018 (Margirier et al., 2020)

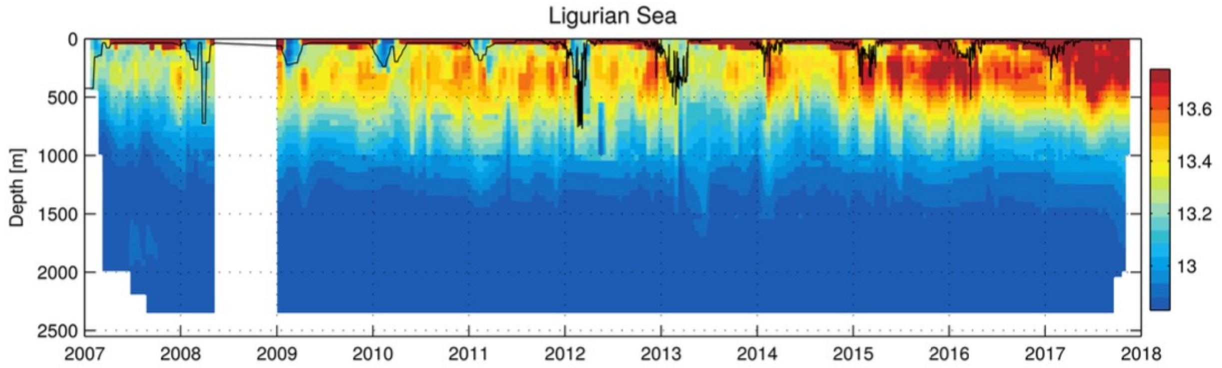


Bosse et al., 2021

De la méso-échelle à la petite échelle
Intégration de processus sur plusieurs échelles de temps

Rapide changement de la convection profonde





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scientific reports

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OPEN

Abrupt warming and salinification of intermediate waters interplays with decline of deep convection in the Northwestern Mediterranean Sea

Félix Margirier[1], Pierre Testor[1], Emma Heslop[2], Katia Mallil[1,3], Anthony Bosse[4], Loïc Houpert[5], Laurent Mortier[6], Marie-Noëlle Bouin[7,8], Laurent Coppola[9], Fabrizio D'Ortenzio[9], Xavier Durrieu de Madron[10], Baptiste Mourre[11], Louis Prieur[9], Patrick Raimbault[4] & Vincent Taillandier[9]

Margirier et al., Scientific Reports, 2020

2007-2017 : LIW en mer de Ligure

dT = +0.06◦C/an dS = +0.012 /an

2014 : changement brutal +0,3◦C /+ 0,08psu se propageant Est → Ouest

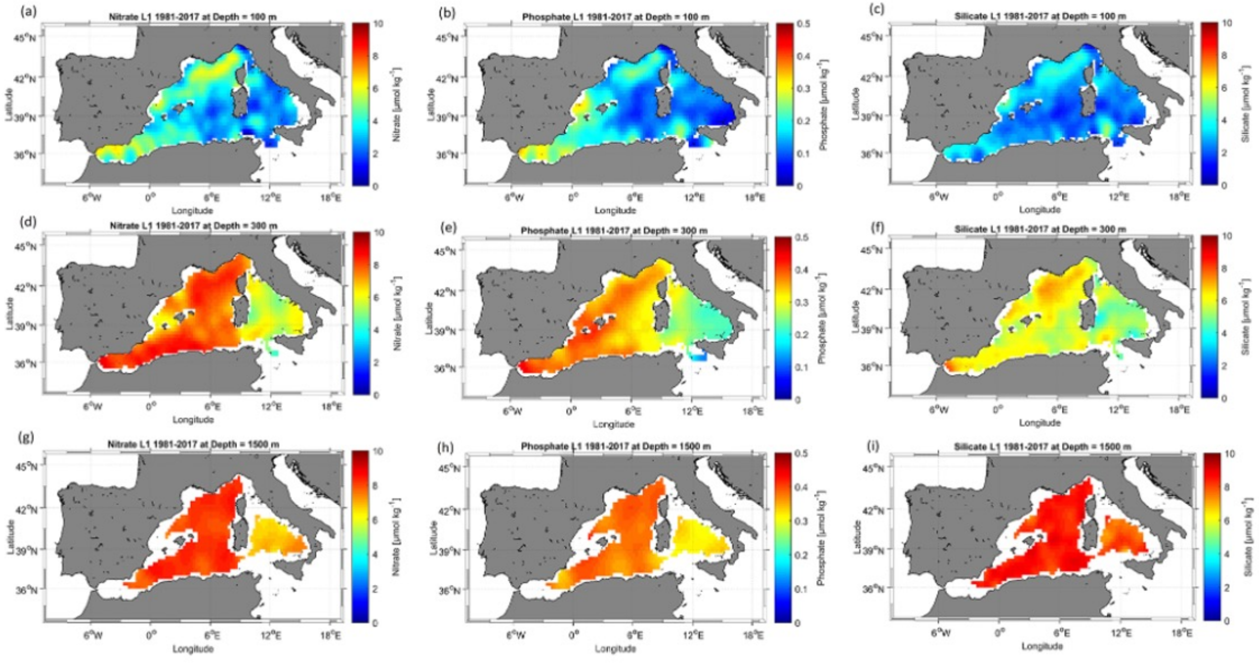
>2014 : ↓ intensité de convection profonde

↑ teneur en chaleur/sel à des profondeurs intermédiaires.

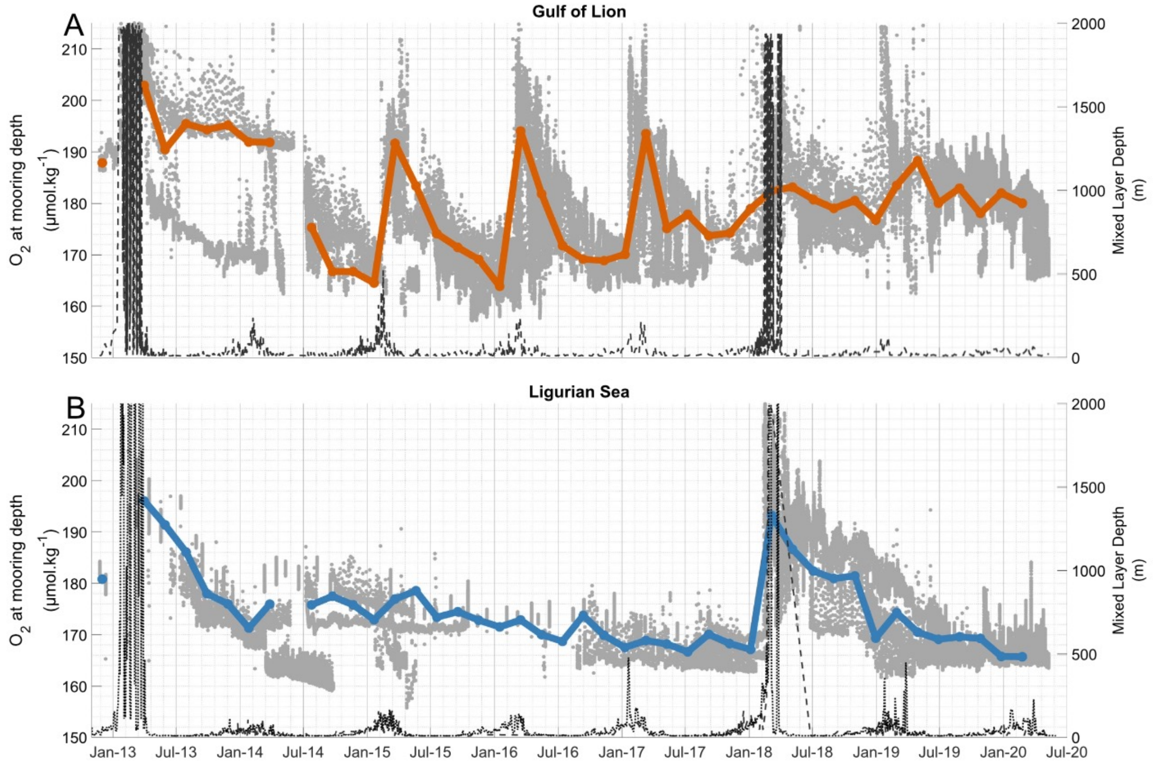
⇒ Futur : nouvel épisode transitoire comme en 2005-2006 ?

Evolution des nutriments & oxygène dissous

Champs de nutriments maillés en moyenne annuelle pour la période 1981-2017 sur une grille horizontale 1/4◦ × 1/4◦



(Belgacem et al. 2021)



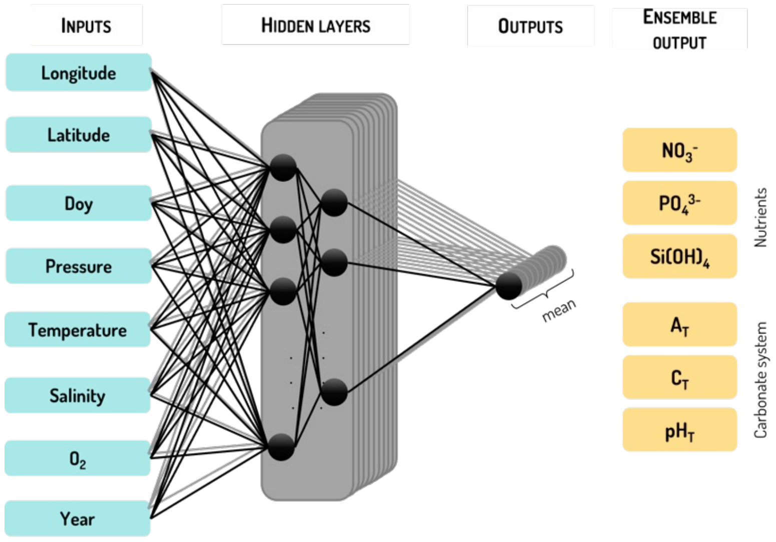
(Fourrier et al. 2022)

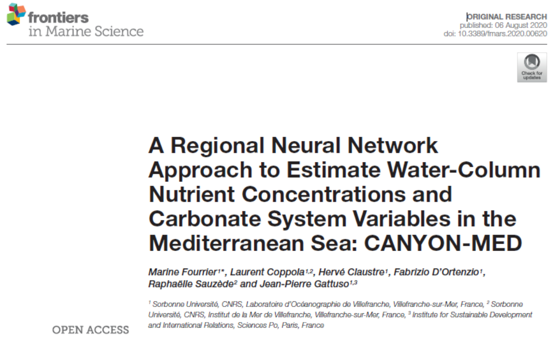
MOOSE-GE représente 25% des données sur la période 1981 à 2017 (MOOSE a débuté en 2010)

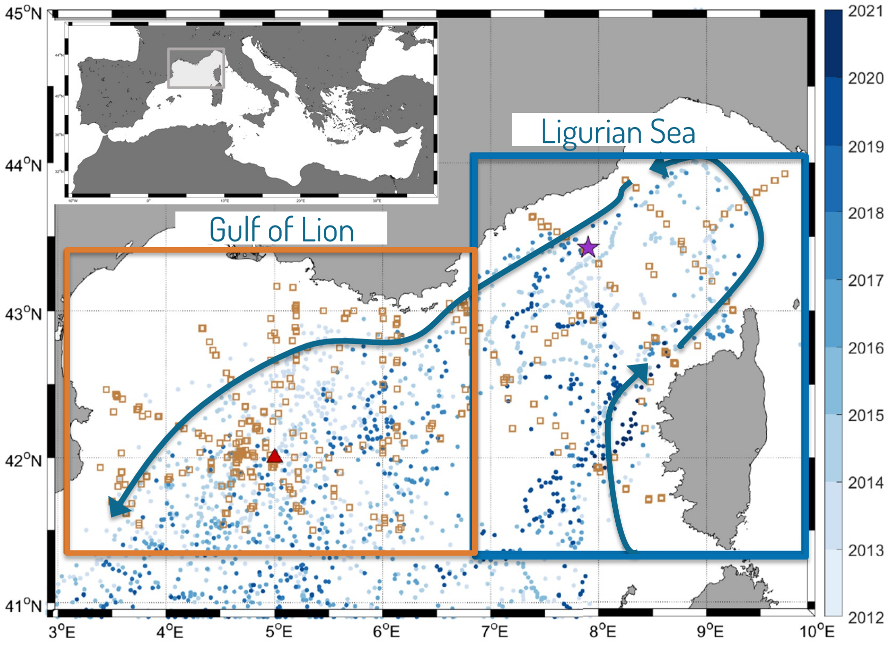
Permet d'améliorer les modèles régionaux (ex. Symphonie, voir présentation C.Ulses)

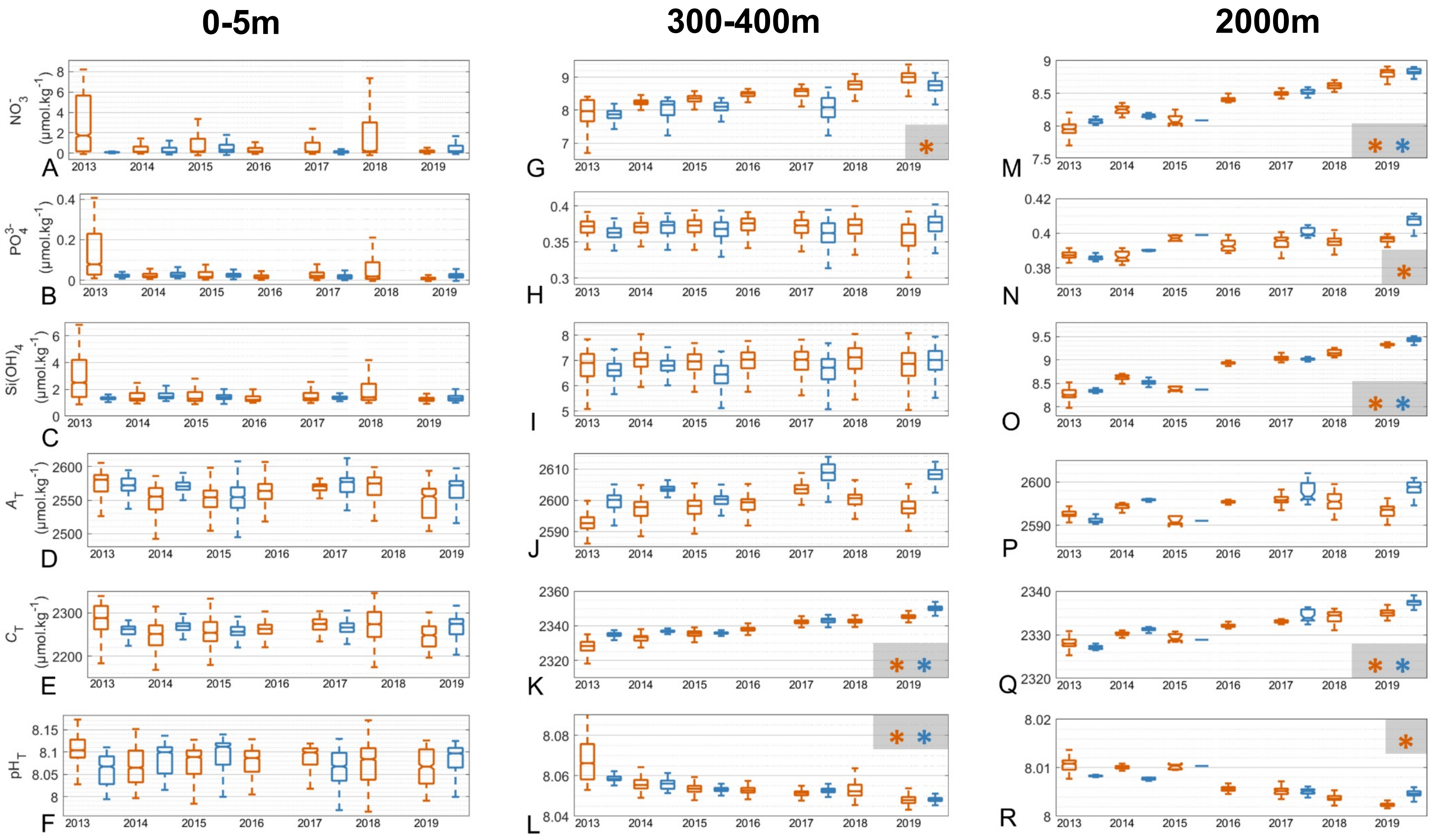
Diminution O2 dans les eaux intermédiaires bien marquée en mer Ligure avec convection hivernale moins intense (-1 µmol/kg/an)

Apports des réseaux de neurones pour la biogéochimie

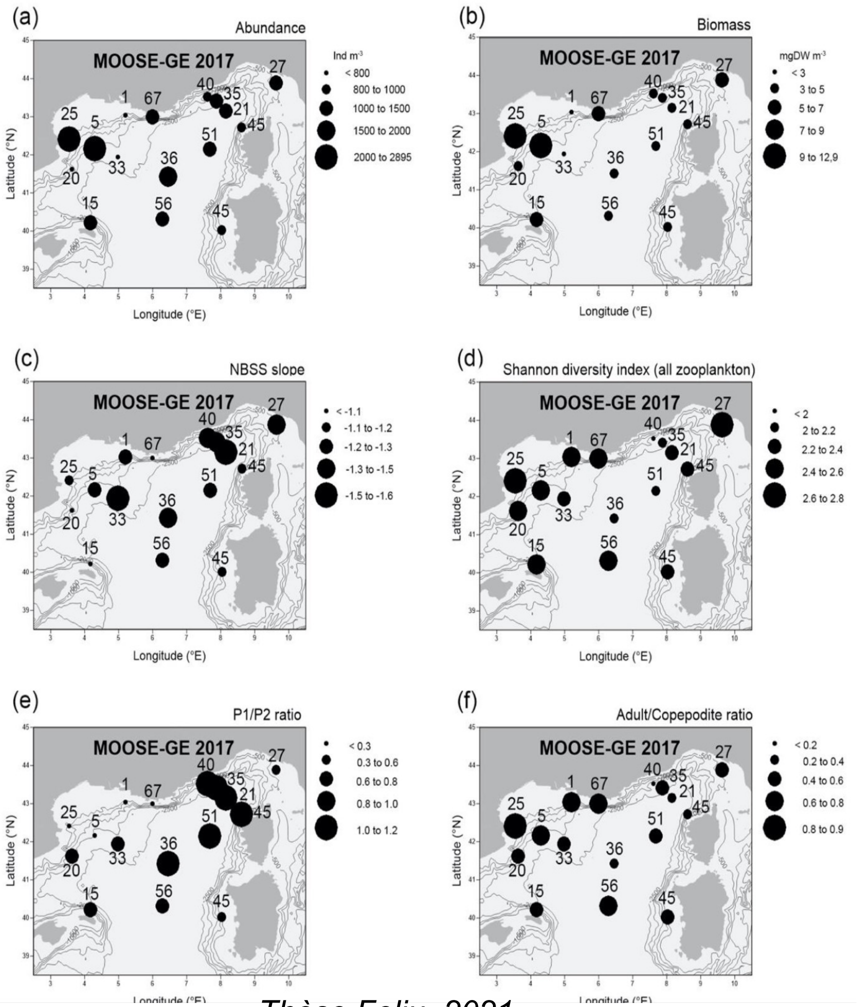








La biodiversité du zooplancton dans le réseau MOOSE

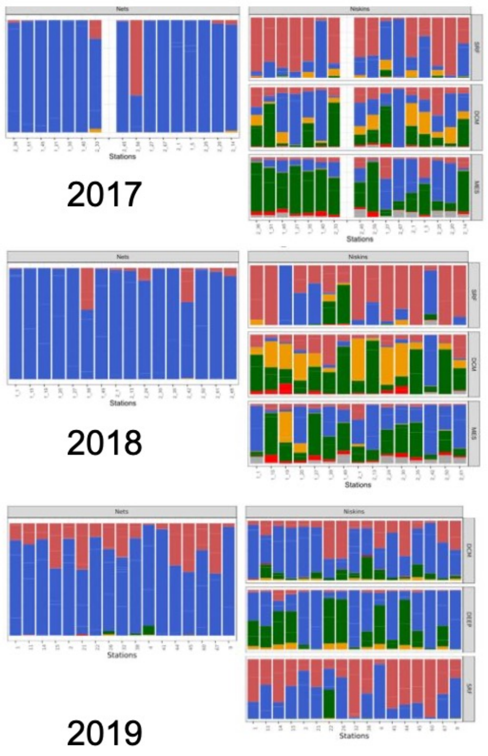


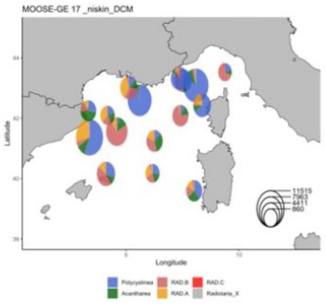
Thèse Feliu ,2021

Suivi des communautés, standardiser les protocoles et la bancarisation, évaluer le rôle fonctionnel et les indicateurs écosystémiques (taxonomie par imagerie, binoculaire)

☑ Bioinformatics tools

☑ First results of protist diversity and biogeography





❑ Play with size fraction

❑ Pull the 3 datasets

❑ Link with other env parameters

❑ Explore specific taxonomic groups

Approche génomique environnementale:
Observer et comprendre **les communautés de plancton dans leur ensemble, l'expression de gènes spécifiques, détecter les nouvelles espèces non indigènes et celles nouvellement introduites** (lien FUTUR-OBS)

frontiers

Rhizaria abundances, diversity and contribution to the silicon cycle in the Mediterranean Sea assessed by combined imaging and metabarcoding approaches

Natalia Llopis Monferrer[1, 2*], Tristan Biard[3], Miguel M. Sandin[4], Fabien Lombard[5, 6], Marc Picheral[5], Amanda Elineau[5], Lionel Guidi[5], Aude Leynaert[1], Paul J. Tréguer[1], Fabrice Not[2]

[1]Univ Brest, CNRS, IRD, Ifremer, LEMAR, F-29280 Plouzane, France, France, [2]Sorbonne University, CNRS, UMR7124, Ecology of Marine Plankton Team, Station Biologique de Roscoff, France, France, [3]LOG, Laboratoire d'Océanologie et de Géosciences, Univ. Littoral Côte d'Opale, Univ. Lille, CNRS, UMR 8187, Wimereux, France, France, [4]Department of Organismal Biology (Systematic Biology), Uppsala University, Norbyv. 18D, 75236 Uppsala, Sweden, Sweden, [5]Sorbonne Université, CNRS, Laboratoire d'Océanographie de Villefranche, Villefranche-sur-Mer, France, France, [6]Institut Universitaire de France, Paris, France, France

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AGU ADVANCING EARTH AND SPACE SCIENCE

Global Biogeochemical Cycles

RESEARCH ARTICLE

10.1029/2019GB006286

Estimating Biogenic Silica Production of Rhizaria in the Global Ocean

Natalia Llopis Monferrer[1,2], Demetrio Boltovskoy[3], Paul Tréguer[1], Miguel Méndez Sandin[2], Fabrice Not[2], and Aude Leynaert[1]

[1]Université de Bretagne Occidentale, CNRS, IRD, Ifremer, LEMAR, Plouzané, France, [2]Ecology of Marine Plankton Team, Station Biologique de Roscoff, Sorbonne University, CNRS, UMR7144, Roscoff, France, [3]Institute of Ecology, Genetics and Evolution of Buenos Aires, University of Buenos Aires-CONICET, Buenos Aires, Argentina

Key Points:

- Polycystines and phaeodarians are highly silicified cells (up to 11.6 μmol bSi mm⁻³)
- Over a large size spectrum, Si content of these siliceous rhizarians is associated with their cell size
- These protists are able to consume dissolved Si and could contribute from 1% to 19% of the biogenic silica production of the global ocean

Supporting Information:

- Supporting Information S1
- Table S1
- Table S2
- Table S3

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Citation: Llopis Monferrer, N., Boltovskoy, D., Tréguer, P., Sandin, M. M., Not, F., & Leynaert, A. (2020). Estimating biogenic silica production of Rhizaria in the global ocean. *Global Biogeochemical Cycles*, 34, e2019GB006286. https://doi.org/10.1029/2019GB006286

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Abstract Siliceous polycystines and phaeodarians are open-ocean planktonic protists found throughout the water column and characterized by complex siliceous skeletons that are formed, at least partly, through the uptake of silicic acid. These protists contribute to the marine organic carbon (C) and biogenic silica (bSi) pools, but little is known about their contribution to the silica (Si) biogeochemical cycle. Here we report the first measurements of the Si uptake rate of polycystine and phaeodarian cells from samples collected in the Mediterranean Sea using the ³²Si-based method. The elementary composition (bSi, particulate organic carbon and nitrogen) of these organisms was also measured. Combining our results with published data on the distribution and abundance of Polycystina and Phaeodaria in the global ocean, we conclude that these organisms could contribute from 0.2 to 2.2 mmol Si m⁻² of the marine standing stock of bSi and from 2 to 58 Tmol Si yr⁻¹ (1% to 19%) of the global oceanic biogenic silica production. The implications for the global marine Si cycle are discussed.

1. Introduction

Rhizarians are eukaryotic, mostly heterotrophic single-celled organisms, ranging in size from tens to hundreds of micrometers, although some are capable of forming gelatinous colonies up to over 1 m in length (Boltovskoy et al., 2017; Suzuki & Not, 2015). These protists are globally distributed, dwelling chiefly in the open ocean, from the surface down to bathypelagic depths. Their distribution and abundance are controlled by environmental factors, such as temperature, salinity, productivity, and nutrient availability (Boltovskoy, 2017a, 2017b; Boltovskoy et al., 2017; Boltovskoy & Correa, 2016). Some rhizarian taxa produce mineral skeletons of strontium sulfate (e.g., subclass Acantharia), calcium carbonate (e.g., order Foraminifera), and opaline silica (e.g., orders Spumellaria and Nassellaria and superorder Phaeodaria).

Silicifying organisms are a critical component of the global oceanic Si cycle. Diatoms, silicoflagellates, sponges, and siliceous rhizarians are all capable of using the silicic acid available in seawater to build elaborated skeletons that are believed to improve essential functions, such as mechanical protection for the cell (Hamm et al., 2003), an armor against predators (Finkel & Kotrc, 2010), an effective pH buffer (Milligan, 2002), or an improvement for the uptake or storage of biosessential elements (Suzuki & Not, 2015). Other studies have suggested that the frustule could confer diatoms an advantage due to its peculiar optical properties (Leynaert et al., 2018). Diatoms are considered the world's largest contributors to the Si cycle, dominating both the standing stock of water column biogenic silica (bSi) and its production rate (Ragueneau et al., 2000, 2006; Tréguer & De La Rocha, 2013). A number of studies ranging from sediment traps to environmental molecular surveys have emphasized the importance of rhizarians in biogeochemical cycles and export of C and bSi to the deep ocean (Biard et al., 2018; Guidi et al., 2016; Gutierrez-Rodriguez et al., 2019; Lampitt et al., 2009). Moreover, recent studies combining genomic and in situ imaging approaches have shown that the contribution of large Rhizaria to the biomass of zooplankton has been largely underestimated (Biard et al., 2016), with their abundance correlating with carbon export fluxes at 150-m depth in oligotrophic oceanic regions (Guidi et al., 2016). Globally, in terms of numbers, some rhizarian taxa can represent approximately 33% of large zooplankton (>600 μm) in the upper water column and up to 5% of the overall oceanic biota carbon reservoir (Biard et al., 2016; Stukel et al., 2018). These new findings suggest an unsuspected role of these organisms in the biological carbon pump, as well as in the Si

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Carbon and nitrogen content to biovolume relationships for marine protist of the Rhizaria lineage (Radiolaria and Phaeodaria)

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Abstract

Rhizaria are large protistan cells that have been shown to be a major component of the planktic community in the oceans and contribute significantly to major biogeochemical cycles such as carbon or silicon. However, unlike for many other protists, limited data is available on rhizarian cellular carbon (C) and nitrogen (N) content and cell volume. Here we present novel C and N mass to volume equations and ratios for nine Rhizaria taxa belonging to Radiolaria (i.e., *Collozoum*, *Sphaerozoum*, *Collosphaeridae*, Acantharia, Nassellaria, and Spumellaria) and Phaeodaria (i.e., *Aulacantha*, *Protocystis*, and *Challengeria*). The C and N content of collodarian cells was significantly correlated to cell volume as expressed by the mass : vol equations ng C cell⁻¹ = −13.51 + 0.1524 × biovolume (μm³) or ng N cell⁻¹ = −4.33 + 0.0249 × biovolume (μm³). Significant C and N content to volume correlations were also identified, and corresponding equations are proposed, for C : vol and N : vol of collodarian colonies (Radiolaria), and C : vol of the genus *Protocystis* (Phaeodaria). Furthermore, average C and N densities (mass per volume) are given for all studied Rhizaria. The densities and mass : vol equations established here could show that, with the exception of *Aulacantha*, biomass of most Rhizaria would have been underestimated using previously published generic protist C : vol ratios. We measured up to 35 times more C content for Acantharia than otherwise estimated, and between 1.4 and 21.5 times more for Collodaria. Our mass : vol data will prove critical for model input and quantitative ecological studies of oceanic ecosystems.

Rhizaria are single-celled eukaryotes (i.e., protists) that are a key component of planktic communities in the ocean (Not et al. 2007; Amacher et al. 2009; Xu et al. 2018). Traditionally, the phylum Radiolaria (Rhizaria) included the orders Acantharia, Nassellaria, Spumellaria, and Phaeodaria (Haeckel 1887). However, Phaeodaria

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Intra-genomic rRNA gene variability of Nassellaria and Spumellaria (Rhizaria, Radiolaria) assessed by Sanger, MinION and Illumina sequencing

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Summary

Ribosomal RNA (rRNA) genes are known to be valuable markers for the barcoding of eukaryotic life and its phylogenetic classification at various taxonomic levels. The large-scale exploration of environmental microbial diversity through metabarcoding approaches has been focused mainly on the V4 and V9 regions of the 18S rRNA gene. The accurate interpretation of such environmental surveys is hampered by technical (e.g. PCR and sequencing errors) and biological biases (e.g. intra-genomic variability). Here we explored the intra-genomic diversity of Nassellaria and Spumellaria specimens (Radiolaria) by comparing Sanger sequencing with Illumina and Oxford Nanopore Technologies (MinION). Our analysis determined that intra-genomic variability of Nassellaria and Spumellaria is generally low, yet some Spumellaria specimens showed two different copies of the V4 with <97% similarity. Of the different sequencing methods, Illumina showed the highest number of contaminations (i.e. environmental DNA, cross-contamination, tag-jumping), revealed by its high sequencing depth; and MinION showed the highest sequencing rate error (~14%). Yet the long reads produced by MinION (~2900 bp) allowed accurate phylogenetic reconstruction studies. These results highlight the requirement for a careful interpretation of Illumina-based metabarcoding studies, in particular regarding low abundant amplicons, and open future perspectives towards full-length rDNA environmental metabarcoding surveys.

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Introduction

Ribosomal RNA (rRNA) genes are known to be valuable taxonomic markers for the barcoding of eukaryotic life and its phylogenetic classification at different levels, mainly due to its intra-genomic tandem repeated structure, the presence of conserved and variable regions and its occurrence in all eukaryotes (Pawlowski *et al.*, 2012; del Campo *et al.*, 2018). The 18S rRNA gene has been widely used in molecular environmental surveys, in particular the short hypervariable regions V4 and V9, thanks to the extensive occurrence in public databases and the availability of generalist primers flanking their sides (Amaral-zettler *et al.*, 2009; Stoeck *et al.*, 2010). The advent of high-throughput sequencing (HTS) techniques has allowed the massive sequencing of molecular environmental diversity supporting its exploration through a metabarcoding approach (de Vargas *et al.*, 2015; Massana *et al.*, 2015; Forster *et al.*, 2016; Pernice *et al.*, 2016). The large number of reads generated by HTS is normally classified into operational taxonomic units (OTUs) based on arbitrary similarity thresholds. OTUs are not only used to identify taxonomic entities but also to describe community structure (Blaxter *et al.*, 2005). The increasing use of the HTS has led to the development of different clustering methods resulting in finer-scale OTUs that focus on single nucleotide differences (Mahé *et al.*, 2015) or on the correction of sequencing errors based on the error rate entropy (so-called amplicon sequence variants or ASVs; Callahan *et al.*, 2016).

HTS produce a vast amount of reads carrying errors that are difficult to distinguish from real biological variation, which is considered as a main factor inflating diversity (Kunin *et al.*, 2010). Intra-genomic rDNA polymorphism and its different copy numbers among taxa can also affect diversity assessments (Gong *et al.*, 2013; Gong and Marchetti, 2019). Other less common causes, yet important, have also been reported as factors inflating

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ORIGINAL PAPER

A morpho-molecular perspective on the diversity and evolution of Spumellaria (Radiolaria)

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Spumellaria (Radiolaria, Rhizaria) are holoplanktonic amoeboid protists, ubiquitous and abundant in the global ocean. Their silicified skeleton preserves very well in sediments, displaying an excellent fossil record extremely valuable for paleo-environmental reconstruction studies, from where most of their extant diversity and ecology have been inferred. This study represents a comprehensive classification of Spumellaria based on the combination of ribosomal taxonomic marker genes (rDNA) and morphological characteristics. In contrast to established taxonomic knowledge, we demonstrate that symmetry of the skeleton takes more importance than internal structures at high classification ranks. Such reconsideration allows gathering different morphologies with concentric structure and spherical or radial symmetry believed to belong to other Radiolaria orders from the fossil record, as for some Entactinaria families. Our calibrated molecular clock dates the origin of Spumellaria in the middle Cambrian (ca. 515 Ma), among the first radiolarian representatives in the fossil record. This study allows a direct connection between living specimens and extinct morphologies from the Cambrian, bringing both a standpoint for future molecular environmental surveys and a better understanding for paleo-environmental reconstruction analysis.

Key words: Spumellaria; rDNA; Molecular diversity; Barcoding; Molecular clock; Molecular evolution.

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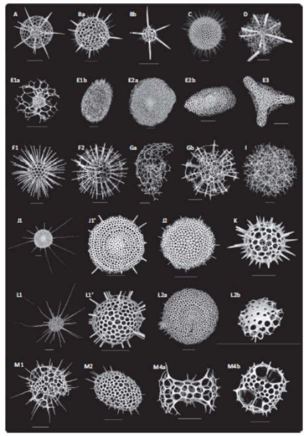
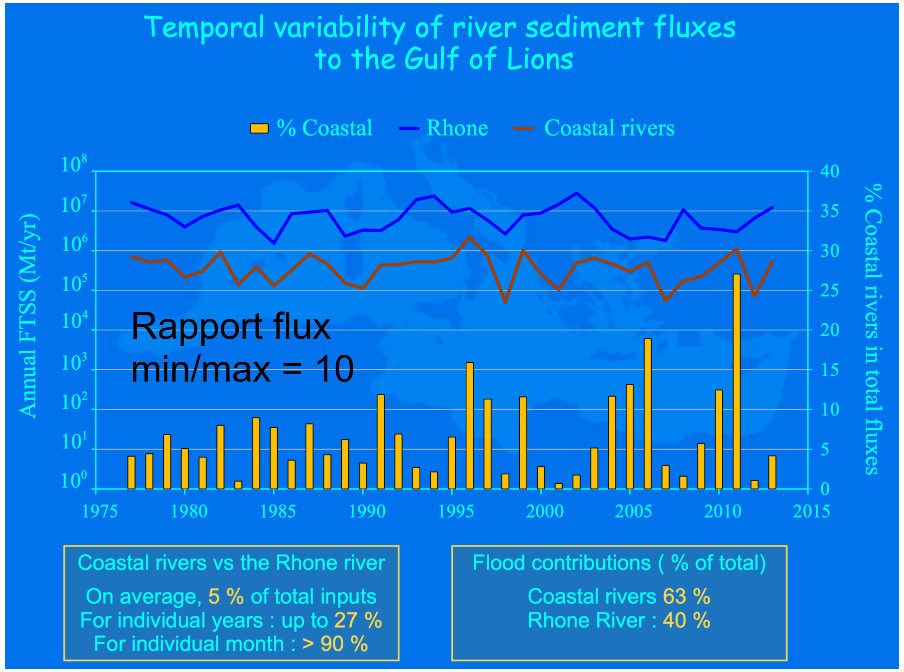
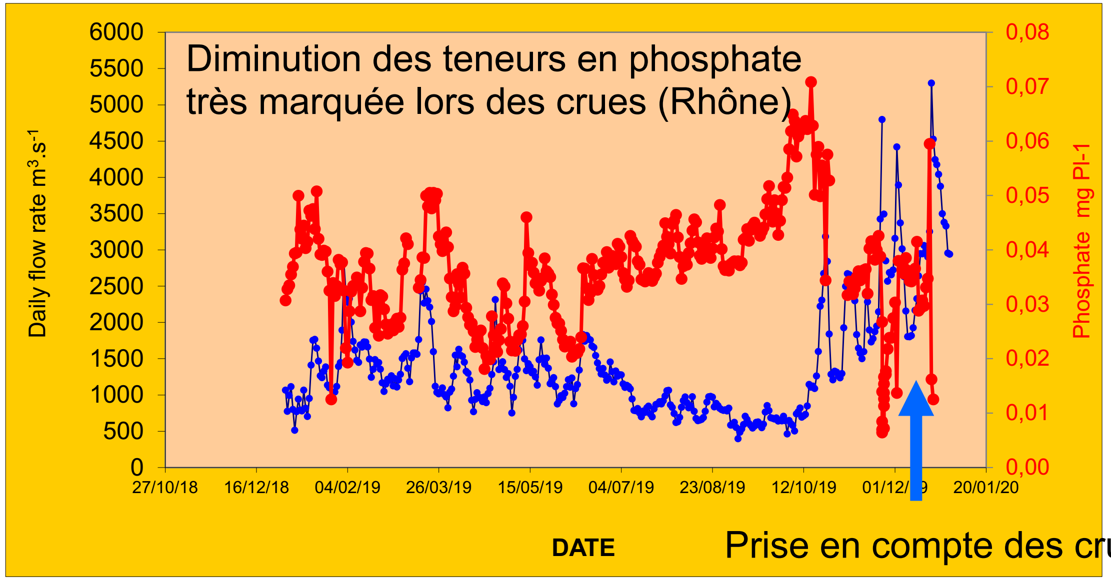
M.M. Sandin et al.



Les apports fluviaux et atmosphériques





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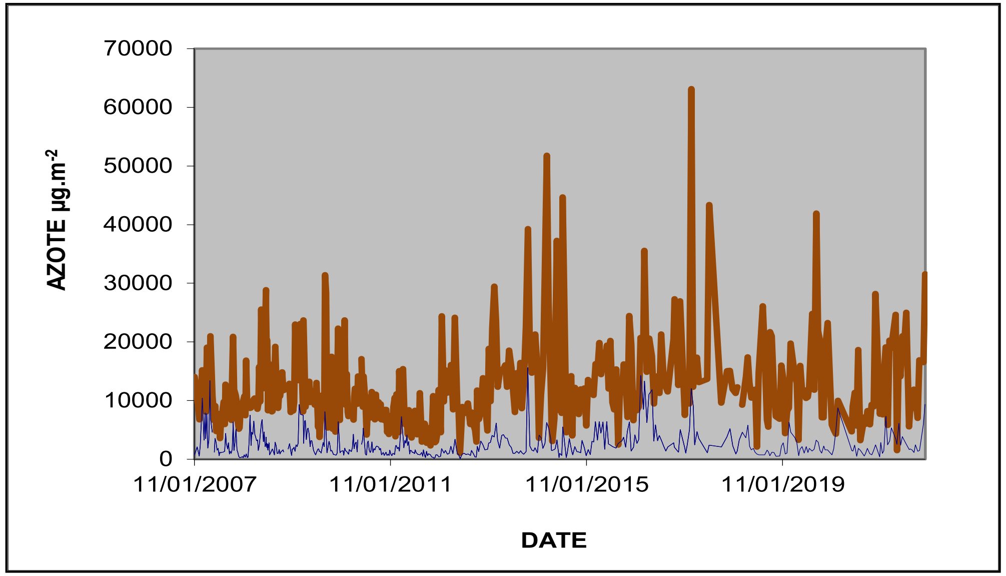

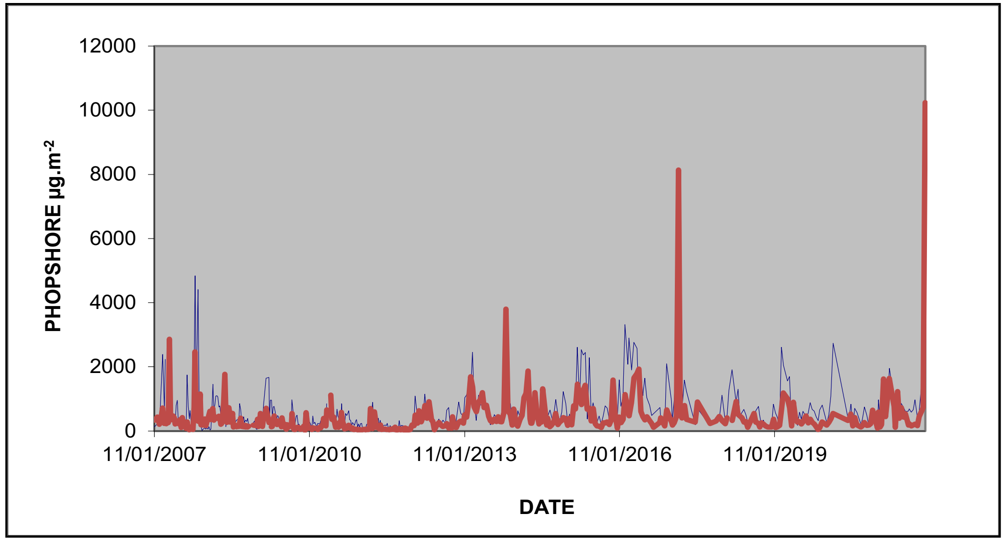

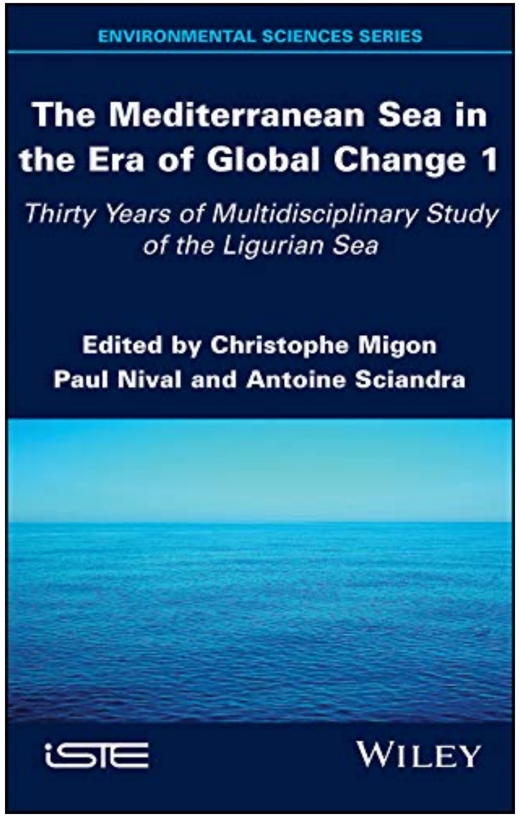

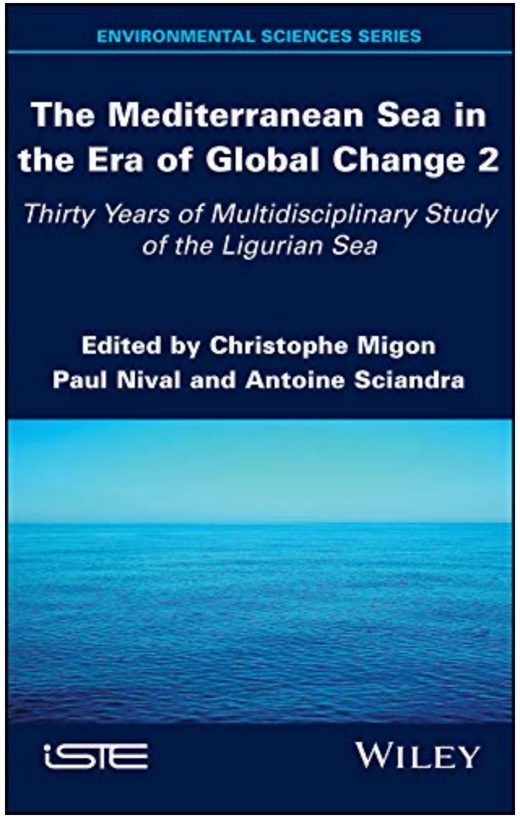

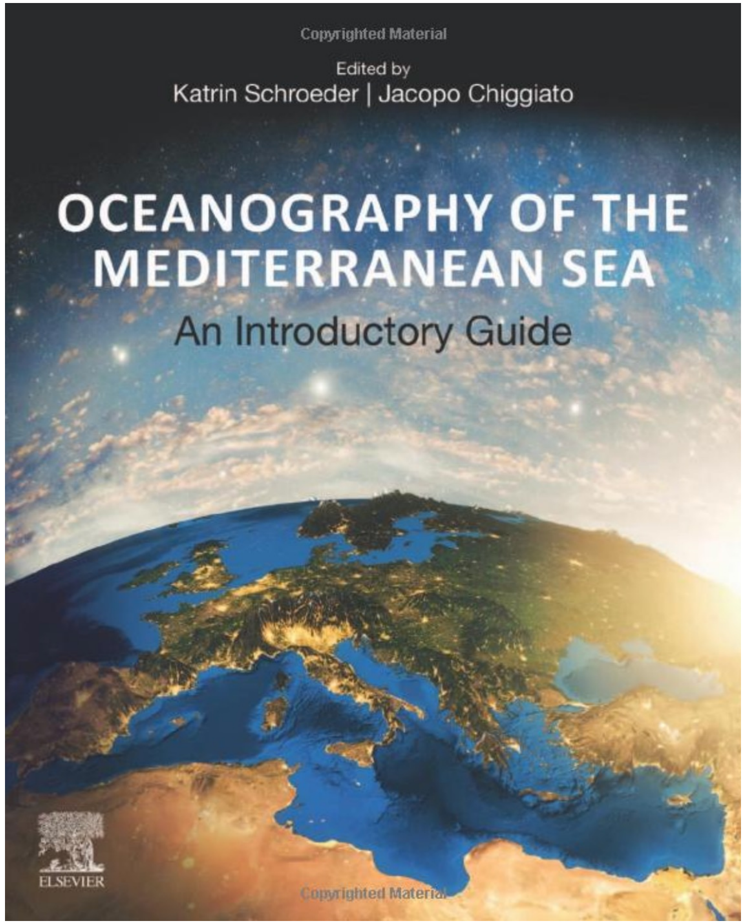

10.3.3.1 MOOSE

The MOOSE observing system[21] is an integrated and multidisciplinary network located in the north-western Mediterranean basin, which has been established in 2010 (Coppola et al., 2019). Its main objective is to monitor the regional long-term evolution of ocean conditions in the context of climate change and anthropogenic pressure in order to detect and identify trends and environmental anomalies of the marine ecosystem. The MOOSE network is supported by French institutes (CNRS-INSU, French Ministry of Higher Education and Research). It involves different partners (Universities, Météo France and IFREMER) and participates in the European and international infrastructures like Euro-Argo, EMSO/OceanSites, OceanGliders and the European Marine Biological Resource Center (EMBRC).

The MOOSE network includes multiscale measurement capabilities to observe trends and anomalies and accurately capture the broad spectrum of hydrodynamic processes (large-scale circulation, mesoscale, and submesoscale eddies) and their impacts on biogeochemical cycles (oxygen ventilation, nutrients supply, phytoplankton production, carbon export and acidification trends). The strategy of MOOSE is to include different platforms operating at different spatial and temporal scales: fixed open sea observatories (moorings, surface buoys and monthly ship visits), two gliders endurance lines, rivers and atmospheric monitoring sites, HF radar stations, annual large-scale RV campaigns and some Argo floats deployment.

Two key areas of the north-western basin have been selected to address the issues identified by MOOSE. The first one is the central and western part of the Ligurian Sea, where the Levantine Intermediate Water formed in the eastern basin flows before spreading into the north-western basin. It constitutes a homogeneous system isolated from direct coastal inputs by rivers, and with a predominant role of the atmospheric forcing. The second one is the Gulf of Lion, which is the most dynamic area of the western basin with intense vertical mixing in winter and episodic events of shelf water cascading (Houpert et al., 2016).

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Monitoring the Environment in the Northwestern Mediterranean Sea

The Mediterranean Ocean Observing System for the Environment (MOOSE) network integrates a range of platforms to detect and identify long-term environmental anomalies.

By L. Coppola, P. Raimbault, L. Mortier, and P. Testor 25 July 2019

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REVIEW
published: 13 September 2019
doi: 10.3389/fmars.2019.00568
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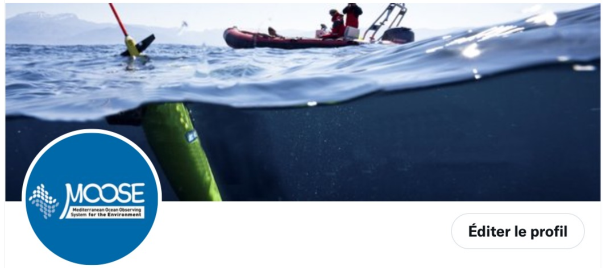
MOOSE
193 Tweets



Éditer le profil

MOOSE
@OS_MOOSE

MOOSE is an observing system based on a multi-sites network of continental-shelf and deep-sea fixed stations and mobile platforms
Traduire la biographie

Nice, France moose-network.fr A rejoint Twitter en avril 2018

139 abonnements **455** abonnés

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