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Generalized changes of benthic communities after construction of wind farms in the southern North Sea

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ABSTRACT

Over the last years, the development of offshore renewable energy installations such as offshore wind farms led to an increasing number of man-made structures in marine environments. Since 2009, benthic impact monitoring programs were carried out in wind farms installed in the southern North Sea. We collated and analyzed data sets from three major monitoring programs. Our analysis considered a total of 2849 sampling points converted to a set of biodiversity response metrics. We analyzed biodiversity changes related to the implementation of offshore wind farms and generalized the correlation of these changes with spatial and temporal patterns. Our results demonstrate that depth, season and distance to structure (soft-bottom community) consistently determined diversity indicators and abundance parameters, whereas the age and the country affiliation were significantly related to some but not all indices. The water depth was the most important structuring factor for fouling communities while seasonal effects were driving most of the observed changes in soft-sediment communities. We demonstrate that a meta-analysis can provide an improved level of understanding of ecological patterns on large-scale effects of anthropogenic structures on marine biodiversity, which were not visible in single monitoring studies. We believe that meta-analyses should become an indispensable tool for management of offshore wind farm effects in the future, particularly in the view of the foreseen development of offshore renewable energies. This might lead to a better picture and more comprehensive view on potential alterations. However, this requires a modern open-source data policy and data management, across institutions and across national borders.

1. Introduction

Ocean sprawl, the expansion of man-made structures into ocean space, has increased strongly in European waters in the last decade (Birchenough and Degraer, 2020; Firth et al., 2016). In particular the development of offshore renewable energy installations such as offshore wind farms led to an increasing number of man-made structures in the marine environment. At the end of 2020, offshore wind facilities installed in European waters were generating a total capacity of 25 Gigawatt (GW; Wind Europe, 2021), which, assuming 6 MW per turbine, amounts to >4000 turbines. Long-term outlooks for the North Sea alone predict an installed capacity of 111 GW by 2030 (Wind Europe, 2021; ~14,000 8 MW turbines) and a total of up to 25,000 wind turbines are expected to be present in the southern North Sea by 2050, supporting the achievement of the current energy commitments and targets agreed across EU waters (de Vrees, 2019). This large-scale introduction of man-made structures (MMS hereafter) will have direct ecological consequences for the ecology and communities present at and around the MMS, the sum of which could cascade to large-scale environmental effects, especially for the communities living on the seafloor (Dannheim et al., 2020).

Offshore natural hard substrates in the North Sea (such as gravel and boulder fields) are generally restricted to low altitudes on the seafloor (Veenstra, 1969). In contrast, many artificial hard structures extend

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throughout the entire water column and connect the seafloor with the intertidal zone. These vertical hard substrates in offshore waters form a habitat type that was naturally absent in the southern North Sea and provide potential habitat to species that were formerly restricted to the rocky coasts of the English Channel and the northern North Sea (De Mesel et al., 2015). Indeed, any kind of underwater hard structure in the North Sea, man-made or natural, is quickly colonized by hard substrate fouling communities (Degraer et al., 2020; Forteath et al., 1982). This may lead to organic matter enrichment in the surrounding soft bottoms through added faeces production and sedimentation which, in turn, can affect community composition in and on the surrounding seabeds (Coates et al., 2014). Furthermore, the presence of the structure may alter the local hydrodynamic environment which can further impact the local seabed communities (Baeye and Fettweis, 2015; Klunder et al., 2018). Exclusion of bottom fisheries can further alter the communities in the direct vicinity of the structures (Bergman et al., 2015). This structure-induced local biodiversity change, associated with a biomass increase, may induce changes in ecosystem functioning. The modified local community is likely to present an altered trophic organization (e.g. more suspension-feeders on the hard substrate) and attract mobile higher-level predators, such as predatory fish that were originally not present in the area (Krone et al., 2013a; Mavraki et al., 2021). Consequently, the presence of such structures has been shown to alter ecosystem processes related to the community-relative trophic composition (Cresson et al., 2014) and the energy flow throughout the local food web (Raoux et al., 2017). This can lead to a modification of secondary production support for higher trophic levels of commercial interest also known as the 'artificial reef effect' (Dannheim et al., 2020).

In order to detect possible changes in the seabed communities and to capture colonization patterns of communities on the MMS, benthic impact monitoring programs were initiated in several wind farms installed in the southern North Sea, with the first in Denmark in 2002 (Leonhard and Christensen, 2006). Analogous programs were also conducted in Belgium, the Netherlands and Germany (De Mesel et al., 2015; Gutow et al., 2014; Lindeboom et al., 2011). Although the methodology varied between these programs, seabed infauna was generally included by collecting grab or core samples at various distances from the structures at various temporal scales (Bergman et al., 2015; Gutow et al., 2014; Leewis et al., 2018; Vandendriessche et al., 2014). Additionally, scrape samples were collected at various depths on the wind turbine foundations and on the surrounding scour protection to sample fouling organisms (Bouma and Lengkeek, 2013; Coolen et al., 2020a; De Mesel et al., 2015; Gutow et al., 2014; Krone et al., 2013b). Since most of the analyses are restricted to describing local patterns (within the wind farm), and given the high natural variation in North Sea macrofaunal communities (Kröncke and Reiss, 2010; Reiss et al., 2006) any generalization from the results obtained at a local scale is challenging.

Meta-analyses are a powerful tool to detect effects on the ecology by combining local results of various studies (Stewart, 2010). This has been demonstrated in many studies on different biological aspects such as trophic interactions (Worm and Myers, 2003; Marczak et al., 2007) and experiments, i.e. combining outcomes of different setups or species (see e.g. Wittmann and Pörtner, 2013; Gurevitch et al., 1992). Considering the development of renewable energies in the North Sea, there is a need for higher level interpretation to identify appropriate temporal and spatial scales to guide future monitoring studies on the effect of hard MMS on soft bottom seabed structures (Dannheim et al., 2020; Wilding et al., 2017). It is important to understand which environmental variables (both natural and anthropogenic) drive macrofauna diversity patterns and to which extent. This level of knowledge is crucial for an improved management of renewable energy development, i.e. to increase positive effects and reduce negative effects that may emerge from the large-scale installation of renewable energy resources in the North Sea. Here, we collated and analyzed existing data sets from three (3) national benthic macrofauna monitoring programs in European offshore wind farms. Our analysis considered a total of 2849 sampling points converted to a set of biodiversity response metrics. We analyzed biodiversity changes related to the implementation of offshore wind farms and generalized the correlation of these changes with spatial and temporal patterns.

2. Material & methods

2.1. Data compilation

We created an integrated database containing data (i) on fouling fauna on turbine foundations and scour protection layers and (ii) on soft sediment infauna. Artificial hard substrate samples were collected by scientific divers whereas infauna samples were taken by grabs and corers in the vicinity of wind turbines within offshore wind farms. The datasets covered the southern North Sea, originating from monitoring and research studies in Belgium, Germany and the Netherlands (Fig. 1; Tables 1 and 2). A metadata template was created to capture biological and environmental information from the different datasets (Supplementary information S1). Where not available, distances to the nearest structure and sampling depths were estimated in ArcGIS (ver 10.3.1; www.esri.com/arcgis). All infauna data was taxonomically matched against the World Register of Marine Species (WoRMS Editorial Board, 2017) and harmonized among the project sub-datasets to the lowest possible taxonomic level. All information was screened for abnormalities (extreme values and missing data) and datasets were excluded if necessary. The resulting selection of datasets/samples is summarized in Table 1.

Data points that were located >10,000 m from a structure were excluded as only a single year in a single dataset was available. All fouling samples had been collected using the same method, so gear type was not included as a predictor in any analysis on fouling data.

Unsurprisingly, there was some difference across datasets: 53% of seabed samples were taken in autumn and 8% in summer. 65% of the seabed samples were obtained in German wind farms and only 7% from the Netherlands. By far, the most samples were taken at <50 m from the structure (Fig. 2). For the fouling data, again most data originated from German locations, but - except for winter months - the frequency of samples per season was more even. Furthermore, most samples were taken in depths <15 m, and were repeated at specific depths (Fig. 3). All data had been collected in the period between the years 2003 and 2012.

2.2. Analyses

Different community descriptors were calculated for each record: taxonomic richness (S sample^{-1}), Simpson diversity index (d sample^{-1}), Shannon diversity index (H sample^{-1}), evenness (J sample^{-1}) and total abundance (N sample^{-1}). Since sampled area varied between records, richness was calculated by rarefaction of all records within the fouling and seabed datasets using the rarefy function of the vegan package (Oksanen et al., 2019), based on the abundance within each sample, corrected for the sample size, *i.e.* rarefying each sample to the smallest area in each dataset (0.078 m^2 for seabed and 0.01 m^2 for fouling data). The abundance per sample was scaled down to these same smallest sample sizes as well. There were four (4) samples for which these indices could not be calculated (i.e. only one species in the sample; 3 fouling samples and 1 seabed sample), were excluded from further analysis. Each sample was assigned to a sampling season. The obtained data were screened again and checked for consistency and completeness of all predictor variables in the respective datasets (Table 3). The final selection of data to be included in analysis included 677 fouling samples and 2172 seabed samples. For data analysis, R version 3.6.1 (R Core Team, 2019) and RStudio version 1.2.5001 (RStudio, 2019) were used.

The selected data were then explored using the protocol by Zuur et al. (2010). The presence of outliers, multicollinearity, and relations between response variables and environmental variables was assessed

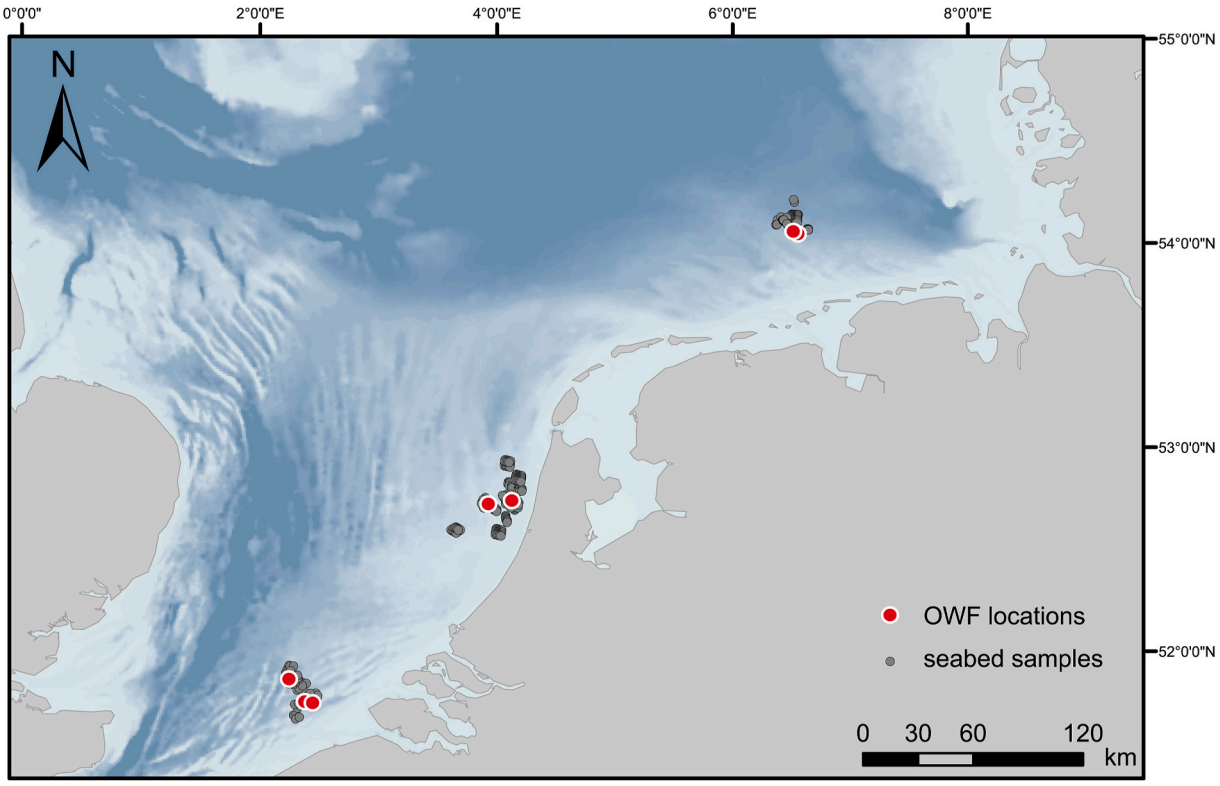


Fig. 1. Data locations. Positions of all data points with seabed sample stations indicated as grey dots and fouling sample stations as red dots. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

Table 1
Overview of the different collated datasets available for the meta-analysis. Number of samples indicate the total number of samples available after cleaning.

Country	Wind farm	Seabed samples	Fouling samples	Source
NL	Egmond aan Zee	49	0	Bergman et al. (2015); Bouma and Lengkeek (2013)
NL	Prinses Amalia	105	92	Coolen et al. (2020a); Leewis et al. (2018); Vanagt and Faasse (2014)
BE	Belwind	357	37	De Mesel et al. (2015); Vandendriessche et al. (2014)
BE	C-Power	231	96	Degraer et al. (2018)
GE	Alpha Ventus	952	234	Gutow et al. (2014)
GE	FINO1 (platform)	478	218	Krone et al. (2013b), Schröder et al. (2013)
Total		2172	677	

using boxplots, Cleveland dotplots (Cleveland, 1985), pairplots, Pearson correlation coefficients, variance inflation factors, and multi-panel scatterplots from the lattice package (Sarkar, 2008).

We tested for functional correlations by applying general additive models (GAMs) in order to assess the influence of the predictors on the calculated response variables. Models were created for each of the five biodiversity metrics from (1) fouling community data and (2) seabed community data, resulting in a total of 10 models (Table 3). The descriptor 'gear type' was excluded from seabed data because of a strong collinearity with country (box corer samples were taken in the Netherlands and van Veen samples in Germany and Belgium). Since samples taken around a specific turbine were considered to be not independent, the turbine ID was included in the models as a random effect.

Models were built using the "gam" function of the "mgcv" package (Wood, 2006). As the relation between diversity metrics and environmental variables can be non-linear, e.g. with maximum richness at intermediate depths (Coolen et al., 2020a), all continuous environmental variables were included in the models as smoothed terms. The maximum number of knots per term was set to three to reduce model complexity (Coolen et al., 2020a). The effective degrees of freedom from the resulting models were used to assess the level of non-linearity (1 = linear, 2 = maximum smoothed) of each variable.

Model structure for the fouling community data:

$$\mathrm{DivMetric}_{ij} = \alpha + f(\mathrm{depth}_{ij}) + f(\mathrm{age}_{ij}) + \beta_1.\mathrm{season}_{ij} + \beta_2.\mathrm{country}_{ij} + \mathrm{turbine}_i + \varepsilon_{ij}$$

$\mathrm{DivMetric}_{ij}$ is the diversity metric of choice for sample j within

Table 2
Meta data per wind farm, with the seabed depth range (m), dominant habitat types, area sampled (m^2) from the seabed and from the turbine foundation.

Wind farm	Seabed depth	Habitat type	Sampled area seabed	Sampled area turbine
Egmond aan Zee	12–20	Circalittoral sand	0.078	0.056
Prinses Amalia	17–23	Circalittoral sand	0.078	0.056
Belwind	22–31	Circalittoral sand	0.1	0.0625
C-Power	20–29	Circalittoral sand & Circalittoral coarse sediment	0.1	0.0625
Alpha Ventus	28–34	Circalittoral sand	0.1	0.01 and 0.04
FINO1 (platform)	29–33	Circalittoral sand	0.1	0.04

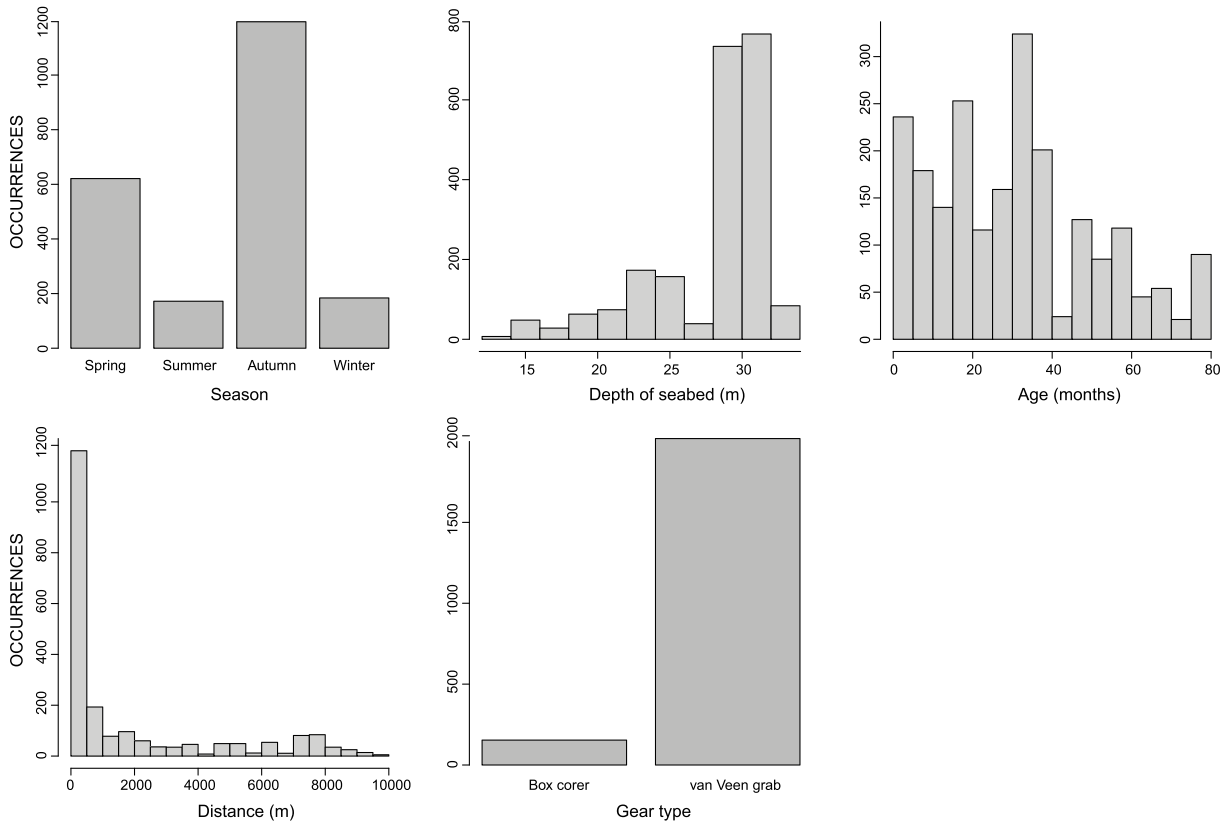


Fig. 2. Data summary seabed. Number of occurrences of variables in data on seabed samples, with top left to bottom right: Season in which the sample was acquired, seabed depth from which the sample was acquired, age of the nearest installation at date of sampling, distance from the nearest installation, gear type used to collect the sample.

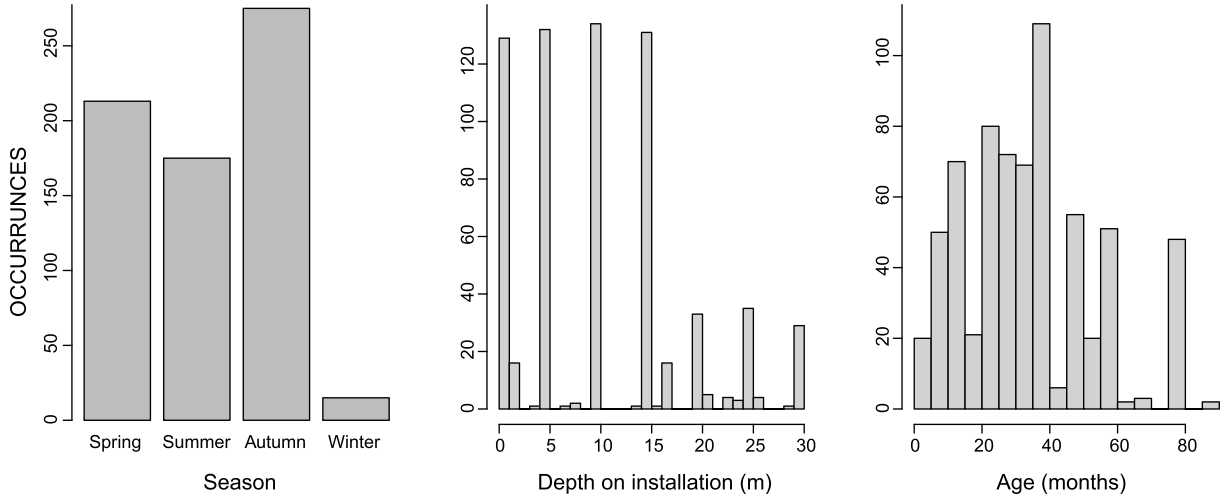


Fig. 3. Data summary fouling. Number of occurrences of variables in data on fouling samples, with left to right: season in which the sample was acquired, depth on the installation from which the sample was taken and age of the installation at date of sampling.

turbine *i*. Smoothing functions are delineated with f(). The residuals ε_{ij} were assumed to be normally distributed with a mean of 0 and variance of σ.

Model structure for the seabed community data:

$$\text{DivMetric}_{ij} = \alpha + f(\text{depth}_{ij}) + f(\text{age}_{ij}) + \beta_1.\text{season}_{ij} + \beta_2.\text{country}_{ij} + f(\text{distance}_{ij}) + \text{turbine}_i + \varepsilon_{ij}$$

Both model structures are similar with the exception of the inclusion of distance to structure for the seabed community data. For each model, the residuals were plotted against the fitted values and visually inspected to confirm the assumptions of homogeneity of variance and normality. Furthermore, residuals were plotted against all variables in and outside the model as well as fitted values to assess model fit. The variance inflation factor was <3 for all variables in all models, therefore collinearity was not an issue for the regarded predictors (Zuur et al., 2010). Model results, the relation between each predictor variable and each response variable, were predicted by using the predict.gam function, while keeping all other predictor variables at a fixed value. The

Table 3
Details of the 10 GAMs to analyze biodiversity indices relations of fouling and seabed data, with model ID, response metric of the model, distribution name with link (log or logit), depth (meters seawater), age (months since construction), season, country (name of country in which the wind farm was based), gear type (box corer or van Veen) and distance (meters from the nearest structure). ✓ indicates inclusion in the model, - indicates exclusion.

Model ID	Data type	Response metric	distribution	link	Predictor variable				
					Depth	Age	Season	Country	Distance
FS	Fouling	Richness (S sample^{-1})	quasiPoisson	log	✓	✓	✓	✓	–
FD	Fouling	Simpson (d sample^{-1})	beta	logit	✓	✓	✓	✓	–
FH	Fouling	Shannon (H sample$^{-1)}$	Gaussian	log	✓	✓	✓	✓	–
FJ	Fouling	Evenness (J sample$^{-1)}$	beta	logit	✓	✓	✓	✓	–
FN	Fouling	Abundance (N sample^{-1})	quasiPoisson	log	✓	✓	✓	✓	–
SS	Seabed	Richness (S sample^{-1})	quasiPoisson	log	✓	✓	✓	✓	✓
SD	Seabed	Simpson (d sample^{-1})	beta	logit	✓	✓	✓	✓	✓
SH	Seabed	Shannon (H sample$^{-1)}$	Gaussian	log	✓	✓	✓	✓	✓
SJ	Seabed	Evenness (J sample$^{-1)}$	beta	logit	✓	✓	✓	✓	✓
SN	Seabed	Abundance (N sample^{-1})	quasiPoisson	log	✓	✓	✓	✓	✓

fixed values were the average depth, age and distance, and the most frequent value for season (autumn) and country (Germany).

3. Results

3.1. Fouling communities

The fouling samples had been collected between 3 and 90 months after installation of the turbine and sampling depth varied between 0 and 30 m. Taxonomic richness varied between 1 and 21 taxa per sample (Table 4). The maximum abundance found was 2.4×10^6 ind. m^{-2}, mostly composed of the amphipod *Jassa herdmani*. The common mussel *Mytilus edulis* was the dominant species in 0–5 m depth, followed by *J. herdmani* in 5–15 m, after which the plumose anemone *Metridium senile* was dominant up to the seabed. These species patterns were similar between wind farms and had been reported extensively for the separate datasets (see references in Table 1) and are therefore not treated further here.

The GAMs explained between 26 and 44% of the variation in the five different response variables (Table 5). Deviance explained varied strongly between different independent variables in the models. The country explained less than 0.1% in all models, while season explained between 2 and 27%. Highest deviance explained was found for the relations between depth and Simpson diversity (25%) as well as between season and richness (27%).

Most of the regarded variables had a significant ($p < 0.05$) influence on biodiversity metrics. The descriptors 'depth' and 'season' were significant for all 5 responses, whereas the descriptor 'age' was only significant for richness, Simpson diversity and abundance. The effective degrees of freedom indicated a non-linear relation (e.d.f > 1.0) between depth and all diversity indices excluding richness and for age with richness, Simpson diversity and Abundance, but not with Shannon diversity and Evenness (Fig. 4). All indices increased with age, with the steepest slopes in richness and Simpson diversity in the first 50 months after construction, after which it levels off (Simpson) or becomes slightly negative (richness). It should, however, be noted that standard errors increase strongly with later ages and a positive slope remains within their range.

The seasonal effect showed the highest richness and abundance in summer and lowest in winter time. The German samples held the highest abundance per sample but the lowest richness, while samples from Belgium held the lowest value for abundance, and highest for richness (Table 6).

Table 4
Sample statistics of the data used as response and predictor variables in the five fouling community models. Columns: minimum, maximum, average and standard deviation of the continuous data used in model calculations. Rows: model variables, with depth (m seawater), age (months after construction), Richness (S sample^{-1}, rarified to a sampled area of 0.01 m^2), Simpson diversity index (d sample^{-1}), Shannon diversity index (H sample^{-1}), evenness (J sample^{-1}) and abundance (N sample^{-1} of 0.01 m^2).

	Minimum	Maximum	Average	Standard Deviation
Depth (m)	0	30.00	10.69	8.14
Age (months)	3	90	34.06	19.44
Richness (S sample^{-1})	1	21	7.31	3.89
Simpson (d sample^{-1})	0	0.91	0.31	0.22
Shannon (H sample$^{-1)}$	0	2.78	0.65	0.46
Evenness (J sample$^{-1)}$	0	1	0.28	0.19
Abundance (N sample^{-1})	1	24,146	1366	2220

3.2. Seabed communities

All available samples had been collected between 1 and 78 months after installation of the nearest turbine and sampling depth varied between 12.5 and 34 m. Distance from the nearest structure ranged between 1 and 9761 m. Rarefied taxonomic richness varied between 1.67 and 59 taxa per sample (Table 7). The highest abundances were found in the polychaetes *Spiophanes bombyx* (up to 25,588 ind m^{-2}) and *Owenia fusiformis* (up to 12,840 ind m^{-2}) as well as in Horseshoe worms of the genus *Phoronis* (up to 45,670 ind m^{-2}).

The GAMs explained between 15 and 59% of the variation in the five different response variables (Table 8). Similar to fouling community models, the response variables for seabed communities varied strongly in their amount of deviance explained. As found for the fouling communities, country affiliation explained no more than 0.1% variation in all models. Highest deviance explained was found for the relations between season and richness (52%), season and abundance (40%) and season and evenness (24%). Deviance of the Shannon diversity was explained best by season of sampling (11%) and age of the community (9%). The predictor variables depth, season and distance were significant for all five response variables, age was significant for all but abundance and country was significant for all but the Simpson diversity. Relations between depth and Simpson and Shannon diversity, as well as between age and abundance and distance with richness were modelled as strictly linear (effective degrees of freedom = 1.0). All other variables had a non-linear relation with at least 1.88 degrees of freedom.

The seasonal effect was strong, with highest richness and abundance in summer and lowest in winter time (Fig. 5). The German samples held both the highest values for abundance and richness per sample; lowest values were recorded for Belgian samples for both of these response variables (Table 9).

Table 5
Summary statistics of all model components for the five models created for fouling communities, with columns for p-value (P, <0.001 = ***; <0.01 = **; <0.05 = *; non-significant = n.s.), effective degrees of freedom (edf) and % deviance explained (DE), rows for sampling depth (m seawater), age (months since construction of wind farm), temperature (°C at water surface), longitude (° east), total deviance explained for the model and adjusted R^2 for the model. N samples = 675. Richness was rarified and abundance scaled down to a sampled area of 0.01 m^2.

	Richness			Simpson Index			Shannon Index			Evenness			Abundance		
	P	edf	DE	P	edf	DE	P	edf	DE	P	edf	DE	P	edf	DE
Depth	*	1.00	1.9%	***	1.99	25%	***	1.98	18%	***	1.99	18%	***	1.95	26%
Age	***	1.98	15%	**	1.87	7.6%	n.s.	1.00	0.4%	n.s.	1.00	1.0%	***	1.97	14%
Season	***	–	27%	**	–	2.4%	***	–	7.9%	***	–	7.4%	***	–	14%
Country	**	–	<0.1%	***	–	0.3%	***	–	0.4%	**	–	0.1%	n.s.	–	0.1%
Total DE			44%			35%			26%			26%			43%
Total R^2			0.44			0.17			0.24			0.14			0.33

4. Discussion

4.1. Biological patterns

Knowledge on benthic responses to the introduction of MMS in the North Sea environment is crucial for monitoring and management of these systems (Lindeboom et al., 2011). To our knowledge, this is the first time that a study of this nature has been conducted to explore general patterns of change of natural benthic communities associated with the installation of offshore wind farms over soft sediment areas. Our study explored the use of ten (10) models parameterized from a unique combination of fouling (hard substrate) and surrounding soft-bottom communities. Our results demonstrated that the predictor variables, such as depth and season (and distance to structure for soft-bottom community) consistently determined diversity indicators and abundance parameters, whereas the age and the country affiliation were significantly related to some but not all indices. Our analysis revealed that water depth was the most important structuring factor for fouling communities and seasonal effects were driving most of the observed change for soft-sediment communities.

4.1.1. Fouling communities

Depth explained up to 25% of the variation in diversity and 26% of abundance. Shallower depth zones showed the largest abundance and were dominated by mussels and amphipods (*Jassa herdmani*). This pattern of colonization has been consistently observed across other offshore wind farms (Degraer et al., 2020). These observed taxa are characterized by a filter feeding strategy and most likely benefit from high food availability (i.e. plankton and detritus) in the upper light penetration zone (Slavik et al., 2019; De Mesel et al., 2015). The lower diversity and evenness in intermediate depths are likely caused by the large abundances of amphipods, with *Jassa herdmani* reaching densities $>10^6$ per m^2 while other species showed much lower densities. The presence of structure forming hydrozoans in this depth zone has been suggested to increase richness (Coolen et al., 2020a). Our analysis showed that age was not significantly related to the Shannon diversity index. Connell and Slatyer (1977) postulated four types of expected successional colonization, categorized depending on the species presence and interactions. Our results suggest that there is an 'inhibitory response' based on this model, in which early colonizers occupy most of the resources, occupying all available spatial resources and which may consume arriving larvae of other taxa, thus preventing other species from establishment on the structure. However, species such as *Mytilus edulis* are also known to provide secondary hard substrates and could be considered as a keystone species, increasing habitat availability, also increasing richness (Coolen et al., 2020a). This would be in contrast to the inhibition model. In an environment with constant disturbance, these combined effects may lead to the observed 'pseudo-equilibrium' in shallower depth zones where losses are quickly compensated by recolonization (via short- and long-distance dispersal) by the predominant species. This would strongly depend on seasonal patterns as observed in our study – season had a clear effect on richness, Shannon diversity and abundance, all of which were highest in summer or autumn and lowest in winter or spring. The decrease in abundance with age may be explained by the aging of individuals of the dominant species, in particular *Mytilus edulis*. With growth in size, space will become limiting and many mussels fall from the structure (Krone et al., 2013b). The remaining individuals will grow to a larger size, at lower abundances.

4.1.2. Surrounding seabed communities

The species diversity of the animal assemblages in the surrounding soft bottoms showed a small (up to 5.5%) but significant relation with the distance to the structure. Very close to the foundation, diversity was higher than at intermediate distances. This response could be attributable to the presence of fouling species being detached and therefore, falling off the structures and inhabiting proximate substrates only, creating an 'artificially' increased diversity in the very local seabed (Fernandez-Gonzalez et al., 2016; Mavraki et al., 2020), in combination with a fining and enriched level of the soft sediments surrounding the structure, resulting in higher abundance and diversity (Coates et al., 2014).

As the studied wind farms were closed for fisheries, a reduced disturbance by bottom trawling may also have affected local richness (Bergman et al., 2015). Additionally, export of organic matter by the fouling community to the seabed (Ivanov et al., 2021) may have altered the seabed diversity as well (Davis et al., 1982; Coates et al., 2014). This can be observed with the slight increase of diversity with the time since construction. However, there is a negative slope visible at higher ages. These data originate from studies in Belgian wind farms. It is unclear whether this decrease at higher wind farm age is caused by a lower biodiversity in Belgium or by other environmental influences. Water depth was a good predictor for all regarded response variables of the soft-bottom communities, confirming the common natural pattern in the shallow North Sea where species richness increases with depths up to 30 m (Armonies et al., 2014). However, the relation of depth and richness remains unclear, as the model shows large errors in depths <25 m, which should be noted when interpreting these results. A similar pattern is visible in the relation between abundance and depth, where shallower depths show very large errors. This may be caused by larger variation in abundance in shallow waters, or by the data originating from only one country. Effects of anthropogenic activities such as the presence of MMS may differ among locations and may be locally restricted (i.e. on small spatial scales; Gutow et al., 2014; Kenworthy et al., 2016). As for fouling communities, season had a very strong effect on most of the responses, in particular for abundance, which was more than 7 times higher in summer than in winter.

4.1.3. The power of meta-analysis for environmental management

As the available dataset was large enough, local (i.e. small-scale) effects contributed only to a small extent to the total variation and only those effects that were present in multiple wind farms independent

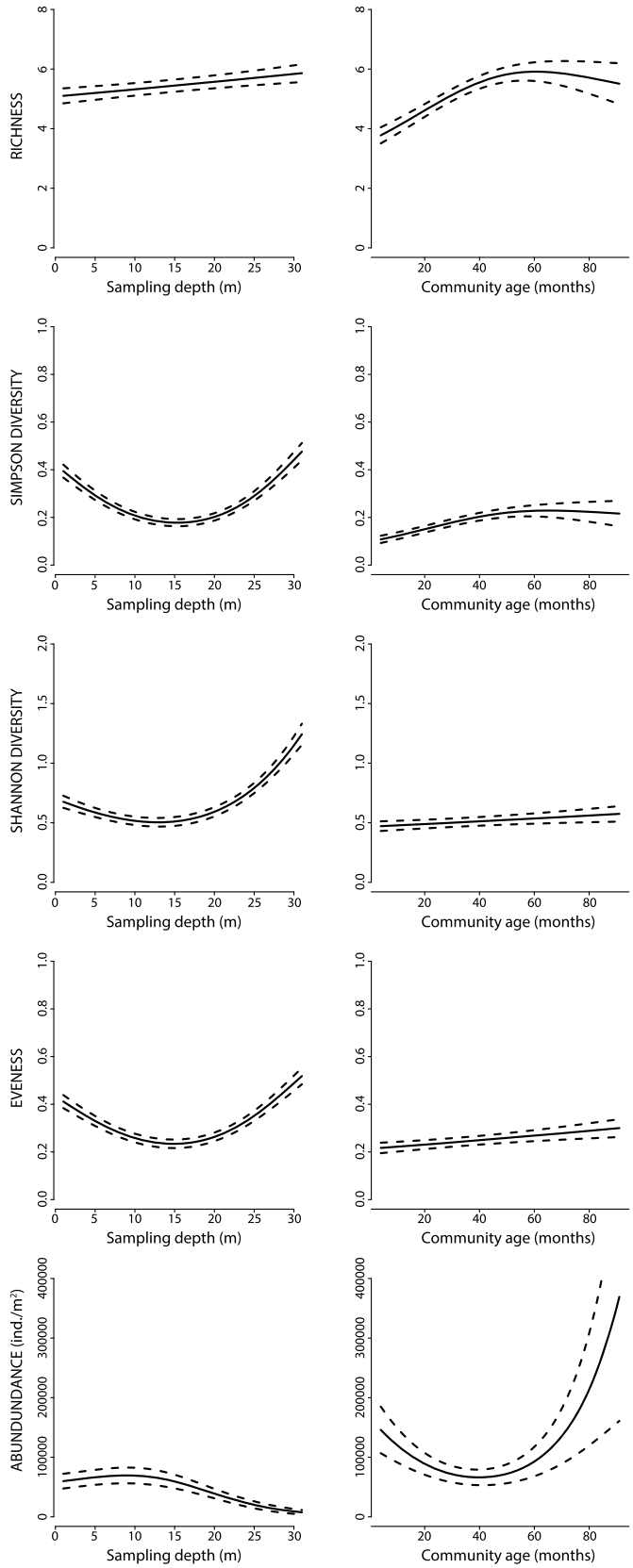


Fig. 4. Non-linear relations fouling. Relations between predictor variables (columns) and response variables (rows), as estimated with GAMs based on fouling community data. Variables within rows are from a single model. Sample size in all models was 678. Continuous line: predicted relation between response variable (y-axis) and predictor variable (x-axis). Dashed lines: standard errors (SE). N sample = 675.

Table 6
Fouling model predicted response values for each category in season and country, with all other predictor variables set to a the mean value for continuous variables and most frequent values for categorical variables. N sample = 675. Richness was rarified and abundance scaled down to a sampled area of 0.01 m^2.

	Richness	Simpson Index	Shannon Index	Evenness	Abundance
Spring	4.39	0.14	0.37	0.18	441.60
Summer	6.43	0.16	0.38	0.17	1109.87
Autumn	5.36	0.19	0.51	0.24	674.82
Winter	3.78	0.17	0.37	0.20	274.72
Belgian	7.37	0.36	0.89	0.46	248.51
Dutch	7.20	0.22	0.75	0.29	432.24
German	5.36	0.19	0.51	0.24	674.82

Table 7
Sample statistics of data used as response and predictor variables in the five seabed community models. Columns: minimum, maximum, average and standard deviation of all data used in model calculations. Rows: Predictor variables, with depth (m seawater), age (months after construction), distance (m from structure), Richness (S $sample^{-1}$, rarified to a sampled area of 0.078 m^2), Simpson diversity index (d $sample^{-1}$), Shannon diversity index (H $sample^{-1}$), evenness (J $sample^{-1}$) and abundance (N $sample^{-1}$ of 0.078 m^2). N sample = 2172.

	Minimum	Maximum	Average	Standard deviation
Depth	12.50	33.88	28.12	3.94
Age	1.00	78.00	31.01	20.62
Distance	1.00	9761.47	1868.51	2648.80
Richness	1.67	58.81	19.90	10.28
Simpson	0.14	0.96	0.83	0.10
Shannon	0.27	3.45	2.28	0.45
Evenness	0.13	1.00	0.78	0.13
Abundance	2.00	3884.00	148.67	288.26

of their location in the southern North Sea were able to dominate the resulting patterns. This is an important step towards understanding the effects of the presence of MMS on the wider North Sea ecosystem. If small effects are present in most wind farms but cannot be detected in the individual studies, meta-analyses may be able to detect any signals due to the increased statistical power resulting from the larger sample size (Cohen, 1988; Gurevitch and Hedges, 1999). For example, Coolen et al. (2020a) applied identical modelling methods to a smaller dataset to assess the effect of age on species richness in fouling communities, but age only explained <0.3% of the variation. Here, when combining this dataset with several others, we showed that up to 12% of the variation in richness can be explained by age. By pooling together multiple datasets, the power to detect changes strongly increased.

The power of meta-analyses to detect previously "undetectable" effects has been demonstrated in many studies on different biological aspects such as trophic interactions (Worm and Myers, 2003, Marczak et al. 2007) and experiments, i.e. combining outcomes of different experiments (Gurevitch et al., 1992). Monitoring studies as those used in the current meta-analysis, are designed to detect possible changes within or in the vicinity of single wind farms. Due to the 'local' nature of each study, however, observed changes can only be considered in a spatially and thus ecologically restricted context. Furthermore, natural variation in environmental conditions may cause large changes in species communities, obscuring effects of the individual wind farm on the benthic community. These limitations can be partly overcome by a meta-analysis. However, merging datasets and performing meta-analyses, is only possible if all the parameters needed for the meta-analysis are available for each of the separate studies (Gurevitch and Hedges, 1999).

In order to allow for useful combinations in the context of a meta-analysis, it is of pivotal importance that a minimum set of parameters are registered in routine monitoring programs. The registration of some of these simple-to-acquire data during monitoring programs is important to address different questions that were originally not intended to be answered when the local monitoring was designed. However, given the increasing installation of offshore wind farms across large areas, answering questions arising on the effect of multiple wind farms on a larger geographical scale (De Borger et al., 2021; Ivanov et al., 2021) requires the compilation of standardized databases. We suggest that future monitoring programs associated with offshore structures include the following minimum set of parameters to register:

- Sampling date;
- Longitude and latitude for each sample;
- Sampling depth;
- Sampling height from seabed in case of fouling samples;
- Sediment composition (median grain size, % fines, total organic carbon content) for seabed samples;
- Substrate type (steel/concrete/presence and type of antifouling treatment) for fouling samples;
- Seawater temperature at sampling depth;
- Whether fishery is allowed at the sample location in case of seabed samples;
    - o If yes: type of fishery
- Seawater salinity at sampling depth;
- Distance to nearest structure for seabed samples;
- Date of construction of that nearest structure.

Most of these variables have also been suggested by the Working Group on Marine Benthal Renewable Developments (WGMBRED), a group of benthic ecology & renewable energy experts that listed the important variables to measure around renewable energy devices (ICES, 2021).

It is important that the timeline of projects is long enough to be able to distinguish smaller long-term changes from larger short-term natural variation. We combined datasets varying in age between 1 month and 7.5 years, elucidating biodiversity parameters are still evolving.

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Table 8
Summary statistics of all model components for the five models created for seabed communities, with columns for p-value (P, <0.001 = ***; <0.01 = **; non-significant = n.s.), effective degrees of freedom (edf) and % deviance explained (DE), rows for sampling depth (m seawater), age (months since construction of wind farm), season, distance (m from structure), and country, total deviance explained (total DE) for the model and adjusted R^2 for the model (Total R^2). N sample = 2172. Richness was rarified and abundance scaled down to a sampled area of 0.078 m^2.

	Richness			Simpson Index			Shannon Index			Evenness			Abundance		
	P	edf	DE	P	edf	DE	P	edf	DE	P	edf	DE	P	edf	DE
Depth	**	2.00	2.7%	***	1.02	0.9%	***	1.00	0.4%	***	1.94	2.3%	***	2.00	2.6%
Age	***	2.00	4.5%	***	1.98	5.8%	***	1.97	9.3%	***	1.93	4.0%	n.s.	1.00	<0.1%
Season	***	–	52.0%	***	–	5.7%	***	–	10.8%	***	–	23.9%	***	–	39.8%
Distance	*	1.00	<0.1%	***	1.95	2.8%	***	1.90	4.1%	***	1.96	5.4%	**	1.88	2.1%
Country	***	–	<0.1%	n.s.	–	0.1%	**	–	<0.1%	***	–	<0.1%	***	–	<0.1%
Total DE			59.0%			15.3%			24.6%			35.7%			44.6%
Total R^2			0.57			0.14			0.23			0.25			0.25

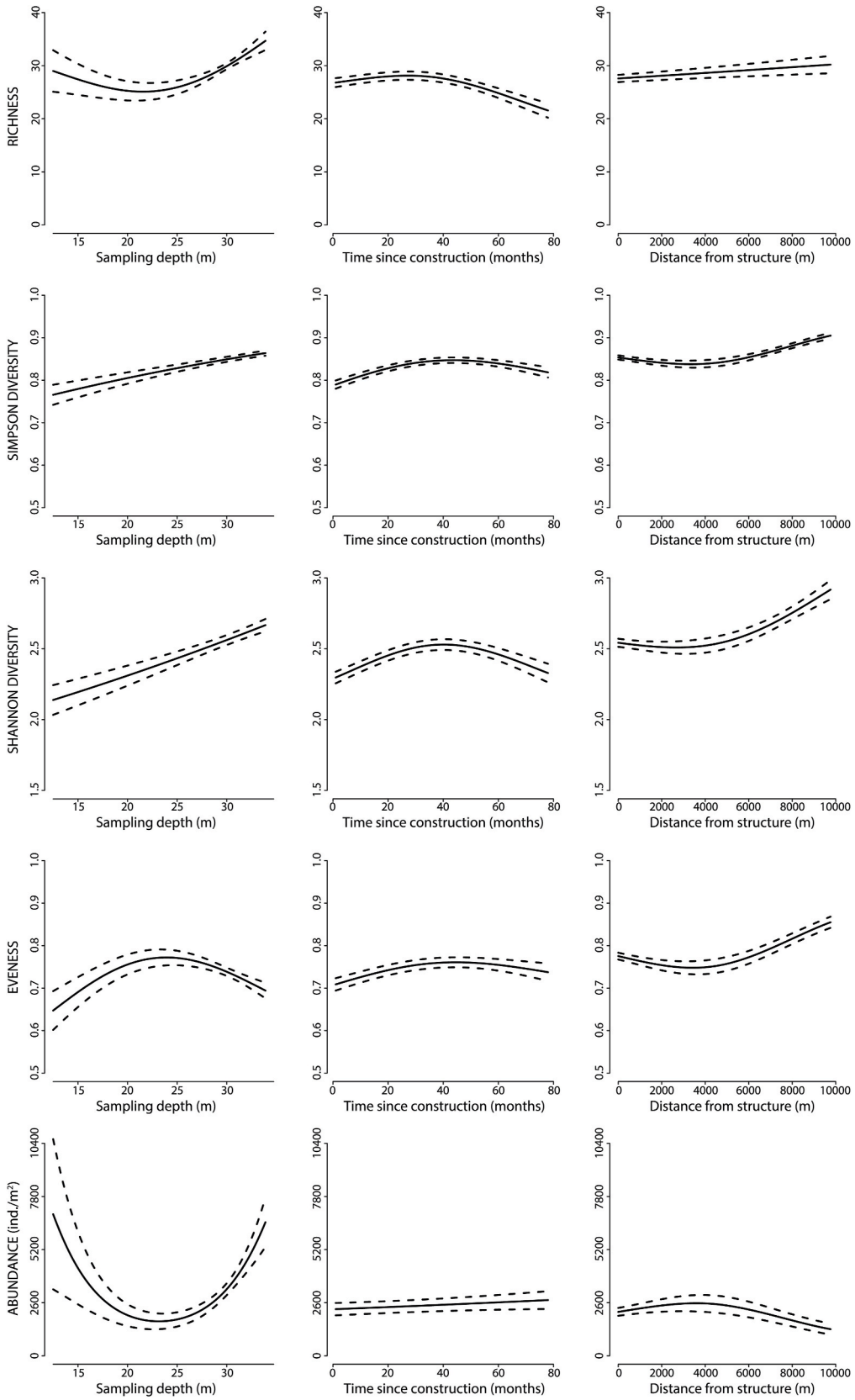


Fig. 5. Non-linear relations seabed. Relations between predictor variables (columns) and response variables (rows), as estimated with gams based on seabed community data. Variables within rows are from a single model. Continuous line: predicted relation between response variable (y-axis) and predictor variable (x-axis). Dashed lines: standard errors (SE). N sample = 2172.

Table 9
Seabed model predicted response values for each category in season and country, with all other predictor variables set to the mean value for continuous predictor variables and most frequent values for categorical predictor variables. N sample = 2172. Richness was rarified and abundance scaled down to a sampled area of 0.078 m^2.

	Richness	Simpson Index	Shannon Index	Evenness	Abundance
Spring	24.29	0.84	2.49	0.77	113.49
Summer	35.17	0.77	2.22	0.62	479.49
Autumn	28.07	0.84	2.51	0.76	188.18
Winter	20.15	0.83	2.44	0.80	63.28
Belgian	17.96	0.84	2.33	0.84	51.42
Dutch	24.94	0.84	2.41	0.80	118.71
German	28.07	0.84	2.51	0.76	188.18

datasets is very labor-intensive. The use of standardized registration templates that include all the variables described above, and can easily be submitted to online repositories such as the Ocean Biodiversity Information System (OBIS, 2022) or directly shared between researchers, would significantly reduce the time needed to perform similar studies. Ideally, this would facilitate international collaborations, sharing data on a regular basis and conducting joint meta-analyses as performed here. This would strongly increase the use of these data, thus improving our understanding of potential impacts.

4.2. Management implications

Meta-analyses of data from independently conducted monitoring projects, proved to be a valuable tool for the generalization of effects of offshore wind farms on their surrounding benthic communities. Long-term small changes, such as alterations to biodiversity over time, can be detected better than in separate local (i.e. spatially restricted) projects despite the effects of season and depth on biodiversity of benthic communities. Furthermore, even though some effects may remain invisible in single monitoring programs, long-term changes on a larger scale may only become apparent if the small-scale data was collected from the start in all the separate initiatives. These large-scale changes may include an altered functioning of communities, changes in nutrient cycles or predator prey-relations (Dannheim et al., 2020). Some aspects that are currently unknown, may become important when offshore wind farms are indeed upscaled to the current outlooks of 25,000 turbines in the southern North Sea (de Vrees, 2019). Patterns observed by that time, can only be detected as changes, if the baseline is measured now and in a way that allows these future assessments. Once the end of life of MMS has been reached, new questions will arise on the effect of removal of such installations (Coolen et al., 2020b). This can only be evaluated against a proper understanding of the effects of their presence (Fowler et al., 2020).

To further improve the potential to perform meta-analyses, we suggest making a registration of a standard minimum number of parameters at a defined high-quality mandatory in renewable energy monitoring programs. Data storage using internationally standardized templates would greatly enhance generalizations of effects and the exchange of knowledge (Murray et al., 2018). This should be considered as a crucial prerequisite for the approval of future monitoring studies. We encourage managers, stakeholders and authorities to demand future projects to follow these requirements and stimulate researchers to standardize and share their data.

We demonstrated that a meta-analysis provided an improved level of understanding of ecological patterns on large-scale ecological effects such as diversity, which couldn't be detected in single monitoring studies. Meta-analyses should be an indispensable tool for management of offshore wind farm effects in the future, particularly in the view of the foreseen development of offshore renewable energies. Combined with an ecosystem approach, i.e. including several ecosystem components from plankton to top predators, this may lead to a better picture and more comprehensive view on potential alterations. However, this requires a modern open-source data policy and data management, across institutions and across national borders.

Credit author statement

Coolen, Joop W.P.: Conceptualization, Data curation, Formal analysis, Funding acquisition, Methodology, Visualization, Roles/Writing - original draft, Writing – review & editing. Vanaverbeke Jan: Formal analysis, Methodology, Writing – review & editing. Dannheim, Jennifer: Conceptualization, Data curation, Funding acquisition, Methodology, Project administration, Writing – review & editing. Garcia, Clement: Conceptualization, Writing – review & editing. Birchenough, Silvana N. R.: Conceptualization, Funding acquisition, Writing – review & editing. Krone, Roland: Data curation, Writing – review & editing. Beermann, Jan: Conceptualization, Data curation, Formal analysis, Funding acquisition, Methodology, Visualization, Roles/Writing - original draft, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

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