INSITE

INfluence of man-made Structures In The Ecosystem

SIGNAL

Influence of Man-Made Structures in the ecosystem: is there a planktonic signal?

CONTINUOUS PLANKTON RECORDER SURVEY

SAHFOS®

Summary report – September 2017

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Consortium PIs & Institutions

Name	Role	Institution	Year 1	Year 2	Total
Dr Willie Wilson	PI	SAHFOS	5 days	5 days	10 days
David Johns	Co. PI	SAHFOS	20 days	40 days	60 days
Post-doc	RI	SAHFOS	212 days	212 days	424 days
Darren Stevens	Database	SAHFOS	25 days	Zero	25 days
Dr.Pierre Helaouet	Numerical Ecologist	SAHFOS	10 days	10 days	20 days

Summary

In the North Sea the presence of man-made structures (MMS), such as oil platforms, has greatly expanded. This research project, part of the **IN**fluence of man-made **S**tructures **I**n **T**he **E**cosystem (INSITE) Programme will examine whether there has been an impact on the abundance, distribution and seasonal timing of the plankton community in the Greater North Sea.

Aim

The research has focused on trying to identify whether MMS have had an impact on the plankton community at large scales in space (local to regional) and in time (month to decade). At those scales, it is well documented that the main factors driving the plankton are environmental (e.g. temperature of the sea or wind strength and direction) and this is why the core of the study uses statistical methods to distinguish the effects of those factors, called drivers, from any potential interactions of the plankton with the MMS. Plankton respond to their environment in a very complex way, over different space and time scales. The signal produced by these organisms is composed of a quantity of entangled sub-signals, in a similar way as a song is composed by many instruments, each having its own rhythm, tone and intensity. To achieve our goal, it was of prime importance to be able to identify the different signals for each planktonic group, to quantify how much they contribute to the main signal, to finally be able to assess whether or not MMS have an impact on the plankton community.

Plankton

Plankton is the collective name for the myriad of, mostly microscopic, plants (phytoplankton) and animals (zooplankton) that inhabit the sea and drift at the mercy of the currents: *planktos* is the Greek word for ‘drifter’. Planktonic organisms occur in vast numbers, with a glass of seawater typically containing many hundreds of thousands to millions of individual organisms. Plankton lie at the base of the marine food web and as such they initiate and sustain all marine ecosystems - many commercially important organisms such as fish are dependent upon them. The plankton community is made up of both phyto- and zooplankton, some of which spend their entire life cycle in the plankton community (holoplankton). The remainder only spend a short part of their life as plankton, these are known as meroplankton, and examples of these are crabs, lobster, barnacles and starfish. As plankton generally grow and reproduce at a rapid rate, their high population turn-over can be useful when looking at impacts on the community as a whole. For example, plankton are known to respond rapidly to climate change, far more so than on longer lived, high trophic organisms. Plankton are also involved in the cycling of the elements, for example, about half of the oxygen in the atmosphere globally is derived from photosynthesis of the phytoplankton. Thus the plankton are arguably the most important living components of the seas. This study will use data from the Continuous Plankton Recorder Survey, run by the Sir Alister Hardy Foundation for Ocean Science (SAHFOS), based in Plymouth. SAHFOS has an archive of plankton abundance covering the entire North Sea (as well as the wider North Atlantic, Arctic, Antarctic and Pacific Oceans) extending back many decades. We used information from almost 55000 samples collected from the North Sea from 1970 to 2015

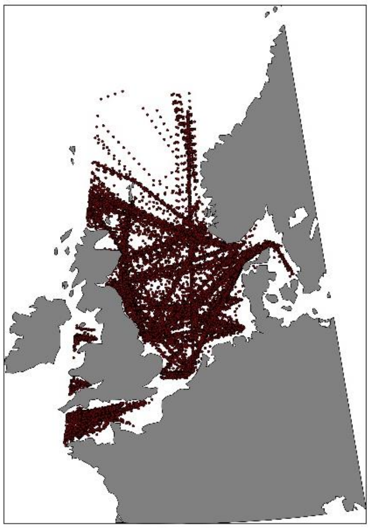


Figure 1. Chart showing the distribution of the 54667 CPR samples collected in the OSPAR Region 2 Greater North Sea between 1970 and 2015.

Physical environment

We focused on two main environmental parameters: Sea Surface Temperature (SST) and wind. SST is essential as it has a well-documented effect on plankton (Reid and Edwards, 2001). Wind can induced water turbulence and is used as an indicator because of its impact on water-column stability which can affect plankton populations (Heath et al., 1999).

Man-Made Structures

Increasing numbers of man-made structures such as artificial reefs, oil platforms, pier pilings, breakwaters, outfall pipelines, and bridge supports are being placed on coastal marine substrate. In this study, we focused only on oil and gas platforms. An important step was to create a usable database gathering, for each platform, key information such as the location, the depth, the weight or the date at which the platform was put at sea. Platforms vastly differ in terms of size, ranging from few to several hundreds of thousands of tons. It was important for us not to treat a platform the size of a car the same way as one the size of a building. We therefore have decided not only to use the presence of MMS, but also the weight of MMS under sea level. Information from more than 1000 platforms was used in this study.

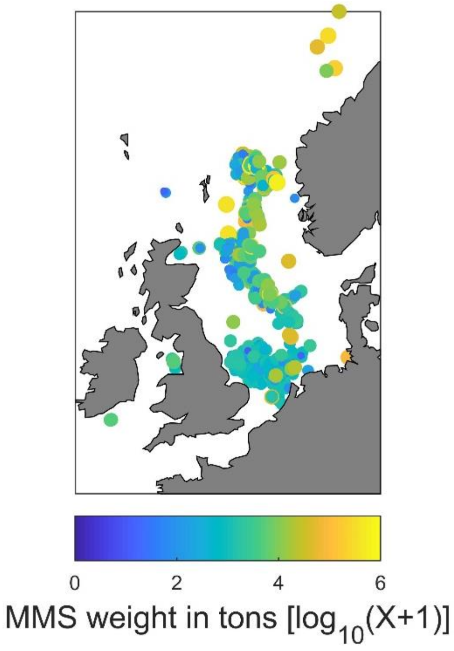


Figure 2: Spatial representation of MMS weight under sea level. Values are logged transform ($\log_{10}$ (X+1)) to enhanced the graphical representation.

Methodology

The first step is to gather data (planktonic, environmental and MMS) from different sources in a single database.

Regularisation

All these datasets are different and we therefore have to homogenise the data to make them comparable. This process, called “gridding”, is designed to transform irregularly spaced data (different locations, different times, etc.) into regularly spaced products. Here we choose to work with ½ a degree grids; a point or pixel represents the average value found in a ½ degree radius. This level of resolution is the best compromise between data precision and data robustness.

Pixel selection

Each node of the obtained grids corresponds to a specific location for a given year. Each month from 1970 to 2015, corresponds to a grid constituted of 1927 points (41 latitudes x 47 longitudes). A vast number of them are on land or do not contain any MMS. This leaves us with 119 points/nodes/pixels that contain MMS. Of the 119 pixels, only 22 of them correspond to complete biological timeseries; a timeseries being a set of values chronologically sorted. In our case, a complete timeseries means a series of values with no gaps for each month of each years from 1970 to 2015 (46 years x 12 months = 552 values). Each of the 22 pixels is given a number to identify it (Figure 2).

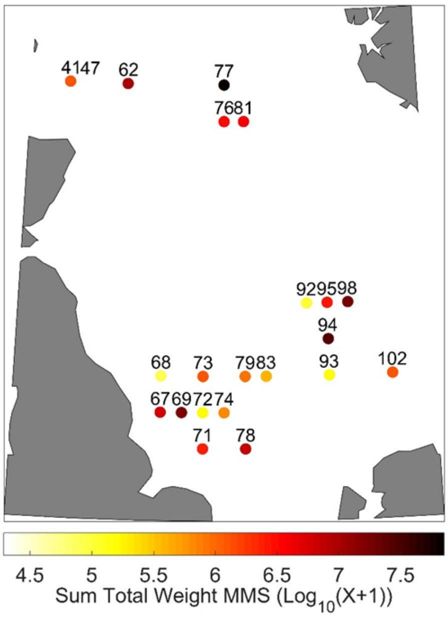


Figure 2: Spatial representation of the 22 selected pixels. The colour corresponds to the sum of total MMS weight under sea level per pixels.

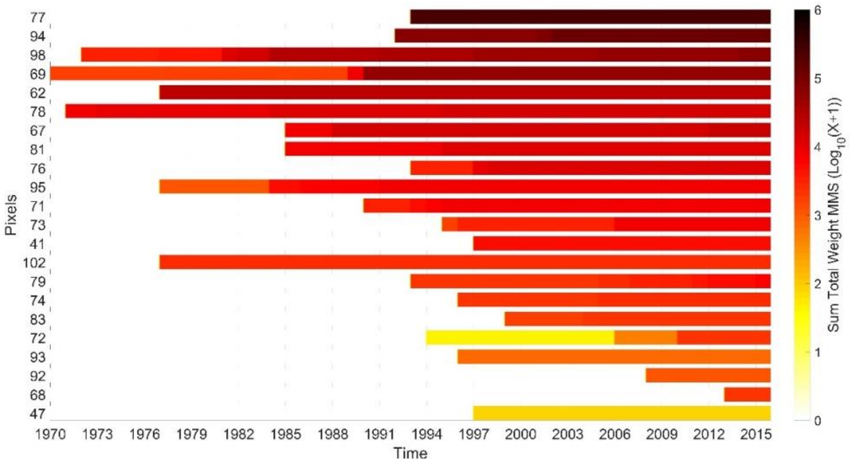


Figure 3: Graphical representation of the total weight of MMS under sea level over the time period for each selected pixel. The weight in expressed in tons and log transformed to enhance the representation.

The 22 selected pixels were sorted by increasing total weight under sea level over the whole time period (Figure 3). Pixel number 77 having the largest quantity of MMS with more than 70 million tons. It is not easy to apprehend such a number but it represents more than 125.000 of the biggest commercial airplane in the world (airbus A380), the quantity of paper used by the US every year or almost 7000 Eiffel tower. At the opposite of the scale, pixels 47 has a total of 19380 tons under sea level. Figure 3 also shows that depending of the location, the “colonisation” over time of each pixels by the MMS was neither achieved at the same paste nor started at the same period.

Timeseries analysis

The next step constitutes the core of the study and its aim is to analyse each signal or biological timeseries. We use an analysis called a distance-based Moran’s eigenvector maps (dbMEM). In a nutshell, this analysis will act like a prism that will decomposed the raw signal (biological timeseries) into different signals along different time scales. As an analogy, we could say that the dbMEM will decompose a song into each instruments (figure 4).

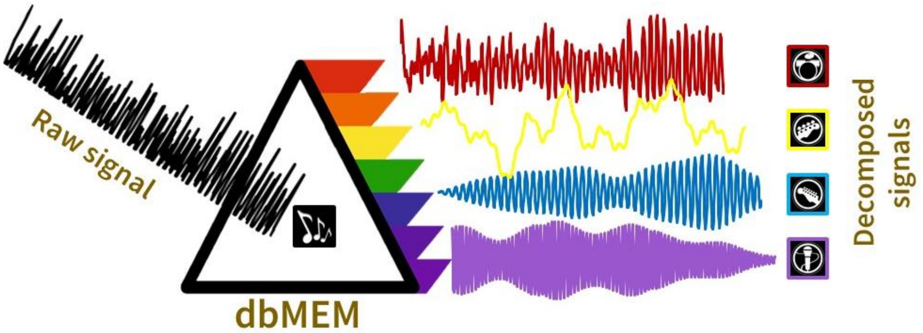


Figure 4: Sketch diagram representing the role of the main analysis of our study: the dbMEM. This analysis will decompose the main signal (or song) into different sub-models (or instruments: drum, bass, guitar and voice).

Each timeseries is decomposed in 4 sub-models, each of them corresponding to a defined temporal window: large scales includes all scales superior to 18 month; seasonal scales, from 18 to 6 months; fine scales from 6 to 1; and very fine scales with everything inferior to the month. Now for each of the 22 selected pixels, we have 10 songs (timeseries) as well as the 4 "instruments" (sub-models) that compose them. The contribution of each instrument (variance of each sub-model) to the main song (total variance contain in each timeseries) is also recorded.

Results

The majority of the selected species or group of species, were decomposed correctly by our core analysis (i.e. dbMEM). It means that their dynamic was structured enough to be picked up by the analysis. Another way of presenting it would be to say that the majority of the songs (species/groups) have melodies (dynamics) clear enough to allow us distinguishing the different instruments (sub-models). Also, it appears that the sub-models corresponding to the highest frequencies (fine scales/guitar and very fine scales/voice) did not contain enough structured variance (melody) to be robustly used. The amount of noise in them was too high for us to work on a clear signal. We therefore decided to focus on the long-term and the seasonal aspect of the plankton dynamic.

The long-term plankton dynamic

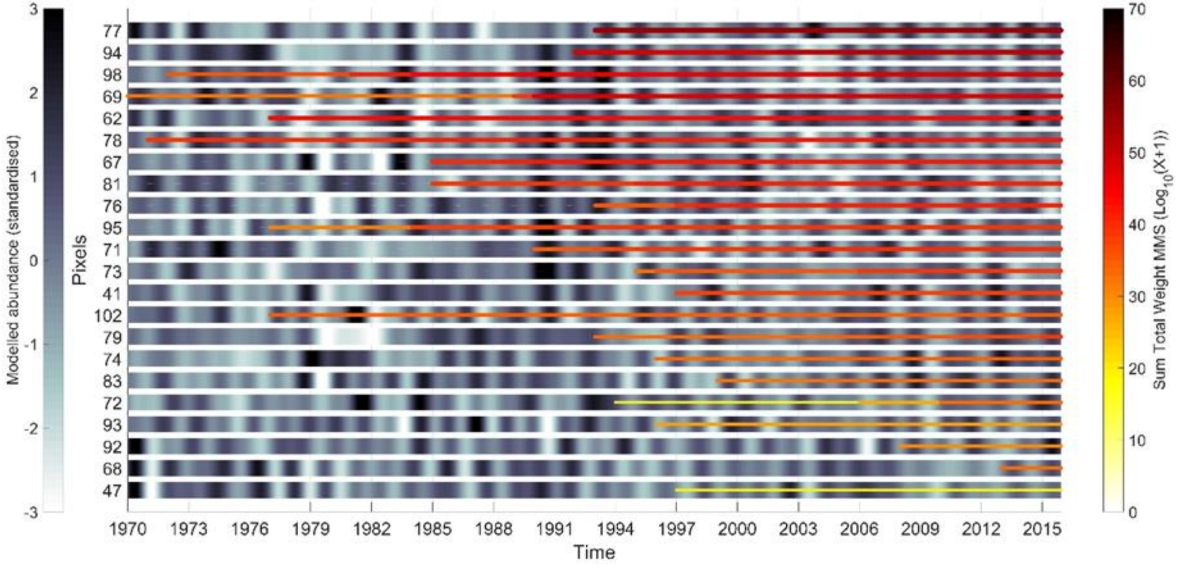


Figure 5: Graphical representation of large scales sub-model (the drum) of meroplankton for each pixels. Superimposed, the sum of total weight under sea level of MMS (in tons). MMS values are log transform ($log_{10}(X+1)$) to enhance the colour scale.

Figure 5 contains a lot of interesting information. First, it shows the long-term dynamic of the meroplankton as a group. We can see periods of relatively low abundances across most of the pixels (characterised by light grey) followed by periods of relatively high abundances (in dark grey or black). For instance, we can see that from the late 1980's to the beginning 1990's, the abundance in meroplankton is significantly increasing. This period, called the "regime shift", is well document and characterised by pronounced changes in large-scale hydro-meteorological forcing (Reid et al., 2016). Increased sea surface temperature and possibly change in wind intensity and direction at the end of the 1970s in the west European basin triggered a change in the location of an oceanic biogeographical boundary along the European continental shelf (Beaugrand, 2004). Second, it showcases the planktonic complexity by showing that the meroplankton reacts quite differently depending of the location. Not all pixels exhibit the same intensity in their dynamics. Finally, it shows that the long-term dynamic of meroplankton is independent from the quantity of MMS (total weight under sea level per pixel).

The use of sea surface temperature (SST) instead of the MMS allows us to demonstrate how much the plankton is driven by this parameter (Figure 6). The match between the two variables become quite apparent (Figure 6) and can be quantified using statistical correlations (Table 1). On the 15 pixels with significant correlations between the long-term meroplankton and the long-term SST dynamics, 10 shows a positive relationships, 3 negative and 2 weak relationships (< 0.1 or > -0.1). Low abundances of meroplankton matches to low values of temperatures (e.g. 1970's and 1980's; blue rectangle). The North Sea "regime shift" (i.e. late 1970's) also coincides with a sharp rise in SST (red rectangle).

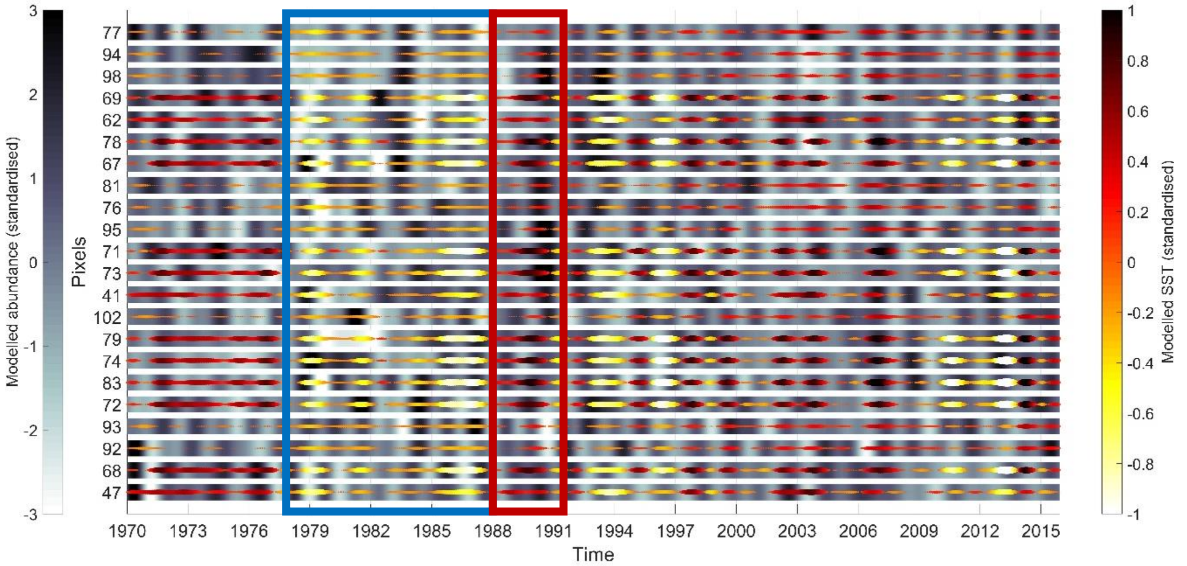


Figure 6: Graphical representation of large scales sub-models of meroplankton for each pixels. Superimposed, the standardised values of long-term SST. When values are positive, SST were above the average and vice versa.

Table 1: Summary table of correlation coefficients (Pearson's *r*) between long-term sub-models of both meroplankton and SST. Cells are in dark grey when the associated probability value (p-value) was >0.01, those should not be considered as the p-value is too high.

Pixels	77	94	98	69	62	78	67	81	76	95	71	73	41	102	79	74	83	72	93	92	68	47
r	▲ 0.11	▲ 0.13	▲ 0.28	▼ -0.11	▬ -0.03	▬ 0.02	▬ -0.04	▬ 0.07	▲ 0.10	▲ 0.18	▼ -0.31	▬ 0.09	▲ 0.17	▲ 0.31	▬ -0.06	▬ -0.09	▬ -0.05	▬ 0.03	▲ 0.41	▲ 0.18	▼ -0.14	▲ 0.22

Similar results are found for the other species/groups. None of the selected species/groups shows a link with the presence or the quantity of MMS. However, a large quantity of species/groups have a significant link with the environment variables (especially with SST). For instance, *Calanus finmarchicus* exhibit an overall negative relationship with SST while its congeneric species *Calanus helgolandicus* has a positive one.

The seasonal plankton dynamic

Seasonality is predominant in most of the plankton, especially in a temperate area such as the North Sea. Most of the species/groups exhibit a clear seasonal pattern, itself driven by the environment. For instance, figure 7 and Table 2, show how much the seasonal signal in meroplankton is positively correlated, or synchronised, with the seasonal signal of SST. Low values of biology always match low values of SST and vice versa.

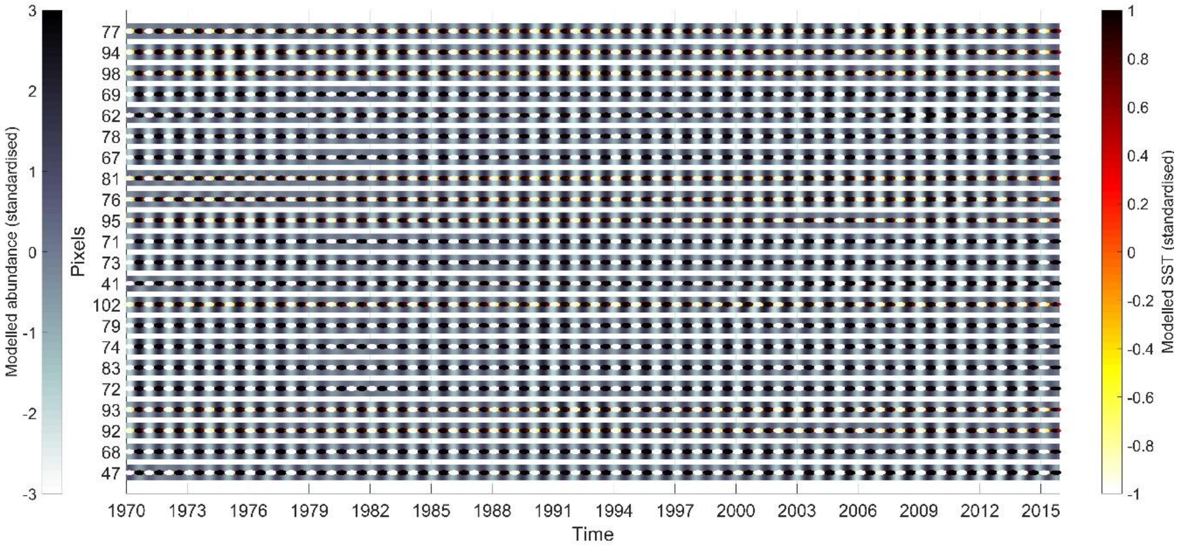


Figure 7: Graphical representation of seasonal scales sub-models of meroplankton for each pixels. Superimposed, the standardised values of long-term SST. When values are positive, SST were above the average and vice versa.

Table 2: Summary table of correlation coefficients (Pearson's *r*) between seasonal sub-models of both meroplankton and SST. All associated probability value (p-value) were >0.01.

Pixels	77	94	98	69	62	78	67	81	76	95	71	73	41	102	79	74	83	72	93	92	68	47
r	▲ 0.75	▲ 0.87	▲ 0.88	▲ 0.87	▲ 0.53	▲ 0.82	▲ 0.85	▲ 0.74	▲ 0.73	▲ 0.89	▲ 0.83	▲ 0.89	▲ 0.52	▲ 0.67	▲ 0.88	▲ 0.82	▲ 0.86	▲ 0.86	▲ 0.72	▲ 0.90	▲ 0.90	▲ 0.59

Again, for most species/groups, seasonal patterns in the biology can be explained by the patterns in environmental parameters. The relationship can be positive, like in the case of meroplankton and SST, or negative, like in the case of *Odontella sinensis* (Diatoms) and SST. Sometimes, a pattern found in the biology did not correspond to any pattern found in the environmental parameters, but even in those cases, we never found a link with the presence or intensity of MMS.

Discussion

The foundation phase of INSITE aimed at getting a sense of what data gathering already exists, and also at understanding the scope of what is currently available in terms of scientific knowledge on the concept of man-made structures influence on the biology. This is precisely what the SIGNAL project aimed to offer to both the scientific community and the industry by using the INSITE programme as an opportunity to investigate new issues, to find innovative solutions and to bring new answers and, of course, new questions.

Theoretically, one potential impact of man-made structures on planktonic communities might have been that the increase in surface area of MMS could have resulted in an increase in surface dwelling organisms (e.g. bivalves, echinoderms, etc.). This phenomenon could have, in turn, changed the dynamic of the species constituting the meroplankton community. It is well know that large scales patterns in plankton, being in time or space, are in majority driven by the physical environment. Hence, if any impact of MMS could be detected, this signal would be buried among the prevailing signals driven by environmental parameters such as sea surface temperature or both wind direction and intensity. This is why this project aimed at disentangle those signals at different scales. However, this studies shows that when a change of plankton dynamic, either a long-term or a seasonal one, is found it is most of the time correlated by a change in the dynamic of the sea surface temperature and/or the wind patterns. Those results indicate that, if oil and gas platforms have an impact on plankton, this impact is marginal at the selected spatio- temporal scales (local to regional, month to decade). Even in areas (i.e. pixels) “colonised” by a huge amount of structures, the plankton dynamic can most of the time be explain by the environment. Furthermore, when biological patterns cannot be explain by the SST or the wind, we cannot detect any clear link with neither the presence nor the quantity of MMS.

Dealing with the biology constitutes a challenge by itself. Plankton in particular are known to exhibit a large quantity of different patterns, driven by an equally large number of causes. Even if they seem primitive and simple, those micro-organisms are surprisingly complex in their behaviours. To make things even more difficult, one dealing with plankton has inevitably to deal with the patchiness associated with it. An observer at sea could take a glass of water, analyse its content, only to find a totally different results when taking another sample at the same place few seconds after. On top of all this, any sampling method has uncertainties that can bring “noise” to the results. This is why we choose to work on gridded products that allow us to combine several samples in order to increase the robustness of our data. This is also why we choose to rule out any location that had incomplete timeseries. Again, it is because SAHFOS as such an extensive database that we were able to aim for such a conservative approach.

SAHFOS is fairly unique in the world due to its extensive database. To be able to afford such a sampling coverage, it is impossible to use research vessels that would go sampling where we want, when we want. Instead, we have to rely on ships of opportunities, mostly merchant ships, which travel from a port to another to deliver passengers and/or goods. This implies that the prime goal of those ships is to safely arrive on time to their destination and to stay away from any danger; among which we can count oil and gas platforms. If this study demonstrates that we cannot clearly identify any impact of MMS on plankton community, this conclusion is valid only at the spatio-temporal scales considered. We do not know what is happening at the scale of the minutes or the hour, few meters from the pillar of a platform. The project has come a long way to fulfil its objectives, but has also revealed challenges. One of them is a serious lack of relevant biological data in the platforms vicinity. Despite that SAHFOS was able to provide extensive data on relevant species, the scale at which those data were collected do not fit correctly with the scales at which known potential physico-chemical effects of the MMS should occur. (e.g. water flow (Wilding, 2014), organic build-up (Davis et al., 1982) or produced waters (Bakke et al., 2013)). Finding a way to monitor the possible effects of MMS cost-effectively, and how such effects will impact MMS management will be dealt with in INSITE Phase 2, the Data Acquisition and Enhancement Phase, starting in 2018.

Introduction & Background

As a result of increasing human activities, the presence of man-made structures (MMS) such as oil platforms, breakwaters or bridge pilings has greatly expanded in the near-shore marine environment (Davis et al., 1982). Currently, the North Sea supports extensive oil and gas exploration which has resulted in over 500 offshore platforms across the region (Fujii et al., 2014). These facilities are the major MMS installed on the seabed and the presence of artificial structures directly interacts with the wave field and acts on local current regimes (Davis et al., 1982). By affecting hydrographic features, MMS could influence biological compartments (i.e. the biocoenosis) through an impact on species phenology (recurring life cycle events), abundance and diversity (in both space and time) with consequences for communities and ecosystem processes.

Studies that dealt with the effects of these structures on their environments mainly focus on sedimentary communities, invertebrates, plants or fishes but with incomplete, and sometimes contradictory, conclusions (Barros et al., 2001; Fabi et al., 2002). To our best knowledge, little attention has been paid up to now to better understand the influence of MMS on the planktonic compartment of the North Sea ecosystem. In recent years, evidence has grown that climate variation impacts the biodiversity, structure and functioning of marine ecosystems (Beaugrand et al., 2010) with well-documented co-variations between changes in climate and both biogeographical and phenological changes in marine species (Aebischer et al., 1990; Beaugrand, 2003; Parmesan and Yohe, 2003). If detected, the influence of MMS on the biocoenosis is expected to be marginal when compared to both the magnitude and rate of climate variation impacts. A crucial issue in this study would therefore be to disentangle the effects of the climatic signal from those of MMS.

Plankton is the collective name for the myriad of, mostly microscopic, plants (phytoplankton) and animals (zooplankton) that inhabit the sea and drift at the mercy of the currents: planktos is the Greek word for ‘drifter’. Planktonic organisms occur in vast numbers, with a glass of seawater typically containing many hundreds of thousands to millions of individual organisms. Plankton lie at the base of the marine ecosystem and as such they initiate and sustain all marine ecosystems. As plankton generally grow and reproduce at a rapid rate, this high population turn-over can be useful when looking at impacts on the community. For example, plankton are known to respond rapidly to climate change, far more so than on longer lived, high trophic organisms. Plankton are also involved in the cycling of the elements, for example, about half of the oxygen in the atmosphere globally is derived from photosynthesis of the phytoplankton. Thus the plankton are arguably the most important living components of the seas.

The North Sea has a particularly rich and diverse community of plankton. There are many complex reasons for this, including, among others: latitude, which drives a strong seasonal cycle; wide depth variations, which change the light environment; a range of tidal and oceanographic currents; multiple inputs of various waters – e.g. the Baltic in the NE and Atlantic water in both the SW and NW, and rivers from around the entire North Sea, which provide rich sources of nutrients that stimulate growth of phytoplankton, like nitrogen and phosphorus; and a relatively high hard surface (coasts, sediments) to volume ratio. The latter might be important in the context of INSITE because there are two types of plankton: organisms that spend their entire life in the plankton (holoplankton) and organisms that spend only part of their life-cycle in the plankton (meroplankton). The meroplankton comprises the larval forms of organisms, such as crabs, lobsters, shellfish and starfish, that live their adult lives in sediments and on rocky surfaces but spend the early part of their lives as members of the plankton. Man-made structures (MMS) could influence the abundance of meroplankton by providing an increased surface area and habitat for hard surface-dwelling organisms, thus leading to an increase in their larvae and juveniles as part of the Meroplankton

The North Sea is one of the best studied marine areas in the world for plankton and foremost among these studies is the Continuous Plankton Survey (CPR), run by the Sir Alister Hardy Foundation for Ocean Science (SAHFOS), based in Plymouth. SAHFOS has an archive of plankton abundance covering the entire North Sea extending back many decades. For the area of interest, OSPAR Region 2 Greater North Sea, SAHFOS has almost 55000 samples from 1958 to present day (Figure 1). In addition to this extensive temporal coverage of sampling, the spatial extent of sampling means that the study area is well covered. This means that plankton data can be mapped in both space and time, and compared to MMS introduction and distribution. The CPR methods have not changed throughout its history (from 1958, see method section) and the survey commenced before the large scale installation of MMS. The data-base contains detailed analyses of the distribution and abundance of the majority of components of the plankton community, including the meroplankton. In fact, the CPR database has information on over 800 planktonic entities and is thus ideal for studying whether MMS have had an impact on the plankton.

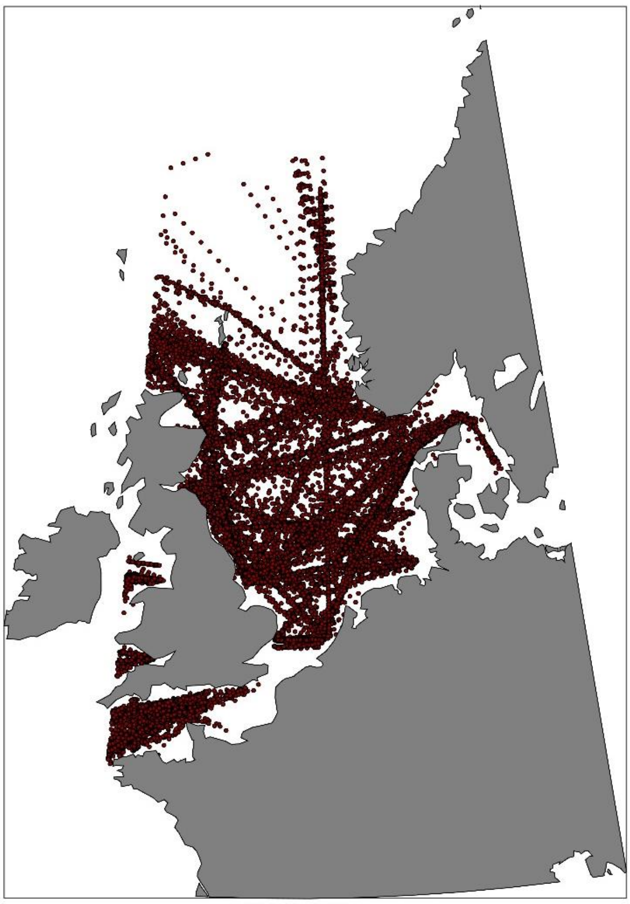


Figure 1. Chart showing the distribution of the 54667 CPR samples collected in the OSPAR Region 2 Greater North Sea between 1970 and 2015.

Methods

The Continuous Plankton Recorder (CPR) survey

Concept

The Continuous Plankton Recorder survey (CPRs) is a large-scale plankton monitoring program. The CPR (the recorder) was towed for the first time during the “Discovery” expedition in the Antarctic in 1925-1927 over 1300 miles (Hardy, 1926). Since 1931 the CPR has been used on regular routes in the North Sea (Hardy, 1939). Since 1991, the CPR survey and the dataset have been managed by the Sir Alister Hardy Foundation for Ocean Science (SAHFOS). Now the CPR survey is the largest multi-decadal plankton monitoring programme in the world. The data on the near-surface abundance of phyto- and zooplankton are available monthly from 1946 and at the end of 2016, this dataset amounts to 3,230,971 positives entries, counted for around 800 phyto- and zooplankton taxa, many of which are identified to the species level. The list of species is consultable on the SAHFOS website (www.sahfos.ac.uk/). CPR data have become increasingly important as a baseline to assess impacts of global change on pelagic ecosystems. This is an important set of tools for all those concerned with biodiversity loss, climate change, eutrophication, pollution, harmful algal blooms and sustainable fisheries (Brander et al., 2003)

Sampling and sub-sampling

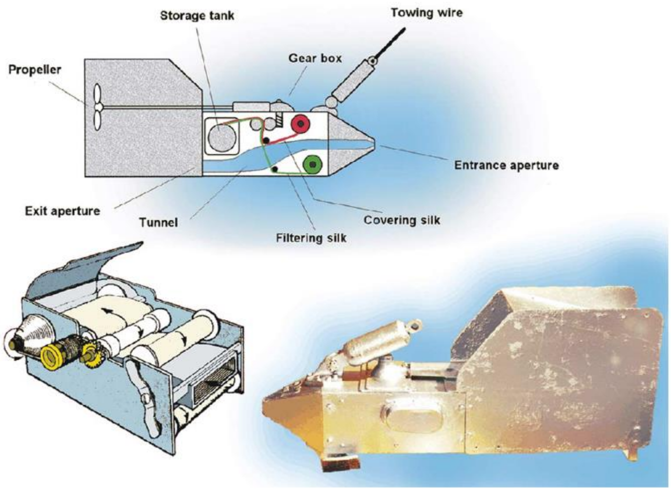


Figure 2. A cross-section of the CPR, its internal mechanism and CPR body.

The CPR is towed behind ships of opportunity on their normal trading routes at their conventional operating speeds (15–20 knots) without any scientists on board. A fixed sub-surface depth (a standard depth of 7 m) was chosen to give the most consistent results in the relatively shallow North Sea (Hays and Warner, 1993). Water enters the CPR through a square aperture 1.27 cm 1.27 cm (1.61 cm2) (Fig. 2) down an expanding tunnel, which effectively reduces the water pressure to minimise damage to the captured plankton, and exits through the rear of the device (Fig. 2). The movement of the water past the CPR turns an external propeller at the rear of the device that operates a drive shaft and gear system, which advances the silk filtering mesh. Plankton in the water are filtered onto this constantly moving band of silk. The filtering silk meets a second band of covering silk, effectively sandwiching the plankton, and is then wound onto a spool in a storage tank containing formalin. The mesh size of the silk is 270 µm in order to give an adequate representation of copepods, cladocera, pteropods, and chaetognaths, but also to give an indication of blooms of large phytoplankton, while reducing clogging by small phytoplankton cells (Hardy, 1939). Despite the relatively large size of the mesh, small phytoplankton, such as coccolithophores, are still retained on the silk. After towing, the CPR is returned to the laboratory and the silk is removed from the storage tank. The silk is divided into samples corresponding to 10 nautical miles (18.5 km) of towing (equivalent to about 3 m3 of sea water filtered assuming 100% filtration efficiency; (Jonas et al., 2004). Positions and times of each sample are estimated with the knowledge of the start and the end of each tow as well as possible changes in the direction and the speed of the ship.

The identification and plankton counting is realised in four steps (The methodology of the step 1 and step 2 have been unchanged since 1958):

- Step 1. It consists of an estimation of the colour of the silk in order to give an index (called greenness index) of concentration of chlorophyll in the environment. There are four different categories of colour (no colour, very pale green, pale green and green).These four levels of the phytoplankton colour index (PCI) represent the amount of phytoplankton pigment on the silk and have been assigned numerical values on a ratio scale based on acetone extracts using spectrophotometric methods(Colebrook and Robinson, 1965).
- Step 2. Phytoplankton are identified and counted to species level when it is possible. More than 200 phytoplanktonic species or taxa are identified. Subsampling of the silk is processed by selected 20 fields under a x400 magnification (295µm diameter view) on one of the diagonals of the silk. These 20 fields amount to 1/10,000 of the area of the filtering silk. Abundance of each phytoplankton taxonomic category is determined by counting the number of fields in which each taxon is detected. This has been derived from the Poisson distribution, which assumes organisms are randomly distributed on the silk (Colebrook, 1960).
- Step 3. This consists of an examination of zooplankton that are generally smaller than 2 mm. Over 70 species or taxa are identified at this stage. Five fields (2.06 mm diameter view) on one of the diagonals of both filtering and covering silks are studied under a x45 magnification. It assumes retained organisms are uniformly distributed on the silk. This procedure examines 1/50 of the silk.
- Step 4. This consists of an identification of the zooplankton greater than *Metridia lucens* stage V in size (>2 mm total length: (Rae, 1952)). More than 150 species or taxa are identified at this step. A category system is used to count the zooplankton in order to reduce the time of the analysis. The method is described in details in Colebrook (1960), (Colebrook & Robinson (1965) and Warner & Hays (1994).

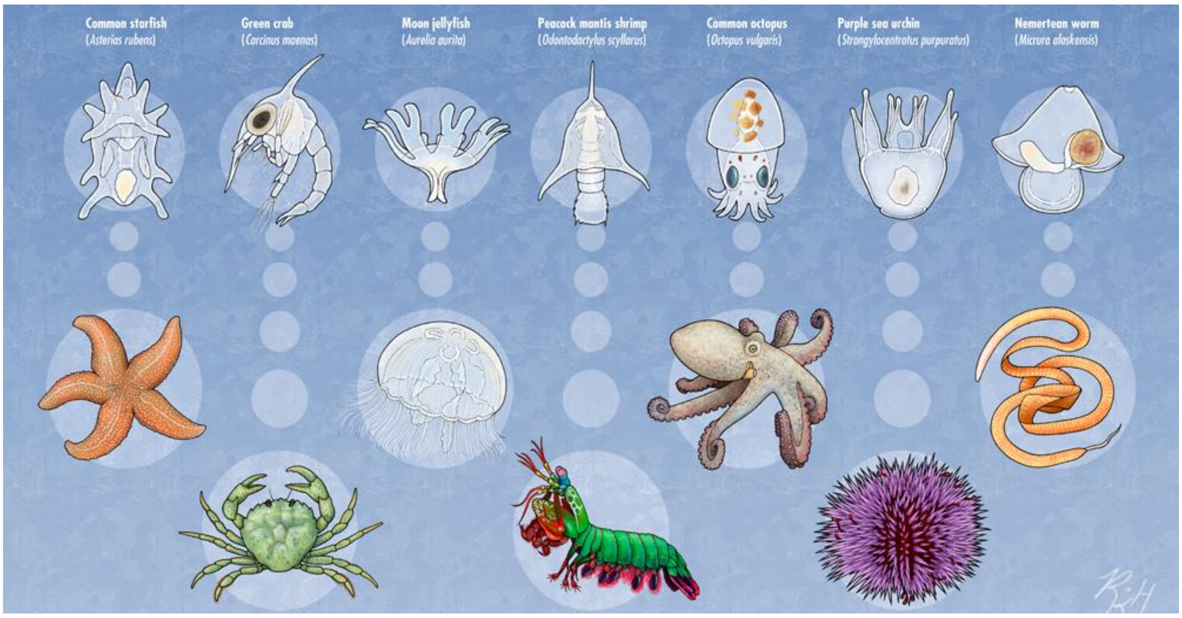
Quality control checks are carried out at all stages of the analysis and the data processing. If high variations are detected between two samples related in space or time, an analyst is asked to re-analyse the sample.

Selection of relevant taxa

From the initial selected taxa (15), we had to drop the dinoflagellate *Ceratium arcticum* because it was totally absent from too many selected pixels or, when present, had too few values to build a timeseries. For similar reasons, the genus Gyrosigma, *Odontella aurita*, *Odontella mobiliensis* and *Odontella regia* despite being potentially interesting, had to be removed from the analysis do to their rarity (too many absences).

Using SAHFOS expertise, a total of 10 planktonic groups or taxa were selected to conduct this study. First, we used two broad types of plankton: organisms that spend their entire life in the plankton (holoplankton) and organisms that spend only part of their life-cycle in the plankton (meroplankton). The meroplankton comprises the larval forms of organisms, such as crabs, lobsters, shellfish and starfish, that live their adult lives in sediments and on rocky surfaces but spend the early part of their lives as members of the plankton. The fact that MMS could play act has artificial rocky surfaces make this group especially important in the context of INSITE.

Echinoderms larvae constitute another group. Again, part of the meroplankton, this group includes well-known animals such as sea stars, sea urchins, sand dollars, and sea cucumbers, as well as the sea lilies. Echinoderms play numerous ecological roles; sand dollars and sea cucumbers burrow into the sand, providing more oxygen at greater depths of the sea floor allowing more organisms to live there. In addition, starfish prevent the growth of algae on coral reefs and probably on other hard substrates. This allows the coral to filter-feed more easily. Also, many sea cucumbers provide a habitat for parasites such as crabs, worms, and snails. In addition to broad groups, some particular species were also used, for instance, the copepods *Calanus finmarchicus* and *C. helgolandicus*. These are small crustacea of prime importance for the ecosystem, they are often an important part in the diet of at least one developmental stage of economically important fish species such as cod, herring or mackerel (Orlova et al., 2005; Skreslet et al., 2005; Sundby, 2000). Phytoplankton were also used in this study because they are extremely important for an ecosystem, they form the base of the food web as they are predominately photosynthetic primary producers. There are many different groups of phytoplankton species found in the world's oceans, but the most common can be broadly split into diatoms and dinoflagellates. Finally, some species that are directly linked to the presence of suspended organic matter in the water column were examined. We know that MMS have an impact on turbulences and those species are especially sensitive to this perturbation.



The meroplankton. Source: Robin K Herman. http://www.rkherman.net/

The environmental parameters

Sea Surface Temperature (SST)

We focused on two main environmental parameters: Sea Surface Temperature (SST) and the wind direction and intensity. SST is essential as it has a well-documented effect on marine ectotherms (Mauchline, 1998; Schmidt-Nielsen, 1990), including plankton (Reid and Edwards, 2001). Metabolic rates of both phytoplankton and zooplankton increase with temperature, even sometimes leading to a growing imbalance between photosynthesis and respiration rates as temperature becomes too high. But temperature has also some indirect effects, primarily associated with the control of the vertical stratification, mixed layer depth (MLD) and consequently the nutrient flux into the upper layer of the sea.

Wind (zonal, meridional and curl)

Wind can induced water turbulence and is used as an indicator because of its impact on water-column stability which can affect plankton populations (Heath et al., 1999). When wind blows over water, the top of the water starts moving and shears against the water below it, making that water moving as well. The momentum from the wind is transferred down into lower layers of the water. Because of the Coriolis force, on average the water moves to the right of the wind in the northern hemisphere; if the wind is blowing northward, the water moves eastward. When the wind is parallel or nearly parallel to the lines of latitude, the wind pattern is termed zonal. When the wind crosses the latitude lines at a sharp angle, the wind pattern is termed meridional. In this study we used both zonal and meridional component of the wind patterns but also a composite of the two: the wind stress curl. We call "Entrainment" how much of the deep, cold ocean water mixes with the relatively warm upper ocean water. The negative wind stress curl leads to water being pushed down and less deep water mixing with the upper ocean. The upper ocean stayed warmer, so the whole heat blob lasted longer.

Both Sea Surface Temperature (SST) and Wind data (wind zonal and wind meridional) come from the National Oceanic and Atmospheric Administration (NOAA). A complete description of the dataset can be found on their website (https://www.esrl.noaa.gov/psd/data/gridded/tables/monthly.html)

Calculation wind stress curl:
The wind stress curl was calculated using post-processed wind fields from NOAA. They were then transformed into the two wind stress components: U (zonal) and V (meridional). Finally, the wind stress curl (Z) was calculated using the formula:

$$Curl = \frac{\Delta\tau_y}{\Delta x} - \frac{\Delta\tau_x}{\Delta y}$$

where:
$\Delta\tau_x = \tau_{south-north}\ wind\ stress\ between\ 2\ points$
$\Delta\tau_y = \tau_{west-east}\ wind\ stress\ between\ 2\ points$
$\Delta x = west - east\ distance\ between\ 2\ points$
$\Delta y = south - north\ distance\ between\ 2\ points$

Man-Made Structures (MMS)

One of the task was to assemble all available data for Man Made Structures (MMS) into a coherent database and structure using the data provided from the community, to assess the completeness of the dataset. Data for MMS were provided by Centre for Environment, Fisheries and Aquaculture Science (Cefas) and by Strategic DECOM. Both datasets were sparsely populated resulting in incomplete records. The data from Strategic DECOM were supplied in two separate tables, linked by the name of the platform. The initial match only produced an approximate 50% match due to the inconsistency in the way the names were stored. The additional 50% of records were matched by hand, and assigned a quality flag based on the confidence of the match. Going forward all data on MMS should be stored with a unique identifier in order to make the data more interchangeable, from the data available it appears the Oslo and Paris Convention for the Protection of the Marine Environment of the North-East Atlantic (OSPAR) have already started this process. Currently, the database now contains 1503 records, though the sparsity of the data for each record is a concern and has a negative impact on the usability of the data.

Table 1: Field descriptions of MMS database. Fields marked * should have standardised vocabularies

Column Name	Description
OSPAR_ID	Unique ID for the Man Made Structure
Country*	Name of Country
Name	Name of Man Made Structure
Location*	Name of Area where structure is located (i.e. name of oil field)
Latitude	Latitude of Man Made Structure location
Longitude	Longitude of Man Made Structure Location
Water_dept	The depth of water at the location of the Man-Made Structure
Operator*	Name of company whom currently own the platform
Production	Year the platform went into production
Finish	The year the platform ceased production
Current_St*	Current State of the platform (i.e. operational, decommissioned, etc.)
Primary_pr*	The primary purpose of the Man Made Structure

Category*	Type of Man Made structure (i.e. Fixed Steel, Subsea Steel, etc.)
Function*	Description of the type of function performed ('Above Water Production, Subsea, etc.)
Weight_sub	Weight below the surface of the water (in tonnes)
Weight_top	Weight above water (in tonnes)
Remarks	Additional comments
Jacket_Wei	Weight of the jacket on the Man Made Structure (in tonnes)
Module_Wei	Weight of the specified Module (in tonnes)
Deck_MSF_W	Deck weight (in tonnes)
Jacket_Ins*	Type of Jacket installation
No__of_Leg	Number of legs on the Man-Made Structure
Manned_Unm*	Manned or Unmanned Man made structure
DataSourceID*	ID of the data provider (to allow for tracking)
QualityFlag*	Quality flag added to indicate level of confidence in the data
Internal_ID	Internal ID to allow for referencial integrity checks
Comment	Further comments

Inverse Distance Weighting (IDW) interpolation

All biotic and abiotic datasets, originating from various sources (i.e. NOAA, OSPAR, DECC and SAHFOS), were gathered. Dedicated algorithms were created to download and read the datasets coming in different formats (e.g. NetCDF, csv, txt). Because the datasets were characterised by different spatio-temporal resolution, they were post-processed to obtain homogenous monthly gridded products (i.e. 0.5 x 0.5 degrees) for the period 1970-2015 using a custom made interpolation algorithm. This dedicated interpolation method, programmed in Matlab®, is based on an Inverse Distance Weighting (IDW) method using a set search radius and number of neighbours. It allows for a fast and controlled gridding of data.

Inverse Distance Weighting (IDW) is a type of deterministic method for multivariate interpolation with a known scattered set of points. The assigned values to unknown points (j) are calculated with a weighted average (w) of the values available within the search radius (i). IDW interpolation are based on the assumption that things that are close to one another are more alike than those that are farther apart. As Tobler stated in 1970 when describing his first law of geography "Everything is related to everything else, but near things are more related than distant things". To predict a value for any unmeasured location, IDW will use the measured values surrounding the prediction location. Those measured values closest to the prediction location will have more influence on the predicted value than those farther away. IDW assumes that each measured point has a local influence that diminishes with distance. It weights the points closer to the prediction location greater than those farther away (Figure 3).

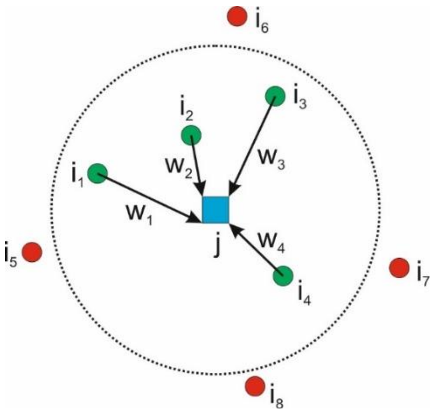


Figure 3: Schematic of Inverse Distance Weighting (IDW) interpolation used to regularise the raw data. The blue point is one node of the defined grid, green points are points within the search radius (dash circle) and red points are points outside the search radius.

After performing an Inverse Weighted Distance (IDW) method on all selected taxa and environmental parameters, we obtain a four dimensions grid (Latitude * Longitudes * Months * Years or 41*47*12*46) with a resolution of ½ a degree.

The distance-based Moran's eigenvector maps (dbMEM)

Spatial eigenfunction analysis is a family of methods for multiscale analysis of univariate and multivariate response data (Griffith and Peres-Neto, 2006). Those methods draw upon several methodologies/concepts such as: distance matrices, minimum spawning trees, principal coordinate analysis, multiple regression modelling, redundancy analysis, variation portioning and the concept of scales in spatio- temporal patterns. The distance-based Moran's eigenvector maps (dbMEM) begins with an eigenfunction decomposition of a truncated matrix of geographic distances among locations. Eigenvectors corresponding to positive eigenvalues are used as spatial descriptors of the data in regression or canonical analysis. This method can be applied to any set of locations providing a good coverage of a given geographic landscape. In the original method described by (Borcard and Legendre, 2002), the truncated matrix of geographic distances is built in such a way that it considers the influence of a sampling location on itself (i.e., the geographic distance matrix has nonzero values in the main diagonal). Although this consideration could be seen as difficult to justify, there are examples of spatial models where it has been applied (Bavaud, 1998). However, in order to make the method fully compatible with the Moran's I coefficient (MC) framework, and therefore more similar to the Griffith topology-based spatial-filtering methodology, (Dray et al., 2006) implemented a modification in the original Borcard & Legendre (2002) Principal Coordinates of Neighbour Matrices (PCNM) spatial-filtering method. Hereafter, we refer to the results of this modified version as distance-based eigenvector maps, to distinguish it from the Griffith method, whose results can be referred to as topology-based eigenvector maps. The distance-based eigenvector procedure (after Dray, Legendre, & Peres-Neto, 2006) can be summarised with the following steps:

- Step 1. Compute a pairwise Euclidean (geographic) distance matrix D among sampling units (D ¼ [dij]).
- Step 2. Choose a threshold value of distance t and construct a truncated connectivity matrix W (i.e. not all sites are connected) using the following rule:

$$\mathrm{W} = (w_{ij}) = \begin{cases} 0 \; if \; i = j \\ 0 \; if \; d_{ij} > t \\ [1 - \left(\frac{d_{ij}}{4t}\right)^2 \; if \; d_{ij} \leq t \end{cases}$$

Where t is chosen as the maximum distance that maintains all sampling units being connected using a minimum spanning tree algorithm. In the dbMEM, the diagonal values of the distance matrix, which of course are originally zeroes, are replace by the value (4*threshold). This change on the diagonal indicates that a site is not connected to itself. Compute the eigenvectors of the centred connectivity matrix. As for the topology-based spatial-filtering methodology, this centring process guarantees that the extracted eigenvectors are orthogonal and linearly independent.

Given the non-Euclidean nature of spatial connectivity matrices, both positive and negative eigenvalues are produced. The non-Euclidean part is introduced by the fact that only certain connections among sites, and not all, are considered in matrix W. As in Griffith's method, the extracted eigenvectors represent the decomposition of the Moran's I coefficients into all mutually orthogonal and linearly uncorrelated map patterns. Eigenvectors having associated positive eigenvalues represent positive spatial association, whereas eigenvectors having negative eigenvalues represent negative spatial association.

- Step 3. An MC for any eigenvector v can be directly calculated as follows:

$$MC(v) = \frac{n}{1^T S 1} v^T \left(I - \frac{11^T}{n}\right) W \left(I - \frac{11^T}{n}\right) v$$

$$MC(v) = \frac{n}{1^T S 1} v^T W v$$

Distance-based eigenvector maps with large eigenvalues represent coarse scales of spatial variability or landscape wide trends (e.g. global or large); eigenvectors with intermediate size eigenvalues represent medium scales (e.g. regional or medium); eigenvectors with small eigenvalues represent fine scales or patchiness (e.g. local or fine).

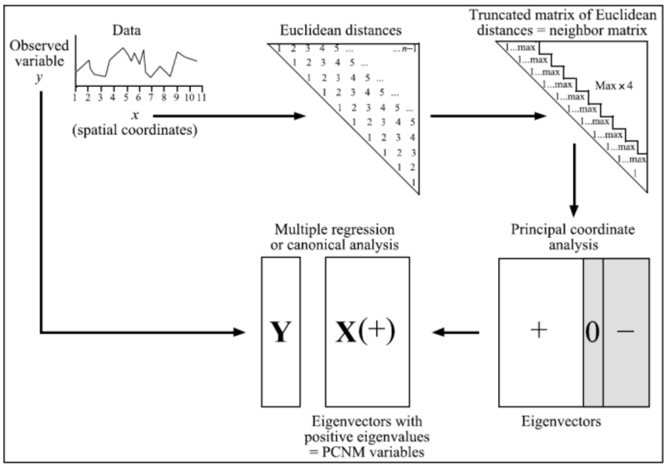


Figure 4: Schematic describing the dbMEM methodology. (From Legendre and Legendre, 1998).

Results

For each taxa and at each location, we explore the potential relationship between all sub-models and the MMS. Because it is unlikely that the MMS could impact the biology at all scales, we chose to explore the results sub-model by sub-model, in other terms, we chose to explore the potential impact of MMS per temporal scales (or instrument).

The majority of the selected species or group of species, were decomposed correctly by our core analysis (i.e. dbMEM). The variance of the signal was correctly captured by the analysis, offering the possibility to rebuild the original signal with good accuracy (Table 1). It means that their dynamic was structured enough to be picked up by the analysis. Another way of presenting it would be to say that the majority of the songs (species/groups) have melodies (dynamics) clear enough to allow us distinguishing the different instruments (sub-models). Also, it appears that the sub-models corresponding to the highest frequencies (fine scales/guitar and very fine scales/voice) did not contain enough variance (melody) to be robustly used (not shown). The amount of noise in them was too high for us to work on a clear signal. We therefore decided to focus on the long-term and the seasonal aspect of the plankton dynamic.

Table 1: Summary table of modelled signals quality. Values corresponds to the r^2 calculated between the global models (all scales) and the raw signal.

	species / groups									
Pixels	**C. finmarchicus**	**C. helgolandicus**	**C. longipes**	**Decapod**	**Echinoderm**	**Holoplankton**	**Meroplankton**	**O. Sinensis**	**PCI**	**P. sulcata**
41	0.74	0.70	0.64	0.81	0.85	0.74	0.82	0.49	0.76	0.53
47	0.73	0.70	0.58	0.77	0.82	0.74	0.76	0.49	0.74	0.56
62	0.81	0.72	0.63	0.76	0.75	0.82	0.76	0.64	0.67	0.62
67	0.91	0.69	0.62	0.89	0.87	0.82	0.87	0.64	0.82	0.60
68	0.76	0.64	0.60	0.80	0.79	0.68	0.89	0.63	0.75	0.62
69	0.73	0.68	0.53	0.84	0.79	0.71	0.80	0.67	0.74	0.63
71	0.69	0.73	0.56	0.92	0.85	0.77	0.87	0.72	0.76	0.64
72	0.72	0.75	0.61	0.85	0.80	0.75	0.82	0.72	0.73	0.66
73	0.79	0.71	0.66	0.87	0.82	0.75	0.89	0.73	0.80	0.59
74	0.68	0.75	0.57	0.84	0.78	0.74	0.81	0.81	0.75	0.61
76	0.77	0.76	0.66	0.61	0.75	0.77	0.66	0.49	0.69	0.60
77	0.77	0.71	0.70	0.58	0.74	0.76	0.61	0.50	0.69	0.63
78	0.62	0.72	0.54	0.88	0.82	0.77	0.88	0.75	0.71	0.62
79	0.82	0.75	0.65	0.83	0.79	0.76	0.86	0.78	0.69	0.66
81	0.76	0.75	0.66	0.56	0.75	0.77	0.60	0.49	0.69	0.63
83	0.80	0.74	0.65	0.83	0.85	0.78	0.87	0.78	0.67	0.62
92	0.74	0.71	0.68	0.85	0.88	0.71	0.81	0.76	0.74	0.67
93	0.76	0.67	0.56	0.86	0.91	0.70	0.83	0.74	0.77	0.59
94	0.74	0.66	0.56	0.84	0.88	0.67	0.79	0.73	0.70	0.58
95	0.75	0.70	0.63	0.85	0.88	0.71	0.81	0.75	0.72	0.69
98	0.77	0.71	0.60	0.78	0.89	0.71	0.79	0.76	0.74	0.57
102	0.68	0.71	0.67	0.86	0.86	0.72	0.83	0.75	0.78	0.65

Table 2: Summary table of modelled signals quality. Values corresponds to the r^2 calculated between the long-term models and the raw signal.

	species / groups									
Pixels	**C. finmarchicus**	**C. helgolandicus**	**C. longipes**	**Decapod**	**Echinoderm**	**Holoplankton**	**Meroplankton**	**O. Sinensis**	**PCI**	**P. sulcata**
41	0.13	0.07	0.02	0.05	0.05	0.10	0.07	0.06	0.04	0.08
47	0.11	0.06	0.01	0.05	0.05	0.11	0.05	0.05	0.04	0.07
62	0.25	0.13	0.05	0.09	0.09	0.21	0.11	0.19	0.08	0.13
67	0.79	0.18	0.01	0.04	0.20	0.51	0.04	0.26	0.47	0.14
68	0.29	0.17	0.04	0.10	0.07	0.18	0.09	0.14	0.22	0.14
69	0.46	0.18	0.06	0.09	0.13	0.24	0.08	0.27	0.31	0.20
71	0.45	0.28	0.06	0.09	0.11	0.21	0.10	0.32	0.40	0.22
72	0.41	0.27	0.13	0.08	0.12	0.24	0.12	0.30	0.31	0.21
73	0.40	0.19	0.11	0.10	0.10	0.26	0.10	0.27	0.31	0.18
74	0.28	0.29	0.08	0.11	0.14	0.13	0.14	0.48	0.41	0.24
76	0.31	0.24	0.06	0.04	0.20	0.31	0.12	0.04	0.13	0.04
77	0.24	0.17	0.08	0.03	0.14	0.24	0.05	0.04	0.12	0.08
78	0.17	0.27	0.14	0.18	0.16	0.19	0.17	0.23	0.23	0.20
79	0.48	0.32	0.12	0.12	0.08	0.31	0.14	0.33	0.29	0.22
81	0.27	0.19	0.04	0.04	0.20	0.29	0.02	0.05	0.13	0.05
83	0.37	0.27	0.16	0.15	0.14	0.25	0.20	0.30	0.23	0.17
92	0.32	0.21	0.11	0.17	0.12	0.22	0.18	0.19	0.28	0.18
93	0.31	0.18	0.08	0.11	0.08	0.19	0.11	0.10	0.19	0.10
94	0.24	0.16	0.04	0.15	0.07	0.19	0.15	0.18	0.23	0.07
95	0.31	0.19	0.06	0.23	0.15	0.24	0.22	0.24	0.25	0.22
98	0.29	0.25	0.07	0.18	0.13	0.26	0.23	0.19	0.27	0.11
102	0.17	0.31	0.15	0.10	0.19	0.24	0.09	0.20	0.22	0.18

Table 3: Summary table of modelled signals quality. Values corresponds to the r^2 calculated between the seasonal models and the raw signal.

	species / groups									
Pixels	**C. finmarchicus**	**C. helgolandicus**	**C. longipes**	**Decapod**	**Echinoderm**	**Holoplankton**	**Meroplankton**	**O. Sinensis**	**PCI**	**P. sulcata**
41	0.24	0.31	0.27	0.55	0.60	0.26	0.51	0.02	0.50	0.01
47	0.23	0.29	0.20	0.51	0.53	0.27	0.45	0.04	0.44	0.02
62	0.27	0.24	0.25	0.37	0.39	0.28	0.32	0.08	0.30	0.04
67	0.03	0.14	0.15	0.64	0.45	0.09	0.57	0.04	0.15	0.08
68	0.16	0.07	0.13	0.45	0.44	0.06	0.59	0.05	0.20	0.04
69	0.07	0.15	0.08	0.52	0.42	0.20	0.42	0.05	0.12	0.07
71	0.04	0.19	0.08	0.67	0.50	0.30	0.53	0.07	0.10	0.04
72	0.09	0.18	0.08	0.53	0.47	0.21	0.42	0.09	0.09	0.04
73	0.13	0.14	0.13	0.53	0.47	0.14	0.57	0.09	0.17	0.06
74	0.07	0.17	0.08	0.52	0.39	0.26	0.42	0.06	0.08	0.02
76	0.17	0.23	0.25	0.24	0.31	0.14	0.27	NaN	0.10	0.17
77	0.21	0.22	0.23	0.24	0.32	0.17	0.20	NaN	0.13	0.19
78	0.08	0.14	0.06	0.47	0.44	0.27	0.49	0.11	0.13	0.06
79	0.07	0.10	0.11	0.45	0.42	0.12	0.51	0.14	0.03	0.05
81	0.18	0.22	0.20	0.19	0.31	0.13	0.17	NaN	0.10	0.18
83	0.10	0.11	0.09	0.43	0.44	0.17	0.47	0.12	0.04	0.07
92	0.11	0.16	0.11	0.43	0.57	0.14	0.36	0.17	0.13	0.11
93	0.11	0.10	0.08	0.55	0.64	0.15	0.53	0.19	0.26	0.09
94	0.14	0.11	0.06	0.47	0.66	0.09	0.42	0.19	0.08	0.04
95	0.14	0.15	0.08	0.39	0.54	0.14	0.32	0.17	0.10	0.11
98	0.15	0.14	0.06	0.29	0.58	0.13	0.29	0.22	0.10	0.09
102	0.07	0.09	0.10	0.55	0.44	0.15	0.51	0.11	0.29	0.09

The comparison between species/group using tables 1 to 3 is interesting. It shows were the variance in each signal is confined or, for each song, what instrument is important to the general melody. For instance, echinoderms are well modelled overall (Table 1), but most of the variance is seasonal (Table 3), the long-term signal (Table 2) being significantly weaker. Conversely, both diatoms *Odontella sinensis* and *Paralia sulcata* have more long-term signal (Table 2) than seasonality (Table 3).

The comparison among pixels is equally interesting. A given taxa can have a very different distribution along time scales of its variance between two different sites. For instance, *Calanus finmarchicus* has equally good quality model overall in pixels 41 and 72 (Table 1). However, in pixel 41, most of the variance is seasonal (Table 3) while in pixel 72, this variance is more contained in the long-term scales. This highlight the complexity of plankton and also tells us that a species could react differently to a pressure depending of its location.

Modelling plankton dynamic at different scales (example of meroplankton at large scales)

Figure 5 contains a lot of interesting information. First, it shows the long-term dynamic of the meroplankton as a group. We can see periods of relatively low abundances across most of the pixels (characterised by light grey) as well as periods of relatively high abundances (in dark grey or black). For instance, we can see that from the late 1980's to the beginning 1990's, the abundance in meroplankton is significantly increasing. This period, called the "regime shift", is well document and characterised by pronounced changes in large-scale hydro-meteorological forcing. Increased sea surface temperature and possibly change in wind intensity and direction at the end of the 1970s in the west European basin triggered a change in the location of an oceanic biogeographical boundary along the European continental shelf (Beaugrand, 2004). Figure 5 also demonstrates the planktonic complexity by showing that the meroplankton reacts quite differently depending of the location. Not all pixels exhibit the same timing in their dynamics or the same intensity.

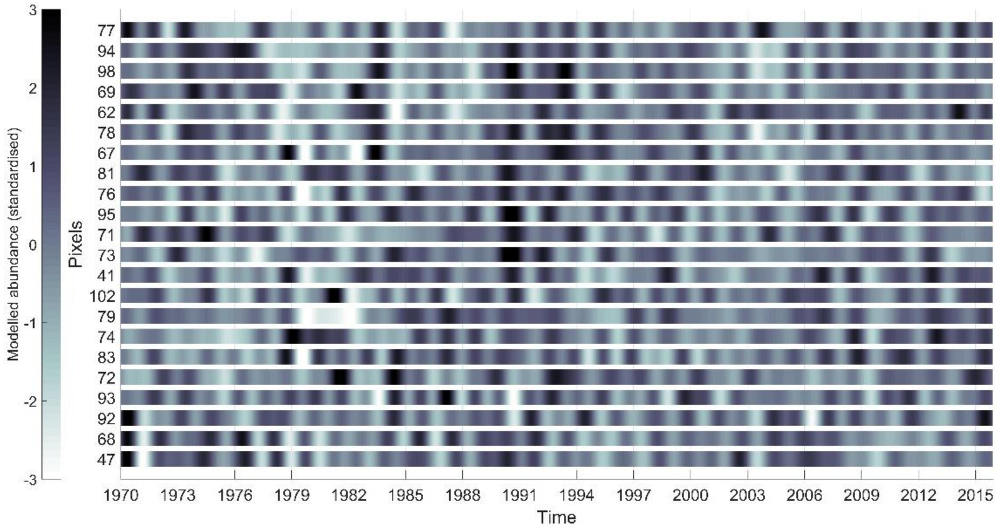


Figure 5: Graphical representation of large scales sub-models of meroplankton for each pixels.

Comparing models with MMS patterns (example of meroplankton at large scales)

It is interesting to superimpose the total weight under water of MMS to the results to see if we can see a correlation in the timing with the biology.

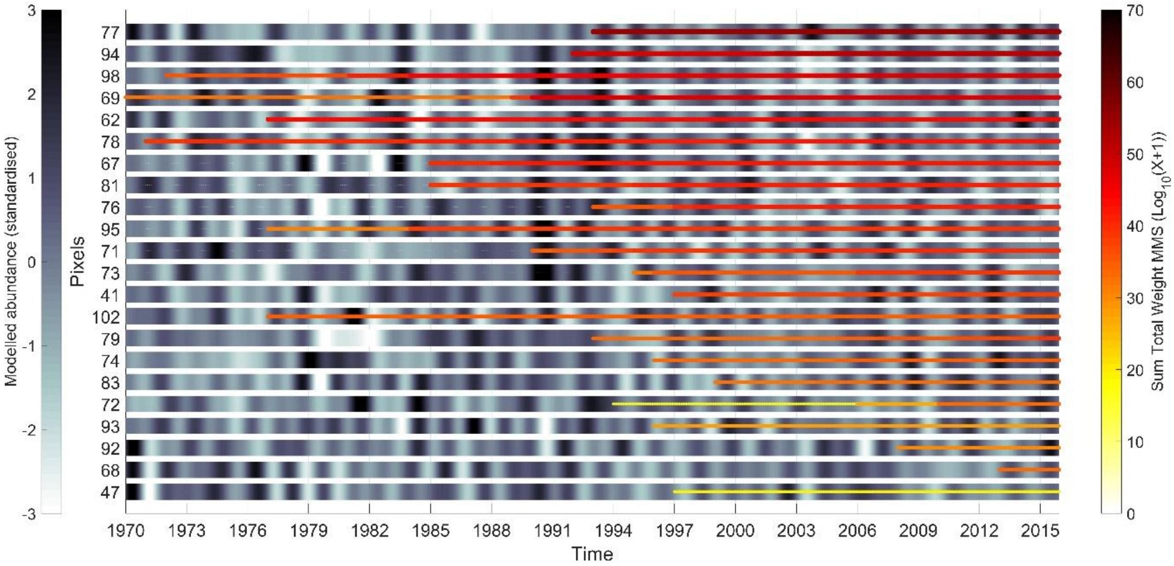


Figure 6: Graphical representation of large scales sub-models of meroplankton for each pixels. Superimposed, the sum of total weight under sea level of MMS (in tons). Values are log transform ($\log_{10}(X+1)$) to enhance the colour scale.

Figure 6 shows that there is no clear link between the meroplankton dynamic at large scales and the quantity of MMS. When meroplankton exhibit changes, it is never synchronised with the appearance of MMS in a given location nor with an increase of them.

Comparing models with SST patterns (example of meroplankton at larges scales)

However, it appears that the long-term dynamic of the meroplankton can be explained by the long-term dynamic of the sea surface temperature (SST). During the 1970’s, the temperature was relatively high (Figure 7, in shades of red) and also characterised by relative high values in meroplankton abundances (Figure7, in black). Conversely, the 1980's are characterised by cold temperatures (in shades of yellow) and low meroplankton abundances. Then, in 1986/87, the "regime shift" took place with a sharp rise in SST followed by a fast increase in abundance.

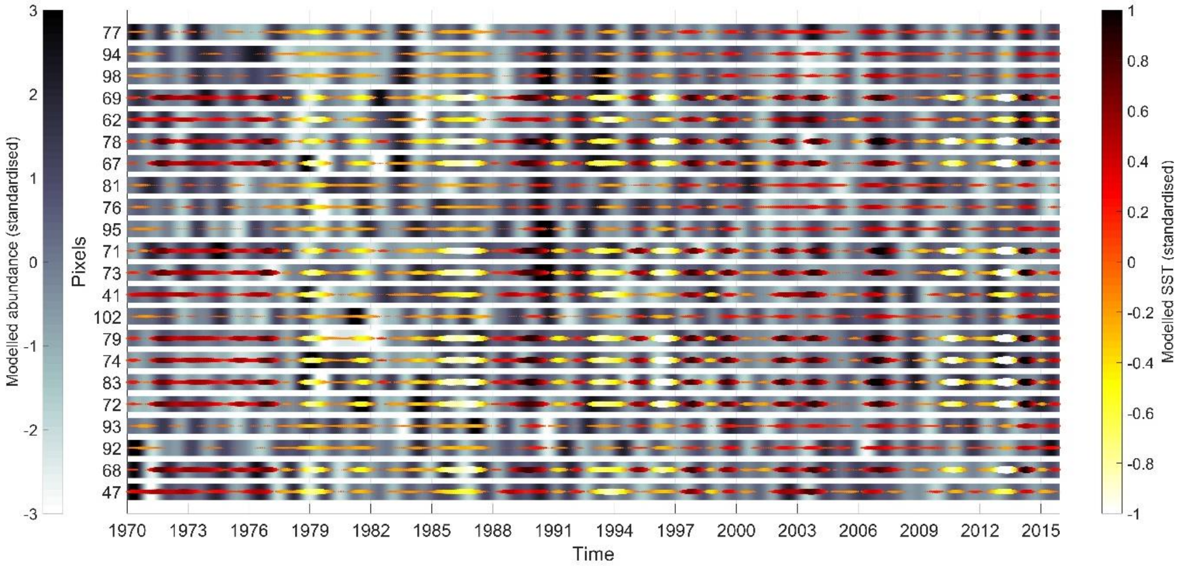


Figure 7: Graphical representation of large scales sub-models of meroplankton for each pixels. Superimposed, the standardised values of long-term SST. When values are positive, SST were above the average.

Comparing models with wind patterns (example of meroplankton at larges scales)

There is a clear relationship between long-term meroplankton sub-models and the zonal component of the wind (Figure 8). When zonal wind values are positive, the wind was blowing from west to east while when values are negative, the wind was blowing from east to west. It seems that the relatively weak abundances of long-term meroplankton (in light grey) corresponds to negative values of the zonal wind corresponding to dominant winds blowing from west to east. We see that to the late 1980's corresponds a significant change in the wind trends: winds suddenly started to strongly blow from West to east. We found no clear link between meroplankton and the meridional wind (i.e. along a longitude circle, Figure not shown).

However, it seems that the log-term wind stress curl and hence Ekman pumping anomalies are related to the long-term meroplankton (not shown). When wind stress curl values are negative, water is being pushed down and less deep water mixing with the upper ocean. The upper ocean stayed warmer and meroplankton values are high.

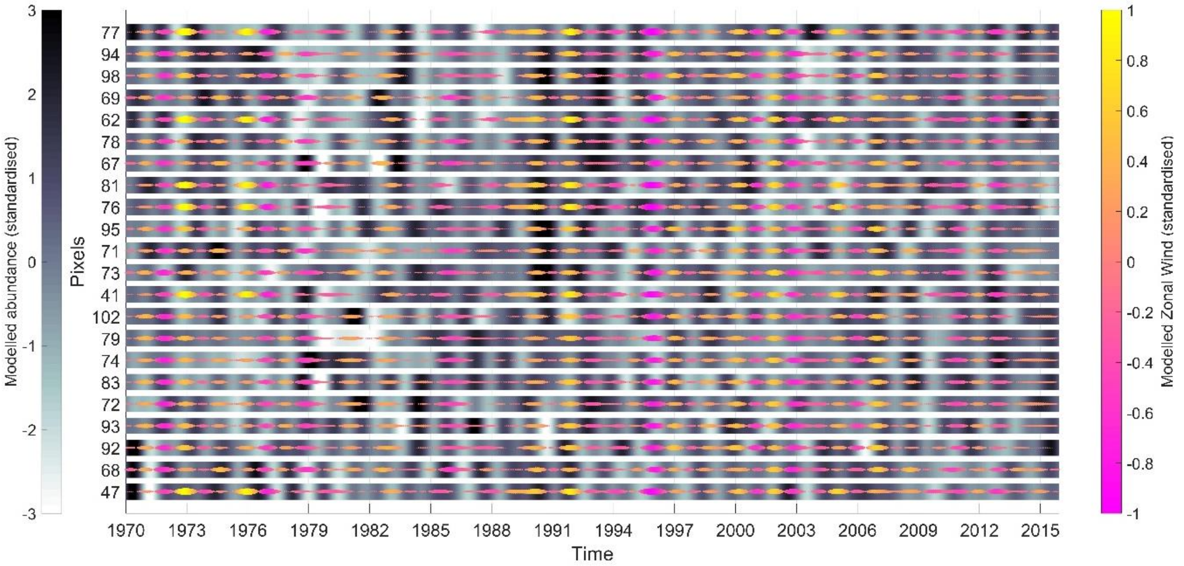


Figure 8: Graphical representation of large scales sub-models of meroplankton for each pixels. Superimposed, the zonal component of the wind: when values are positive, the wind is blowing from west to east; when negatives, the wind is blowing from east to west.

Summary of results (all species/groups, all parameters)

Considering that we have 10 taxa, two sub-models for each of them and 22 locations, it would be fastidious to present and comment all 20 graphical representations. Instead, we have created summary tables of correlations per temporal scales (sub-models) of interest. In each table, cells are in dark grey when the calculated probability value (p-value) was >0.05, those should not be considered as p-values were too high. Cells are in light grey when 0.01 > p-value > 0.05, those can be considered bearing in mind that in up to 5% of the cases, the correlation could fallacious. Cells are not shaded when p-value < 0.01, those exhibits a fairly high level of confidence. The arrows are here to help the reader identifying if the correlation was positive (> 0.1, green arrows), negative (< -0.1, red arrows). Finally, a “NaN” was used when the correlation was impossible to calculate.

By comparing table 4 and 5, we can see that there more non-significant correlations when using the long-term sub-models. This make sense if we consider that the seasonality is predominant in most of the plankton, especially in a temperate area such as the North Sea. Most of the species/groups exhibit a clear seasonal patterns itself driven by the seasonality in SST.

Table 4: Summary table of correlation coefficients (Pearson's *r*) between long-term sub-models of all species/groups and all environmental parameters. Cells are in dark grey when the associated probability value (p-value) was >0.05, those should not be considered as the p-value was too high. Cells are in light grey when 0.01 > p-value > 0.05, those can be considered.

		Pixels																						
		41	47	62	67	68	69	71	72	73	74	76	77	78	79	81	83	92	93	94	95	98	102
Sea Surface Temperature	C. finmarchicus'	-0.20	-0.15	-0.22	-0.31	-0.32	-0.19	-0.23	-0.15	-0.25	-0.15	-0.12	-0.20	-0.04	-0.23	-0.18	-0.07	-0.14	-0.07	-0.11	-0.03	0.13	0.01
	C. helgolandicus'	0.36	0.41	0.11	0.35	0.39	0.35	0.22	0.28	0.37	0.25	0.33	0.38	0.11	0.19	0.39	0.21	0.38	0.29	0.31	0.36	0.30	0.26
	C. longipes'	0.10	0.18	-0.06	0.43	-0.05	0.22	0.13	0.12	0.30	0.12	0.25	0.24	0.05	0.30	0.15	0.18	0.03	0.21	-0.10	0.04	0.02	0.14
	Decapod'	0.31	0.23	0.06	-0.03	-0.14	0.13	-0.12	0.29	0.25	0.05	0.07	0.17	0.02	0.03	0.09	0.01	0.17	0.54	0.08	0.07	0.21	0.39
	Echinoderm'	-0.05	0.03	0.04	-0.07	-0.02	0.20	0.05	0.22	0.03	-0.09	0.13	0.15	0.06	0.04	0.12	0.05	0.12	0.29	0.22	0.20	0.18	0.04
	'Holoplankton'	0.02	0.03	-0.23	-0.11	-0.09	0.03	0.04	0.09	-0.11	0.10	0.02	-0.13	0.19	-0.01	-0.11	0.14	0.11	0.16	0.01	0.16	0.14	0.12
	'Meroplankton'	0.17	0.22	-0.03	-0.04	-0.14	-0.11	-0.31	0.03	0.09	-0.09	0.10	0.11	0.02	-0.06	0.07	-0.05	0.18	0.41	0.13	0.18	0.28	0.31
	O. Sinensis'	0.07	0.09	0.11	0.03	0.10	-0.06	-0.06	-0.10	0.01	-0.15	-0.08	0.33	-0.03	0.06	-0.08	-0.05	0.13	0.01	0.00	0.03	-0.08	-0.25
	'PCI'	0.09	0.04	0.00	0.37	0.08	0.40	0.36	0.30	0.02	0.06	-0.06	-0.16	0.15	0.14	-0.06	0.08	0.18	0.28	0.14	0.15	0.16	0.11
	P. sulcata'	-0.07	0.00	0.00	0.32	-0.04	0.09	0.13	-0.04	-0.11	0.03	0.01	0.17	-0.02	-0.13	0.24	-0.12	0.11	0.09	0.08	0.14	-0.01	0.01
Wind Curl	C. finmarchicus'	0.14	-0.07	0.29	-0.03	-0.02	-0.05	0.09	-0.09	0.01	0.01	0.03	-0.02	-0.03	0.03	-0.01	-0.01	NaN	0.03	0.08	NaN	NaN	-0.07
	C. helgolandicus'	-0.18	-0.12	-0.02	-0.21	0.00	-0.23	-0.08	-0.10	-0.03	-0.04	-0.14	-0.13	-0.01	-0.13	-0.02	-0.01	NaN	-0.16	0.04	NaN	NaN	-0.26
	C. longipes'	0.00	0.00	0.15	0.00	0.00	0.00	0.00	-0.23	-0.26	-0.14	-0.12	0.02	0.07	-0.10	-0.10	0.09	NaN	-0.24	0.00	NaN	NaN	0.00
	Decapod'	-0.08	-0.08	0.09	0.03	0.07	0.04	0.16	-0.02	0.06	-0.07	0.14	0.00	-0.08	-0.10	0.12	-0.09	NaN	-0.13	-0.16	NaN	NaN	-0.11
	Echinoderm'	0.14	0.33	0.19	-0.17	-0.10	-0.10	-0.14	-0.12	-0.18	-0.26	0.19	0.19	-0.09	-0.18	0.11	-0.16	NaN	-0.17	-0.34	NaN	NaN	0.00
	'Holoplankton'	0.07	0.04	0.17	-0.14	0.04	-0.21	-0.06	-0.01	0.06	0.12	0.02	-0.09	-0.05	-0.03	-0.04	-0.09	NaN	-0.12	0.16	NaN	NaN	-0.10
	'Meroplankton'	0.00	0.00	0.11	0.06	0.03	0.00	0.11	-0.04	0.15	-0.11	-0.01	-0.13	-0.04	-0.13	0.16	-0.03	NaN	-0.12	-0.04	NaN	NaN	0.00
	O. Sinensis'	0.09	0.13	-0.17	-0.12	-0.18	-0.15	-0.08	-0.09	-0.07	-0.21	0.14	0.13	-0.04	-0.17	0.00	-0.17	NaN	-0.12	-0.14	NaN	NaN	-0.04
	'PCI'	0.08	0.08	0.23	-0.04	0.05	-0.03	-0.03	-0.08	0.09	-0.04	0.04	-0.03	-0.04	-0.01	0.06	-0.07	NaN	-0.13	0.01	NaN	NaN	0.00
	P. sulcata'	0.13	0.20	0.11	0.00	0.01	-0.08	0.00	0.06	0.17	0.05	0.02	0.04	-0.05	0.13	-0.01	0.00	NaN	0.00	-0.12	NaN	NaN	0.02
Wind Zonal	C. finmarchicus'	0.09	0.08	0.06	0.02	0.05	0.10	-0.02	0.10	0.05	0.01	-0.01	-0.06	0.07	0.12	-0.06	0.07	0.08	0.00	0.15	0.03	0.09	0.00
	C. helgolandicus'	0.16	0.18	0.02	0.15	-0.06	0.16	0.00	0.02	0.01	-0.05	0.08	0.13	0.08	0.11	0.02	-0.02	0.01	0.16	0.00	-0.05	0.00	0.05
	C. longipes'	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.19	0.10	0.11	0.20	0.10	-0.01	0.11	-0.18	-0.08	0.20	-0.13	-0.14	0.00	0.00
	Decapod'	0.26	0.26	0.11	-0.08	-0.01	-0.14	-0.19	-0.07	0.12	-0.05	0.17	0.15	0.04	0.00	0.14	0.00	0.13	0.05	0.10	0.16	0.08	0.07
	Echinoderm'	0.10	0.01	0.10	0.07	0.07	-0.01	0.10	-0.01	0.16	0.21	0.18	0.19	0.13	0.08	0.14	0.01	0.31	0.15	0.11	0.28	0.20	0.07
	'Holoplankton'	0.02	0.08	-0.02	0.08	-0.03	0.23	0.07	0.02	-0.06	-0.11	0.13	-0.13	0.11	0.10	-0.10	0.11	0.13	0.03	-0.02	0.02	0.04	0.07
	'Meroplankton'	0.12	0.22	0.15	-0.09	-0.12	0.00	-0.10	-0.03	-0.03	0.00	0.16	-0.02	0.04	0.03	0.05	-0.06	0.16	0.03	0.08	0.17	0.14	0.00
	O. Sinensis'	0.33	0.38	0.02	0.04	0.08	-0.03	-0.12	-0.05	-0.01	0.11	0.11	-0.11	-0.07	0.06	0.09	0.05	0.01	0.00	-0.15	0.01	0.08	-0.10
	'PCI'	0.00	0.00	0.09	0.03	0.01	0.00	0.00	-0.02	-0.09	0.00	0.11	-0.11	0.00	0.06	0.04	0.09	0.05	0.13	0.04	0.07	0.06	-0.05
	P. sulcata'	0.00	-0.10	0.02	-0.08	-0.07	0.11	-0.07	-0.05	-0.18	-0.13	-0.01	0.02	-0.10	-0.11	0.01	0.00	0.10	0.00	-0.10	0.12	0.09	-0.19
Wind Merional	C. finmarchicus'	-0.27	-0.31	-0.34	0.00	0.00	0.00	0.00	-0.11	-0.07	-0.14	0.07	0.00	0.00	-0.06	0.00	0.00	0.00	-0.09	0.00	0.00	-0.12	0.00
	C. helgolandicus'	0.12	0.00	-0.17	0.00	0.00	0.22	0.16	0.18	0.19	0.09	0.23	0.13	0.00	0.15	0.17	0.14	0.13	0.16	0.13	0.11	0.00	0.19
	C. longipes'	-0.41	0.00	-0.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.00	0.22	0.33	0.00	0.29	0.29	0.00	0.11
	Decapod'	0.14	0.00	-0.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.17	0.00	0.11	0.00	0.12	0.16	0.00	0.00	0.08
	Echinoderm'	0.00	0.13	-0.27	-0.01	0.00	0.00	0.13	0.00	0.00	-0.12	0.14	0.22	0.16	0.00	0.11	0.13	0.28	0.00	0.32	0.22	0.17	0.07
	'Holoplankton'	0.08	0.00	-0.18	0.00	0.00	0.00	0.01	0.09	0.00	0.00	0.12	0.10	0.00	0.00	0.16	0.00	0.00	0.11	0.00	0.00	-0.09	0.12
	'Meroplankton'	0.00	0.00	-0.49	0.00	0.00	0.00	0.10	0.00	0.14	0.12	0.00	0.00	0.17	0.20	0.00	0.08	0.00	0.00	0.13	0.00	0.00	0.00
	O. Sinensis'	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.21	0.00	0.08	0.31	0.18	0.39	0.27	0.19	0.13
	'PCI'	0.00	0.00	-0.23	0.00	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	P. sulcata'	0.00	0.16	0.16	0.00	0.00	0.15	0.27	0.14	0.00	0.14	0.00	0.00	0.33	0.11	0.00	0.00	0.00	0.00	0.22	0.10	0.00	0.23

Table 5: Summary table of correlation coefficients (Pearson's *r*) between seasonal sub-models of all species/groups and all environmental parameters. Cells are in dark grey when the associated probability value (p-value) was >0.05, those should not be considered as the p-value was too high. Cells are in light grey when 0.01 > p-value > 0.05, those can be considered.

		41	47	62	67	68	69	71	72	73	74	76	77	78	79	81	83	92	93	94	95	98	102
Sea Surface Temperature	C. finmarchicus'	0.45	0.43	0.50	0.07	0.23	-0.09	-0.36	-0.12	-0.14	-0.47	0.53	0.41	-0.70	-0.35	0.53	-0.56	-0.19	-0.20	-0.36	-0.20	-0.32	-0.41
	C. helgolandicus'	0.76	0.71	0.71	0.41	0.51	0.25	0.03	0.13	0.34	0.07	0.75	0.77	0.12	0.32	0.75	0.22	0.18	0.14	0.19	0.20	0.08	0.08
	C. longipes'	0.86	0.87	0.81	0.16	0.43	-0.11	-0.02	-0.03	0.05	0.03	0.53	0.49	-0.34	-0.43	0.53	-0.12	0.09	-0.39	0.06	0.07	0.01	-0.57
	Decapod'	0.67	0.68	0.66	0.87	0.90	0.88	0.86	0.88	0.92	0.85	0.76	0.76	0.86	0.89	0.73	0.88	0.92	0.76	0.89	0.88	0.85	0.73
	Echinoderm'	0.72	0.72	0.70	0.56	0.69	0.58	0.55	0.57	0.58	0.58	0.54	0.54	0.68	0.60	0.54	0.65	0.76	0.72	0.75	0.77	0.77	0.68
	'Holoplankton'	0.73	0.71	0.76	0.21	0.59	0.06	-0.07	0.01	0.10	-0.04	0.75	0.74	0.09	-0.06	0.74	-0.08	-0.03	0.28	-0.30	-0.15	-0.32	0.13
	'Meroplankton'	0.52	0.59	0.53	0.85	0.90	0.87	0.83	0.86	0.89	0.82	0.73	0.75	0.82	0.88	0.74	0.86	0.90	0.72	0.87	0.89	0.88	0.67
	O. Sinensis'	-0.83	-0.62	-0.47	-0.08	-0.03	-0.19	-0.19	-0.17	-0.23	-0.15	NaN	NaN	0.02	-0.24	NaN	-0.22	-0.18	0.14	-0.14	-0.13	-0.09	0.20
	'PCI'	0.48	0.47	0.46	0.68	0.73	0.44	0.44	0.43	0.42	0.31	0.53	0.36	0.44	0.03	0.51	0.02	0.08	0.82	0.42	0.14	0.31	0.79
	P. sulcata'	-0.02	-0.20	-0.04	-0.03	-0.16	-0.07	-0.12	-0.10	-0.03	-0.07	-0.65	-0.64	-0.05	0.02	-0.65	-0.44	-0.36	0.38	-0.40	-0.14	-0.14	0.30
Wind Curl	C. finmarchicus'	-0.62	-0.59	-0.57	0.08	0.08	-0.14	-0.19	-0.01	0.12	-0.06	0.16	0.17	0.01	-0.04	0.47	0.09	NaN	0.01	-0.24	NaN	NaN	0.51
	C. helgolandicus'	-0.07	-0.13	-0.01	-0.12	0.00	-0.11	-0.23	-0.23	-0.17	-0.31	0.22	0.22	-0.31	-0.33	0.41	-0.34	NaN	-0.32	0.09	NaN	NaN	-0.44
	C. longipes'	0.04	0.00	0.15	0.13	0.16	-0.11	-0.09	-0.20	-0.16	-0.24	0.27	0.24	-0.15	-0.31	0.08	-0.20	NaN	-0.43	0.50	NaN	NaN	-0.13
	Decapod'	-0.58	-0.55	-0.46	0.27	0.19	0.26	0.07	0.06	0.05	0.06	0.18	0.20	0.08	-0.02	0.38	0.06	NaN	0.03	-0.47	NaN	NaN	0.06
	Echinoderm'	-0.70	-0.66	-0.57	0.29	0.20	0.31	0.16	0.23	0.21	0.20	0.02	-0.01	0.16	0.24	0.31	0.18	NaN	0.08	-0.77	NaN	NaN	0.09
	'Holoplankton'	-0.34	-0.39	-0.28	-0.29	-0.08	-0.43	-0.44	-0.41	-0.25	-0.40	0.24	0.26	-0.42	-0.48	0.41	-0.37	NaN	-0.34	0.17	NaN	NaN	-0.52
	'Meroplankton'	-0.68	-0.63	-0.60	0.27	0.22	0.26	0.10	0.08	0.08	0.07	0.17	0.08	0.08	0.02	0.41	0.05	NaN	0.12	-0.52	NaN	NaN	0.11
	O. Sinensis'	-0.28	-0.21	-0.18	0.51	0.00	0.24	-0.09	-0.10	-0.40	-0.06	NaN	NaN	-0.29	-0.25	NaN	-0.44	NaN	-0.33	0.44	NaN	NaN	-0.29
	'PCI'	-0.75	-0.68	-0.58	0.25	-0.02	0.27	0.25	0.20	-0.13	-0.15	0.20	0.12	0.15	-0.16	0.48	-0.12	NaN	-0.04	-0.30	NaN	NaN	0.15
	P. sulcata'	0.00	0.28	-0.07	0.03	0.00	0.20	0.00	0.00	-0.09	0.24	-0.08	-0.06	0.16	0.23	-0.18	0.01	NaN	-0.11	0.38	NaN	NaN	-0.12
Wind Zonal	C. finmarchicus'	-0.59	-0.60	-0.38	-0.40	-0.45	-0.31	-0.09	-0.15	-0.24	-0.08	-0.04	-0.24	-0.11	-0.12	0.21	-0.28	-0.08	-0.29	-0.27	0.05	0.00	-0.55
	C. helgolandicus'	-0.03	-0.07	0.05	0.45	0.34	0.44	0.48	0.46	0.44	0.51	0.12	0.07	0.50	0.59	0.21	0.53	0.51	0.46	0.37	0.30	0.22	0.35
	C. longipes'	0.07	-0.02	0.10	0.34	0.36	0.36	0.34	0.42	0.39	0.30	0.21	0.13	0.13	0.20	0.14	0.23	0.30	0.22	0.29	0.11	0.02	-0.03
	Decapod'	-0.46	-0.44	-0.21	-0.17	-0.08	-0.11	-0.13	-0.06	-0.01	0.07	-0.04	-0.12	0.02	0.19	0.06	0.15	0.26	0.02	0.16	0.38	0.33	-0.06
	Echinoderm'	-0.59	-0.58	-0.39	-0.47	-0.36	-0.43	-0.40	-0.40	-0.40	-0.21	-0.23	-0.32	-0.17	-0.17	-0.01	-0.10	-0.10	-0.07	-0.03	0.23	0.25	-0.11
	'Holoplankton'	-0.30	-0.37	-0.18	0.45	0.11	0.60	0.64	0.56	0.47	0.55	0.15	-0.02	0.55	0.52	0.25	0.48	0.38	0.51	0.29	0.27	0.00	0.50
	'Meroplankton'	-0.59	-0.55	-0.38	-0.19	-0.14	-0.11	-0.17	-0.08	-0.08	0.04	-0.07	-0.13	0.02	0.16	0.16	0.15	0.23	-0.11	0.09	0.38	0.36	-0.11
	O. Sinensis'	-0.32	-0.14	-0.15	-0.34	0.00	-0.20	0.26	0.21	0.42	0.14	NaN	NaN	0.43	0.15	NaN	0.42	0.43	0.50	0.42	0.20	0.15	0.35
	'PCI'	-0.71	-0.67	-0.42	-0.42	0.08	-0.44	-0.54	-0.36	0.13	-0.06	-0.18	-0.33	-0.28	0.00	0.08	0.11	0.22	0.00	0.32	0.39	0.31	-0.07
	P. sulcata'	0.00	0.36	0.00	0.04	0.03	0.01	0.11	0.11	0.06	-0.09	0.08	0.13	-0.14	-0.17	0.07	-0.19	0.16	0.09	0.03	0.05	0.17	0.21
Wind Merional	C. finmarchicus'	-0.68	-0.64	-0.73	-0.52	-0.72	-0.48	-0.31	-0.38	-0.54	-0.24	-0.73	-0.74	-0.01	-0.31	-0.74	-0.20	-0.47	-0.34	-0.49	-0.45	-0.41	-0.40
	C. helgolandicus'	-0.28	-0.29	-0.18	0.35	0.07	0.42	0.59	0.50	0.27	0.56	-0.39	-0.42	0.61	0.30	-0.51	0.52	0.31	0.49	0.31	0.30	0.46	0.38
	C. longipes'	-0.17	-0.21	-0.06	0.48	0.39	0.59	0.63	0.57	0.46	0.54	0.06	0.10	0.39	0.67	0.13	0.55	0.58	0.49	0.64	0.66	0.72	0.11
	Decapod'	-0.80	-0.80	-0.78	-0.55	-0.59	-0.56	-0.54	-0.55	-0.56	-0.57	-0.60	-0.68	-0.63	-0.56	-0.65	-0.59	-0.41	-0.70	-0.48	-0.42	-0.41	-0.67
	Echinoderm'	-0.84	-0.84	-0.79	-0.76	-0.80	-0.86	-0.80	-0.84	-0.88	-0.80	-0.77	-0.79	-0.76	-0.85	-0.77	-0.82	-0.77	-0.80	-0.79	-0.75	-0.78	-0.75
	'Holoplankton'	-0.41	-0.48	-0.46	0.41	-0.19	0.57	0.80	0.63	0.30	0.71	-0.48	-0.57	0.75	0.54	-0.55	0.65	0.28	0.52	0.31	0.42	0.43	0.70
	'Meroplankton'	-0.83	-0.83	-0.82	-0.55	-0.63	-0.57	-0.58	-0.59	-0.62	-0.60	-0.62	-0.61	-0.68	-0.63	-0.52	-0.64	-0.41	-0.74	-0.48	-0.42	-0.46	-0.70
	O. Sinensis'	0.00	0.00	0.00	0.13	-0.09	0.29	0.63	0.59	0.65	0.67	NaN	NaN	0.61	0.52	NaN	0.63	0.74	0.73	0.83	0.77	0.81	0.68
	'PCI'	-0.86	-0.86	-0.80	-0.57	-0.22	-0.66	-0.63	-0.67	-0.06	-0.40	-0.82	-0.82	-0.71	0.00	-0.81	0.00	0.27	-0.65	0.28	0.29	0.15	-0.70
	P. sulcata'	0.00	0.24	0.00	0.00	0.25	0.13	0.08	0.09	0.24	0.12	0.34	0.33	0.00	0.00	0.35	0.24	0.58	0.02	0.63	0.56	0.69	0.24

Discussion

Theoretically, one potential impact of man-made structures on planktonic communities might have been that the increase in surface area of MMS could have resulted in an increase in surface dwelling organisms (e.g. bivalves, echinoderms, etc.). This phenomenon could have, in turn, changed the dynamic of the species constituting the meroplankton community. It is well know that large scales patterns in plankton, being in time or space, are in majority driven by the physical environment. Hence, if any impact of MMS could be detected, this signal would be buried among the prevailing signals driven by environmental parameters such as sea surface temperature or both wind direction and intensity. This is why this project aimed at disentangle those signals at different scales. However, this studies shows that when a change of plankton dynamic, either a long-term or a seasonal one, is found it is most of the time correlated by a change in the dynamic of the sea surface temperature and/or the wind patterns. Those results indicate that, if oil and gas platforms have an impact on plankton, this impact is marginal at the selected spatio- temporal scales (local to regional, month to decade). Even in areas (i.e. pixels) “colonised” by a huge amount of structures, the plankton dynamic can most of the time be explain by the environment. Furthermore, when biological patterns cannot be explain by the SST or the wind, we cannot detect any clear link with neither the presence nor the quantity of MMS.

Dealing with the biology constitutes a challenge by itself. Plankton in particular are known to exhibit a large quantity of different patterns, driven by an equally large number of causes. Even if they seem primitive and simple, those micro-organisms are surprisingly complex in their behaviours. To make things even more difficult, one dealing with plankton has inevitably to deal with the patchiness associated with it. An observer at sea could take a glass of water, analyse its content, only to find a totally different results when taking another sample at the same place few seconds after. On top of all this, any sampling method has uncertainties that can bring “noise” to the results. This is why we choose to work on gridded products that allow us to combine several samples in order to increase the robustness of our data. This is also why we choose to rule out any location that had incomplete timeseries. Again, it is because SAHFOS as such an extensive database that we were able to aim for such a conservative approach.

SAHFOS is fairly unique in the world due to its extensive database. To be able to afford such a sampling coverage, it is impossible to use research vessels that would go sampling where we want, when we want. Instead, we have to rely on ships of opportunities, mostly merchant ships, which travel from a port to another to deliver passengers and/or goods. This implies that the prime goal of those ships is to safely arrive on time to their destination and to stay away from any danger; among which we can count oil and gas platforms. If this study demonstrates that we cannot clearly identify any impact of MMS on plankton community, this conclusion is valid only at the spatio-temporal scales considered. We do not know what is happening at the scale of the minutes or the hour, few meters from the pillar of a platform. The project has come a long way to fulfil its objectives, but has also revealed challenges. One of them is a serious lack of relevant biological data in the platforms vicinity. Despite that SAHFOS was able to provide extensive data on relevant species, the scale at which those data were collected do not fit correctly with the scales at which known potential physico-chemical effects of the MMS should occur. (e.g. water flow (Wilding, 2014), organic build-up (Davis et al., 1982) or produced waters (Bakke et al., 2013)). Finding a way to monitor the possible effects of MMS cost-effectively, and how such effects will impact MMS management will be dealt with in INSITE Phase 2, the Data Acquisition and Enhancement Phase, starting in 2018.

Conclusions & Recommendations

This study demonstrates that we cannot clearly identify any impact of MMS on plankton community at the spatio-temporal scales considered. It therefore provides stakeholders with a new scientific evidence base needed to better understand the influence of man-made structures on the ecosystem of the North Sea.

The SIGNAL project has come a long way to fulfil its objectives, but has also revealed challenges. For instance, the SIGNAL project only dealt with oil & gas platforms, while a lot of other man-made structures could have been used. There are a number of databases that could be useful but we need local and wider operator data. We need to establish quality controlled systems and protocols to enable the storage and the sharing of data. Also, the SIGNAL project treated man-made structures as physical entities, not considering their activities such as the presence of discharged water. Finally, cumulative negative impacts on the ecosystem were beyond the scope of this programme. However, the presence and/or quantity of MMS could mitigate or enhance the effects of natural parameters, in the same way the effects of overfishing synergised with climate change to impact the fish stocks (Beaugrand et al., 2003)

All these limitations, as well as other issues such as how to monitor the possible effects of MMS cost-effectively, should be dealt with in INSITE Phase 2, the Data Acquisition and Enhancement Phase, starting in 2018.

Outreach & Products

The SIGNAL project has been presented as a poster during the last Annual Science Conference (ASC) of the International Council for the Exploration of the Sea (ICES) in Florida (18-21 September 2017, Fort Lauderdale, Florida, USA).

The MMS database built during this project was circulated among all projects within the INSITE programme.

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