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Capabilities of Baltic Sea models to assess environmental status for marine biodiversity

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ABSTRACT

To date there has been no evaluation of the capabilities of the Baltic Sea ecosystem models to provide information as outlined by the Marine Strategy Framework Directive. This work aims to fill in this knowledge gap by exploring the modelling potential of nine Baltic Sea ecosystem models to support this specific European policy and, in particular, models' capabilities to inform on marine biodiversity. Several links are found between the Model-Derived Indicators and some of the relevant biodiversity-related descriptors (i.e. biological diversity and food webs), and pressures (i.e. interference with hydrological processes, nutrient and organic matter enrichment and marine acidification). However several gaps remain, in particular in the limited representation of habitats other than the pelagic that the models are able to address for descriptor sea-floor integrity and inability to assess descriptor non-indigenous species. The general outcome is that the Baltic Sea models considered do not adequately cover all the requested needs of the MSFD, but can potentially do so to a certain extent, while for some descriptors/criteria/indicators/pressures new indicators and/or modelling techniques need to be developed in order to satisfactorily address the requirement of the MSFD and assess the environmental status of the Baltic Sea.

1. Introduction

The Directive 2008/56/EC, known as the Marine Strategy Framework Directive (MSFD), establishes a framework for community action in the field of marine environmental policy [1]. It was formally adopted by the European Union in July 2008. The MSFD outlines a legislative framework for an ecosystem-based approach to the management of human activities that supports the sustainable use of marine goods and services. The overarching goal of the Directive is to achieve Good Environmental Status (GEnS)[1] by 2020 across the European marine environment. The Directive defines GEnS as 'the environmental status of marine waters where these provide ecologically diverse and dynamic oceans and seas which are intrinsically clean, healthy and productive, and the use of the marine environment is at a level that is sustainable, thus safeguarding the potential for use and activities by current and future generations'. With the aim to support its implementation, the MSFD sets out in Annex I 11 qualitative *descriptors*[2] (D1-D11, Table 1), either state or pressure *descriptors*. Later, a Commission decision defines also 29 related *criteria* and 56 related *indicators* [4] that are used in the assessment of the status of the seas. An example of *criteria* and *indicators* defined for biological diversity (D1) is shown in Table 2.

With the aim to facilitate the implemention of the MSFD, Borja et al. [5] proposed an operational definition of GEnS, i.e. 'GEnS is achieved when physicochemical and hydrographical conditions are maintained at a level that main structuring components of the ecosystem are present, allowing the functionality of the system to provide resistance and resilience against deleterious effects of human pressures/activities/impacts, maintaining and delivering

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[1] Following the recommendation of Mee et al. [2] the acronym GEnS for Good Environmental Status is used here to discern from Good Ecological Status (GEcS) defined by the Water Framework Directive [3].

[2] *Descriptors/criteria/indicators/pressures* are here identified in italics when strictly referring to those defined by the Marine Strategy Framework Directive.

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Table 1
The 11 *descriptors* identified by the Marine Strategy Framework Directive and related number of *criteria* and *indicators*.

#	Type	*Descriptor*	# of *criteria*	# of *indicators*
D1	state	Biological diversity	7	14
D2	pressure	Non-indigenous species	2	3
D3	state	Exploited fish and shellfish	3	8
D4	state	Food webs	3	3
D5	pressure	Human-induced eutrophication	3	8
D6	state	Sea-floor integrity	2	6
D7	pressure	Hydrographical conditions	2	3
D8	pressure	Contaminants	2	3
D9	pressure	Contaminants in fish and seafood	1	2
D10	pressure	Litter	2	4
D11	pressure	Energy and noise	2	2

Table 2
D1 Biological diversity *descriptor* and related *criteria* and *indicators*.

Criteria	*Indicator*
1.1 Species Distribution	1.1.1 Distributional range
	1.1.2 Distributional pattern
	1.1.3 Area covered by the species
1.2 Population size	1.2.1 Population abundance and/or biomass
1.3 Population condition	1.3.1 Population demographic characteristics
	1.3.2 Population genetic structure
1.4 Habitat distribution	1.4.1 Distributional range
	1.4.2 Distributional pattern
1.5 Habitat extent	1.5.1 Habitat area
	1.5.2 Habitat extent
1.6 Habitat condition	1.6.1 Condition of the typical species and communities
	1.6.2 Relative abundance and/or biomass
	1.6.3 Physical, hydrological and chemical conditions
1.7 Ecosystem structure	1.7.1 Composition and relative proportion of ecosystem components

the ecosystem services that provide societal benefits in a sustainable way'. Despite the fact that several attempts have been made to assess the environmental status of marine waters in an integrative manner e.g. [6], significant gaps still remain for understanding marine ecosystem structures and functions and their response to human pressures e.g. [5]. There are several challenges related to the assessment of GEnS within the MSFD. The assessment of an ecosystem's health requires the setting of adequate reference conditions and/or environmental targets to which data should be compared [7]. The use of robust and appropriate indicators that can assess whether an ecosystem and its services are well maintained and sustainably used is one of the essential steps for the practical implementation of conservation and management policies such as the MSFD [8]. On the other hand, an accurate evaluation requires integrating knowledge across different ecosystem components and linking physical, chemical and biological aspects [9]. To this end, ecological models are a powerful tool for predicting and understanding the consequences of anthropogenic and climate-driven changes in the natural environment e.g. [10].

Within this framework, Piroddi et al. [11] assess the most commonly used capabilities of models in five regional European seas (North Sea, Baltic Sea, Mediterranean Sea, Black Sea and Bay of Biscay) to provide information about indicators outlined in the MSFD, particularly on biodiversity-related *descriptors*. They built a catalogue of European models and their derived indicators to assess which models are able to demonstrate the linkages between indicators and ecosystem structure and function, and the impact of pressures on ecosystem state through indicators. A brief summary of the models' catalogue is given in Section 2.1. Thus, Piroddi et al. [11] provide an extensive overview at pan-European scale. As the Baltic Sea is facing several health issues including an enlargement of the eutrophication problem [12] despite the adopted nutrient reduction measures [13], it was found relevant to investigate the Baltic Sea case in more details. To date there has been no evaluation of the capabilities of the ecosystem models of the Baltic Sea to provide information as outlined by the MSFD. This work aims to fill in this knowledge gap by providing a review of the capabilities of nine Baltic Sea ecosystem models to assess the environmental status of marine waters with particular focus on marine biodiversity. Yet, it is acknowledged that this study does not aim to serve as review of all the existing ecosystem models of the Baltic Sea, but instead highlights a process of exploring modelling potential to support this specific European policy. As in Piroddi et al. [11], models were analysed for potentially addressing the MSFD biodiversity-related *descriptors*: biological diversity (D1), non-indigenous species (D2), food webs (D4) and sea-floor integrity (D6). A short description of the characteristics of the Baltic Sea, the main features of the models and the criteria used for deriving indicators and assessing models' capabilities are given in Sections 2.2, 2.3 and, 2.4, respectively. The Baltic Sea Model-Derived Indicators (MDI) and their capabilities to inform on biodiversity-related *descriptors* and *pressures* are presented in Section 3.1, while Section 3.2 gives a more detailed analysis of the capabilities of each of the Baltic Sea models to address, potentially address or not address at all the biodiversity-related *indicators*. Finally, Section 4 highlights the current gaps between the MSFD and the models and suggests the use of different methods and tools as well as the development of new indicators and models to better link ecosystem models to the political framework of the MSFD.

2. Material and methods

2.1. The catalogue of european ecological models in brief

This section summarises the methodology used and the results gained from the analysis of the modelling capabilities of five European regional seas (North Sea, Baltic Sea, Mediterranean Sea, Black Sea and Bay of Biscay) to assess environmental status for marine biodiversity and presented in Piroddi et al. [11].

With the aim of developing new indicators and modelling tools to assess environmental status for marine biodiversity, it is necessary to initially evaluate the capabilities of the state-of-the-art models to do so. The work flow requires a series of sequential steps (Fig. 1). After the identification of the relevant *descriptors* in relation to marine biodiversity (biological diversity (D1) , non-indigenous species (D2) , food webs (D4) and sea-floor integrity (D6) with some relevance for commercial fish (D3) and human-induced eutrophication (D5)), the catalogue of European models that can specifically address these *descriptors* is produced (see the Supplementary material for a detail description of the structure of the catalogue). Every model output is then linked to relevant *descriptors* and related *criteria* and *indicators*, and MDI are then identified. Every MDI is then used for the assessment of its capability to relate to both *descriptors* (Table 1) and *pressures* (Table 3).

At European scale 44 ecological models were analysed for their capabilities to inform on the biodiversity-related *descriptors* [11, see Table 1]. The models are either operational i.e. tested and validated (24), or under development i.e. not yet validated (18), or conceptual (2). The type of models were grouped into 7 categories:

- biogeochemical: represents the dynamics and cycling of biogeochemical compounds of the lower trophic levels of the food web (1 model)
- meta-community: describe specific mechanistic processes to predict empirical community patterns, i.e. species composition and abundance (1)

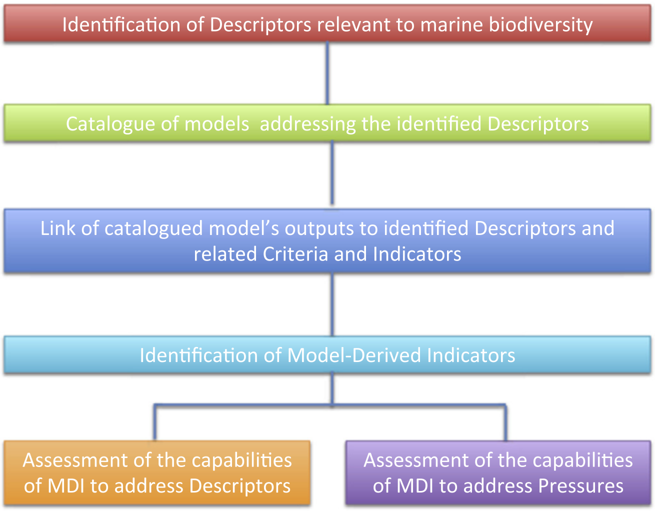

Fig. 1. The work flow required for the assessment of the capabilities of the models to address environmental status for marine biodiversity.

Table 3
Pressures identified by the Marine Strategy Framework Directive.

	Pressure
1	Physical disturbance (sum)
2	Underwater noise
3	Marine litter
4	Interference with hydrological processes
5	Contamination (sum)
6	Contamination by radionucleids
7	Nutrient and organic matter enrichment
8	Introduction of microbial pathogens
9	Non-indigenous species
10	Extraction of living resources (sum)
11	Marine acidification

- individual-based: represents individual organisms in a population having specific state characteristics, such as age, size, developmental stage, and physiological conditions (3)
- bio-optical: analyse and predict the optical properties of biological materials (6)
- food web: represent networks formed by feeding interactions between species to understand trophic patterns, population dynamics and implication for system stability and substance/energy flows (9)
- species distribution/habitat suitability: combine observations of species occurrence or abundance with environmental variables to predict distribution across selected habitats/spatial predictions on the suitability of locations for a target species, community or biodiversity (9)
- coupled hydrodynamic-biogeochemical: capture global scale patterns in physical-chemical components affecting lower trophic levels of the food web (15). When coupled to food web models they are known as end-to-end models.

From the 44 models, 201 MDI were identified, of which 129 are operational, 66 under development and 6 conceptual ones i.e. an indicator idea without practical measure/metric yet available. MDI were grouped into 7 major categories, based on what the indicators inform on:

- Biomass (115 MDI)
- Diversity (26)
- Physical, hydrological and chemical characteristics (24)
- Primary/secondary production (18)
- Spatial distribution (12)
- Ecological Network Analysis (4)
- Species life-history (2).

Among the biodiversity-related components of the MSFD such as microbes, phytoplankton up to fish, birds and marine mammals, the less frequently used food web models (9) were the ones that assessed most of the biodiversity-related components, while the more frequently applied coupled hydrodynamic-biogeochemical models (15) were the least inclusive in terms of number of components evaluated.

The majority of indicators (136) were derived from the Ecopath with Ecosim (Ewe, http://www.ecopath.org) software applications, which was also the only model applied to every regional sea. Of the 11 *descriptors* of the MSFD (Table 1), the evaluated models were able to address 8 of them but not contaminants (D8), litter (D10) and energy and noise (D11). Of the biodiversity-related GEnS *descriptors* models especially addressed biological diversity (D1) and food webs (D4), while non-indigenous species (D2) and seafloor integrity (D6) were poorly addressed. In total 27 MDI were identified under these 4 *descriptors*, of which the modelling capabilities to address them were highly heterogeneous, from 1 single model addressing only once a single *indicator* (e.g. 'Parameters describing the characteristics of the size spectrum of the benthic community' within D6) to all of the 44 models addressing 108 times a single *indicator* (e.g. 'Interactions between structural components' within D1). Considering their spatial coverage, the majority of MDI (53) related to the Mediterranean Sea and Bay of Biscay, followed by the North-East Atlantic Ocean (46), the Black Sea (29), the Baltic Sea (22) and other non-EU seas (11).

Among the predominant habitat types of the MSFD (water column, seabed and ice-associated habitats) the water column - and in particular the marine shelf - was the most comprehensively evaluated habitat by the models.

41 out of 44 models are in use to address collectively all the pressure impacts outlined in the MSFD (Annex III). The most addressed *pressure* is 'Inputs of nutrients and organic material' (44 models), followed by 'Marine Acidification' and 'Interference with the hydrological regime' (25). The least addressed *pressures* (1) were 'Introduction of microbial pathogens' and 'Contamination from radionucleids'.

The gap analysis of the models importantly showed that among the 4 biodiversity-related *descriptors* (D1, D2, D4 and D6), some of the related *indicators* were not addressed by any of the MDI. Also, the geographical coverage of the models was very heterogeneous, with several regional seas needing improvements in terms of number of models, model types, and capabilities to address MDI, as for example the Baltic Sea, which is the focus of the rest of this review.

2.2. Baltic Sea, biodiversity and human pressures

The Baltic Sea (Fig. 2) features brackish waters and, consequently, both freshwater and marine species cohabit and are distributed according to the water salinity patterns that characterizes different areas. The classical knowledge of the Baltic Sea inhabited by relatively few species, i.e. having low inter-specific biodiversity, decreasing from more saline to more fresh waters, have been recently challenged. Ojaveer et al. [14] showed that not only does the Baltic Sea hosts some 6000 species, but furthermore that phytoplankton and zooplankton biodiversity is very high with more than 4000 taxa. Only the diversity of bottom dwelling zoobenthos and macroalgae is still considered comparably low.

The main threats to the biodiversity of the Baltic Sea includes: fisheries, maritime activities (including shipping), physical damage

Fig. 2. The Baltic Sea and its partition in subasins (Credits: HELCOM).

and disturbance, recreational activities, eutrophication, hazardous substances, alien species, noise pollution, hunting, and climate change [15]. Overfishing, eutrophication, and drastic decline of marine mammals have been the most prominent changes in the Baltic Sea during the twentieth century [16].

Since the 1800 s, the Baltic Sea has changed from an oligotrophic clear-water sea to an eutrophic marine environment e.g. [17]. High nutrient concentrations stimulate growth of algae, which leads to imbalanced functioning of the system and extreme events that can cause: excess of filamentous algae and phytoplankton blooms, altered communities of fauna and flora, production of excess organic matter, increase in oxygen consumption, oxygen depletion and mortality of benthic organisms e.g. [18,19].

The spatial geographical, oceanographic, and climatological characteristics of the sea render the Baltic ecosystem highly susceptible to the environmental impacts of human activities at sea and in its catchment area [20]. The environmental status of the Baltic Sea is generally impaired [20]. The overall ecosystem health is degraded when the eutrophication and biodiversity status as well as the status of hazardous substances are evaluated together. In 2007 the Baltic Sea Action Plan (BSAP) [21], which aims to reach a healthy Baltic Sea by 2021, has been signed by the nine countries that surround it. The novelty of the BSAP is that the status of the ecosystem as wanted in the future is at the center, defining the management decisions that directly link abatement measures to the status of the Baltic Sea. Furthermore, a multi-model approach to characterize the nutrient loads, the retentions that occur between these sources and the sea, and the effects of various management strategies to reduce loads has been specifically developed to support the BSAP, providing more robust insights into patterns of loading and response when models agree, and priorities for additional research when models disagree [22].

In a recent assessment of the eutrophication status of the Baltic Sea it was found that the spatial extent of the eutrophication problem is expanding and now considered unacceptable for all the 17 evaluated open sea sub-basins [12], while earlier Bothnian Bay was classified unaffected by eutrophication [20]. Nutrient levels, rates of primary production (in terms of chlorophyll-a), Secchi depths and oxygen levels were used as indicators of direct and indirect effects of eutrophication of the sea. Even though a straight comparison with the previous eutrophication assessment [20,23] cannot be done as the assessment methodology and targets were different, it is a remarkable finding considering that the current management strategies for the Baltic Sea [13] do not require any nutrient reduction measure to the Bothnian Bay.

The expected combination of a rise in temperature and a decrease in salinity will result in a decrease in abundance and habitat occupied by marine species of fishes in the Baltic Sea. In contrast, habitats of freshwater species of fishes, particularly those whose growth or survival are enhanced by warmer temperatures, will increase. These changes in the fish community will affect fisheries and may require modifications to existing fisheries management policies. Long-term predictions of fish stock development are highly uncertain due to the uncertainties arises because salinity and temperature will change simultaneously and because these changes will have counteracting effects on biological phenomena. Furthermore, changes in salinity balance will affect other key hydrographic characteristics, such as inflows into the Baltic and thus oxygen concentrations in deeper water areas [16].

Other relevant human-induced pressures on the Baltic Sea include those related to shipping and contaminants e.g. [24]. Some of the shipping routes in the Baltic Sea are the busiest in the world. Potential negative environmental impacts related to the shipping are: the introduction of non-indigenous, potentially invasive species; emissions of nitrates, sulphates and carbon dioxide and a risk of accidental oil or chemical pollution. Contamination of the Baltic Sea certain fish species with dibenzo-p-dioxins and dibenzofurans has lead to recommendations to restrict the Baltic herring consumption e.g. [25–27]. Model simulations indicate that contamination in the water column will continue to decrease especially if supported by further reduced emissions measures [28]. Tributyltin in paint used on ships and maritime installations contaminated the seabed, and although banned since 2008, concentrations remain high in certain areas, especially near dockyards e.g. [29,30].

2.3. Baltic Sea models in brief

Nine Baltic Sea ecosystem models were analysed for their potential of addressing one or more of the biodiversity-related *descriptors* (Table 4). Of those, seven are operational and two under development. The operational models include five coupled hydrodynamic-biogeochemical models, one food web model and one end-to-end model. Each model covers the entire Baltic Sea domain, except BaltProWeb that simulates the Baltic Proper basin only (see Fig. 2 for location). The still under development models include one coupled hydrodynamic-biogeochemical model and one end-to-end model.

The type and number of living components and marine habitats within the models are shown in Table 4 and Fig. 3, while the main features of the models are described extensively in the Supplemental material. Generally, the five operational coupled hydrodynamic-biogeochemical models are similar in that they describe the main functional groups of the pelagic ecological domain of the Baltic Sea. Main differences among them refer to their level of complexity (i.e. number of functional groups, see Fig. 3), vertical resolution, and sediment parameterisations. They all describe at least the dynamics of nitrogen, oxygen, phosphorous, phytoplankton, zooplankton and dead organic matter. Only three models are also Higher Trophic Level (HTL, i.e. include larger size classes than zooplankton up to top predators), of which one is under development. Finally, the under development coupled hydrodynamic-biogeochemical model NEMO-BFM adds to this framework a considerable level of complexity in terms of number of

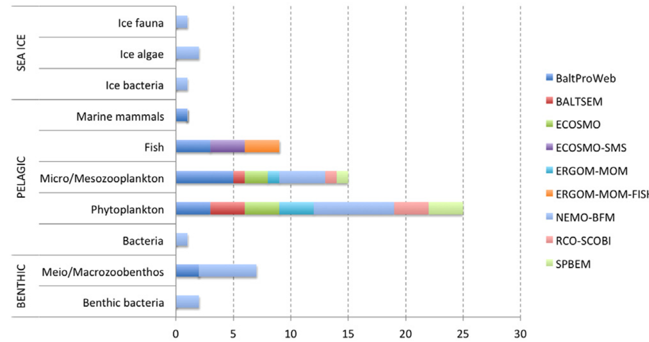

Fig. 3. Type (*y*-axis) and number (*x*-axis) of living components of the Baltic Sea models in different marine habitats.

state variables (i.e. non-Redfield model), number of functional groups (higher diversity for cyanobacteria, spring blooms composition and zooplankton) and number of habitats (pelagic, benthic and sea ice).

2.4. Criteria for the identification of MDIs and assessment of models' capabilities

The testing of an indicator-based approach to assess Baltic marine biodiversity has been conducted on a set of 22 national case studies and an overall assessment of the Baltic Proper subbasin [15]. The main criteria used for assessing the status of marine biodiversity within a given area were:

- a sufficient number of indicators that describe a sufficiently broad array of biodiversity components for a given site or area;
- the definition of a desirable state for the selected indicators, including both a quantitative reference status (or target), as well as an acceptable deviation from this reference (the highest possible value being 50% from the reference value);
- the assessment of the overall status of the biodiversity by using the indicators and their reference levels and acceptable deviations as components in an overall assessment matrix termed BEAT (the HELCOM Biodiversity Assessment Tool).

Indicators were grouped under 4 categories according to the biodiversity segment of the HELCOM BSAP, and an additional category for supportive features:

- Category I, Marine Landscapes: Area-based habitat indicators (all types) and large geographic features
- Category II, Communities: Community indicators on structure and function of phytoplankton, zooplankton, zoobenthos, macrophytes, fish community, bird community, endangered habitats and biotopes

Table 4
The Baltic Sea models and related number of Model-Derived Indicators (MDI) and living components in different habitats.

Name	Status	Type	# of MDI	Pelagic LTL	Pelagic HTL	Sea Ice	Benthic
BaltProWeb	oper.	food web	10	8	4	–	2
BALTSEM	oper.	hydr-bgc	7	4	–	–	–
ECOSMO	oper.	hydr-bgc	7	5	–	–	–
ECOSMO-SMS	un. dev.	end-to-end	+3	–	3	–	–
ERGOM-MOM	oper.	hydr-bgc	7	4	–	–	–
ERGOM-MOM-fish	oper.	end-to-end	+3	–	3	–	–
NEMO-BFM	un. dev.	hydr-bgc	14	12	–	4	7
RCO-SCOBI	oper.	hydr-bgc	7	4	–	–	–
SPBEM	oper.	hydr-bgc	7	4	–	–	–

- Category III, Species: Single-species indicators of high profile species mainly fish, birds and mammals as well as indicators on endangered and alien species
- Category IV, Supporting features: Indicators of environmental parameters including e.g., water clarity, water temperature, oxygen concentrations, nutrients.

Similar criteria are used here while identifying the MDI, taking in consideration all possible diversity biological components (from LTL to HTL) and habitats (from benthic to pelagic to ice-associated habitats) and the possibility to have/set targets and/or reference values. Each MDI is then liked to the related MSFD criteria among the biodiverisity-related *descriptors*. Finally, depending on their capabilities with respect to each *indicator*, the models are classified as:

- currently able to address ✓
- potentially able to address with some changes to the model ✓
- not able to address and requiring different/new modelling tools/ techniques ✗.

The criteria of classification is based on the minimum requirements, i.e. if a MDI already exists and addresses a certain *indicator*, the related model is classify as ✓, even though modifications for increasing the capabilities of the model to address biodiversity are anyhow encouraged. Similarly, if a MDI already exists and potentially can address a certain *indicator*, the related model is classified as ✓, even though such *indicator* might be addressed only to a certain extent and the usage/development of new features/model might be advisable. Finally, if a certain type of model is not able to address a certain *indicator* even after modifications, the model is classified as ✗ and some recommendations are provided, indicating suitable types of models with reference to that specific *indicator*.

3. Results and discussion

3.1. Model-derived indicators vs. descriptors and pressures

Of the 201 indicators derived from the full set of models, only 22 MDI are addressed by the Baltic Sea ecosystem models relevant to one or more *descriptors* (Table 5 and Fig. 4). Of the analysed biodiversity-related *descriptors* (biodiversity (D1), non-indigenous species (D2), food webs (D4) and sea-floor integrity (D6)) the Baltic models do not currently address *non-indigenous species* at all. Of the remaining *descriptors*, the Baltic models are able to also address commercial fish (D3), human-induced eutrophication (D5) and hydrological alteration (D7), but not contaminants (D8), contaminants in food (D9), litter (D10) and energy and noise (D11).

Biodiversity MDIs (19) are the most frequently addressed by the set of Baltic models (69 times), although mainly indirectly, linking MDIs mostly to species distributional ranges (*indicator* 1.1.1), to population biomasses (1.2.1), and to physical, hydrological and chemical conditions of the habitats (1.6.3). The second most addressed (46 times) *indicator* is *Food webs* by 13 MDIs (Table 5). Even though not the main targets of this study, *human-induced eutrophication* and *hydrological alteration* are both discretely addressed (22 times the former and 29 times the latter) by 5 and 6 MDIs, respectively. Of the remaining addressed *descriptors*, the least addressed (9 and 10 times, respectively) are *commercial fish* and *sea-floor integrity*, both by 3 MDI (Table 5).

The analysed Baltic models are capable of addressing biodiversity and food webs (D1 and D4) to some extent, while commercial fish (D3) is addressed only by the HTL models and human-induced eutrophication (D5), sea-floor integrity (D6) and hydrological alteration (D7) only by the Lower Trophic Level (LTL) models (Fig. 4).

All of the Baltic Sea LTL models provide indicators such as phytoplankton/zooplankton biomass and distributional ranges, relevant to biodiversity and food webs (D1 and D4, Table 5). While all of the LTL models provide information on the oxygen level in water and sediments, relevant to *biodiversity* and sea-floor

Table 5
Model-Derived Indicators (MDI) from MSFD descriptors and number of Baltic Sea models addressing them.

MDI	D1 Biological diversity	D4 Food webs	D6 Sea-floor integrity	D3 Commercial fish	D5 Human-induced eutrophication	D7 Hydrological alteration
Temperature	6	–	–	–	–	6
Salinity	6	–	–	–	–	6
pH	2	–	–	–	–	2
Oxygen penetration depth	7	–	7	–	7	7
Denitrification layer depth	1	–	1	–	1	1
Bacteria biomass	1	1	–	–	–	–
Phytoplankton biomass	7	7	–	–	7	–
Zooplankton biomass	7	7	–	–	–	–
Chlorophyll-a concentration	–	–	–	–	1	–
Primary production	–	7	–	–	7	–
Secondary production	–	9	–	–	–	–
Bacteria distributional range	1	–	–	–	–	–
Phytoplankton distributional range	6	–	–	–	6	–
Zooplankton distributional range	6	–	–	–	–	–
Fish: Herring biomass	3	3	–	3	–	–
Fish: Cod Biomass	3	3	–	3	–	–
Fish: Sprat Biomass	3	3	–	3	–	–
Marine mammal biomass (seals)	1	1	–	–	–	–
Zoobenthos biomass	2	2	2	–	–	–
Sea-ice algae biomass	1	1	–	–	–	–
Sea-ice bacteria biomass	1	1	–	–	–	–
Sea-ice fauna biomass	1	1	–	–	–	–
Total	69	46	10	9	29	22

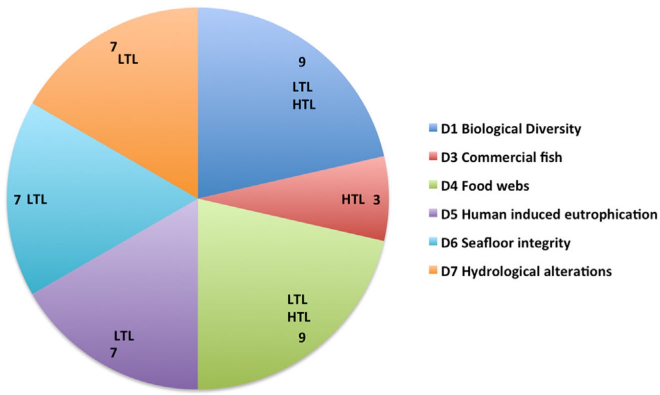

Fig. 4. Baltic Sea models and addressed MSFD *descriptors*.

integrity (D6), zoobenthos biomass is provided only by BaltProWeb and NEMO-BFM and is relevant also for D6, besides D1 and D4. Only BaltProWeb, ERGOM-MOM-Fish and the under development ECOSMO-SMS provide information on fish biomass (herring, sprat and cod), relevant to *descriptors* D1, D3 (commercial fish) and D4. Finally, BaltProWeb provides information on marine mammal biomass (i.e. grey seals), relevant also to D1, D3 and D4. The physical and chemical conditions, such as temperature, salinity, pH and oxygen penetration depth are important indicators relevant also to hydrological alteration (D7) and are addressed by all the LTL models, while denitrification layer depth only by the under development NEMO-BFM.

The analysed Baltic Sea models are totally able to address to some extent 8 of the 11 *pressures* defined by the MSFD (Fig. 5 and Table 6), but not 'contaminants in radionuclides', 'introduction of microbial pathogens' and, most importantly, 'non-indigenous species'. Of the addressed *pressures*, 'interference with the hydrological regime', such as thermal regime changes, is addressed by each LTL model and by each MDI up to 66 times (Table 6). Also 'nutrients and organic matter enrichment' and 'marine acidification' are highly addressed by each of the by LTL models and by several MDI (13 and 11, respectively) several times (42 and 34, respectively, Table 6). The least addressed *pressures* are 'underwater noise' and 'marine litter', both in relation to marine mammals and addressed by the BaltProWeb model only, followed by "contamination" and "extraction of living resources" addressed only 9 and 10 times, respectively.

3.2. Capability to address the biodiversity-related MSFD indicators

In this section the capabilities of the evaluated Baltic Sea models to address the biodiversity-related *indicators*, i.e. with

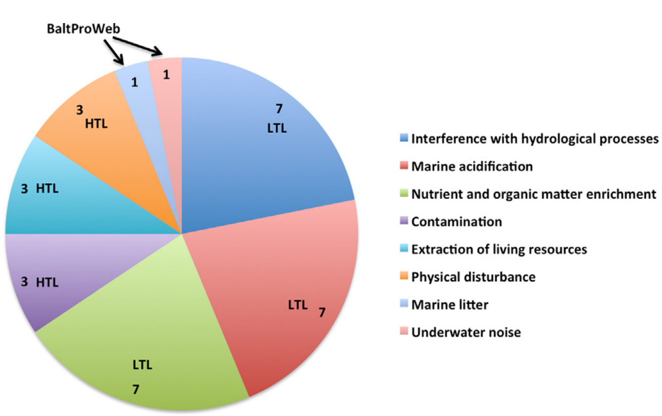

Fig. 5. Baltic Sea models and addressed MSFD *pressures*.

reference to biodiversity (D1), non-indigenous species (D2), food webs (D4) and sea-floor integrity (D6), according to the criteria described in Section 2.4, are analysed in detail.

In general, the capabilities of the Baltic Sea models to address the MSFD *indicators* is quite heterogeneous (Table 7), from every model able to address several *indicators* linked to 'Phytoplankton distributional range' and 'Zooplankton distributional range', to none of the models producing or capable to produce any MDI addressing *indicators* such as 'Population genetic structure' within D1. The MDI 'Phytoplankton biomass' is referred to be capable of addressing *indicator* 1.2.1 'Population biomass' and 4.3.1 'Abundance trends of functionally important selected groups/species' by each Baltic model. However, depending on the model complexity, the number of Plankton Functional Types (PFTs) could be increased with the aim of increasing biodiversity at the population/community levels. For example, the reduction in the duration of the coastal sea-ice cover during the past century and the associated changes in vertical mixing are considered to have contributed to the increasing dominance of dinoflagellates over diatoms during the spring bloom in some parts of the Baltic Sea [31]. The type of blooming PFT has large consequences on the Baltic food web: while diatoms are usually large cells that sink rapidly, enriching the seabed of organic matter that can lead to anoxic conditions, dinoflagellates tend to be mostly consumed and recycled in the upper water column, feeding a more efficient microbial loop [32]. Besides the under-development NEMO-BFM model, none of the Baltic Sea LTL models currently simulates the abundance and distributional range of the spring dinoflagellates. It is suggested that all of the Baltic Sea LTL models would take such unique feature of the Baltic Sea vernal bloom into consideration for a better representation of e.g. the carbon paths/dynamics including the oxic, suboxic and anoxic conditions of the sea-floor within different areas of the Baltic Sea.

Considering the different levels in the ecosystem structure defined in *descriptor* biological diversity (D1), biodiversity is especially addressed at the level of communities (for phytoplankton and zooplankton) and populations (for fish and marine mammals) in several indicators within D1. However, *indicators* representing biodiversity strictly at species and habitat levels are missing. For example, all of the Baltic LTL models simulate at least one generic group of cyanobacteria. However, the cyanobacteria bloom in the Baltic Sea is mainly composed of two dominant species: *Nodularia spumigena* and *Aphanizomenon flos-aquae*, which especially differ for the fact that the former is toxic, while the latter is not e.g. [33]. This is addressed by the 2 groups of cyanobacteria represented in the under-development NEMO-BFM model, but should also be included in other models. This would enable a better understanding of the abundance and distributional range of both species within the Baltic Sea, and would provide valuable information for improving management and mitigation measures. Besides the existing biogeochemical models, other types of model might also extensively address such *indicator* as for example individual-based models.

None of the *descriptor* non-indigenous species (D2) related *indicators* (2.1.1 to 2.2.2) are addressed by any of the Baltic models, but could potentially be after some modifications to models. For example, the distribution and abundance in the Baltic Sea of the invasive and potentially toxic dinoflagellate *Prorocentrum minimum* e.g. [34] could be potentially modelled by any of the Baltic LTL models after the implementation of a new PFT that would represent the target species.

Many of the habitat-related *indicators* within D1, such as 'Habitat distributional range', 'Habitat distributional pattern', 'Habitat area' and 'Habitat volume', cannot currently be addressed by the evaluated models and the development/usage of other types of tools such as habitat suitability models are thus suggested.

Table 6
List of Model Derived Indicators (MDI) and corresponding MSFD *pressures* and number of Baltic Sea models addressing them.

MDI	Physical disturbance	Underwater noise	Marine litter	Interference with hydrological processes	Contamination	Nutrient and organic matter enrichment	Extraction of living resources	Marine acidification
Temperature	–	–	–	6	–	–	–	–
Salinity	–	–	–	6	–	–	–	–
pH	–	–	–	2	–	–	–	2
Oxygen penetration depth	7	–	–	7	–	7	–	–
Denitrification layer depth	1	–	–	1	–	1	–	–
Bacteria biomass	–	–	–	1	–	1	–	1
Phytoplankton biomass	–	–	–	7	–	7	–	7
Zooplankton biomass	–	–	–	7	–	7	–	7
Chlorophyll-a concentration	–	–	–	1	–	1	–	1
Primary production	–	–	–	7	–	7	–	7
Secondary production	–	–	–	9	–	9	–	9
Bacteria distributional range	–	–	–	1	–	1	–	1
Phytoplankton distributional range	–	–	–	6	–	6	–	6
Zooplankton distributional range	–	–	–	6	–	6	–	6
Fish: Herring biomass	3	–	–	3	3	–	3	–
Fish: Cod Biomass	3	–	–	3	3	–	3	–
Fish: Sprat Biomass	3	–	–	3	3	–	3	–
Marine mammal biomass (grey seals)	–	1	1	1	–	–	1	–
Zoobenthos biomass	2	–	–	2	–	2	–	–
Sea-ice algae biomass	1	–	–	1	–	1	–	1
Sea-ice bacteria biomass	1	–	–	1	–	1	–	1
Sea-ice fauna biomass	1	–	–	1	–	1	–	1
Total	22	1	1	82	9	58	10	50

Within the set of models analysed, descriptor food webs (D4) is discretely represented. In particular, *indicator* 4.3.1 linked to phytoplankton and zooplankton biomass and abundance is addressed by all of the models, while those linked to other trophic levels and living components, such as bacteria and fishes in *indicators* 4.1.1 and 4.2.1, are addressed only by some models, and an increase in the number of PFT is instead required for the rest of the models.

Several gaps are found when relating the analysed Baltic Sea models to the *indicators* of *descriptor* sea-floor integrity (D6) 6.1.1 to 6.2.4. In particular, the living components of the benthic habitat, except for the under-development NEMO-BFM, are poorly represented by the current set of models and required either an increase in complexity of the models, or the usage or development of new type of software such as habitat suitability models, which could not only describe both the biotic and abiotic parts of the system, but could also map those areas impacted by human activities such as fishing, drilling, enriching in organic matter and polluting.

The indicated suggestions are obviously not meant to be exhaustive among all the type of existing models, since newly developed models specifically targeted for the requirements of the MSFD should also be taken into consideration.

4. Conclusions

The conceptual workflow that allowed the identification of the biodiversity-related *descriptors*, the available models and their Model-Derived Indicators (MDI) (Fig. 1) has been presented. After a short review of the main characteristic of the Baltic Sea in relation to biodiversity and human pressures (Section 2.2), and a summary of the main features of the selected nine Baltic Sea models (Section 2.3), the analysis of the MDIs in relation to the number of models (Table 5), the type of living components (Fig. 3), and the related *descriptors* and *pressures* (Section 3.1) addressing them has been been discussed. Finally, a more detailed analysis that links the biodiversity-related *indicators* to each Baltic model (Section 3.2) has highlighted the current and potential capabilities of the available Baltic Sea models, together with some suggested developments of new features and/or modelling techniques.

22 MDI and 9 ecosystem models were found to be able to inform on and support the MSFD, which are 11% and 20%, respectively, of the total number found by Piroddi et al. [11] at European level. Despite the capability of the Baltic Sea ecosystem models to address several *pressures* and *descriptors*, several gaps still remain before the set of models would be entirely capable of assessing the environmental status of the Baltic Sea as requested by the MSFD. The gap analysis of the Baltic Sea study shows that some MSFD *descriptors*, such as food webs (D4), are described by the Baltic models to some extent, while others, such as non-indigenous species (D2) are not addressed at all, although there is potential for all of the models to address such descriptor. Sea-floor integrity (D6) is currently poorly addressed despite the tight coupling between the pelagic and benthic habitats in the shallow Baltic Sea, thus the usage and development of tools such as habitat suitability models is encouraged for the Baltic Sea. Most of the MDIs refer to biomass, while diversity in a more strict sense is poorly addressed apart from the under development NEMO-BFM, which adds considerable ecosystem complexity to the LTL Baltic Sea food web. Concerning habitat types, ice-associated habitats are described only by one model under development, despite sea ice covering the northern Baltic Sea every year. While all of the LTL models include some form of parameterisation of benthic chemical processes, only 2 models describe the living component of the Baltic seabed, which remains poorly represented.

Finally, the detailed analysis of the MSFD *indicators* in relation to each Baltic model in Section 3.2, where each model is classified

Table 7
Capabilities of the Baltic Sea models to address the biodiversity-related *indicators*: ✓ if the model is currently capable; (✓) if the model can be capable after some model's modifications; ✗ if the model is not capable and other model types are required.

Indicator	MDI	BaltProWeb	BALTSEM	ECOSMO	ERGOM	NEMO-BFM	RCO-SCOBI	SPBEM	Developments
1.1.1 Species Distributional range	Phytoplankton distrib. range	✓	✓	✓	✓	✓	✓	✓	
	Zooplankton distrib. range	✓	✓	✓	✓	✓	✓	✓	
	Bacterioplankton distrib. range	(✓)	(✓)	(✓)	(✓)	✓	(✓)	(✓)	e.g. new group/PFT
1.1.2 Species Distributional pattern within range	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
1.1.3 Area covered by the species	-	(✓)	(✓)	(✓)	(✓)	(✓)	(✓)	(✓)	e.g. new group/PFT representing benthic species
1.2.1 Population abundance and/or biomass	Phytoplankton biomass	✓	✓	✓	✓	✓	✓	✓	
	Zooplankton biomass	✓	✓	✓	✓	✓	✓	✓	
	Bacterioplankton biomass	(✓)	(✓)	(✓)	(✓)	✓	(✓)	(✓)	e.g. new group/PFT
	Zoobenthos biomass	(✓)	(✓)	(✓)	(✓)	✓	(✓)	(✓)	e.g. new group/PFT
	Sea ice algae biomass	(✓)	(✓)	(✓)	(✓)	✓	(✓)	(✓)	e.g. new group/PFT
	Sea ice fauna biomass	(✓)	(✓)	(✓)	(✓)	✓	(✓)	(✓)	e.g. new group/PFT
	Sea ice bacteria biomass	(✓)	(✓)	(✓)	(✓)	✓	(✓)	(✓)	e.g. new group/PFT
	Herring biomass	✓	(✓)	✓	✓	(✓)	(✓)	(✓)	e.g. coupling to HTL model
	Sprat biomass	✓	(✓)	✓	✓	(✓)	(✓)	(✓)	e.g. coupling to HTL model
	Cod biomass	✓	(✓)	✓	✓	(✓)	(✓)	(✓)	e.g. coupling to HTL model
	Grey seal biomass	✓	(✓)	(✓)	(✓)	(✓)	(✓)	(✓)	e.g. coupling to HTL model
1.3.1 Population demographic characteristics	Herring biomass (body size)	✓	(✓)	✓	✓	(✓)	(✓)	(✓)	e.g. coupling to HTL model
	Sprat biomass (body size)	✓	(✓)	✓	✓	(✓)	(✓)	(✓)	e.g. coupling to HTL model
	Cod biomass (body size)	✓	(✓)	✓	✓	(✓)	(✓)	(✓)	e.g. coupling to HTL model
	Grey seal biomass (body size)	✓	(✓)	(✓)	(✓)	(✓)	(✓)	(✓)	e.g. coupling to HTL model
1.3.2 Population genetic structure	-	✗	✗	✗	✗	✗	✗	✗	e.g models of population genetics structure
1.4.1 Habitat distributional range	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
1.4.2 Habitat distributional pattern	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
1.5.1 Habitat area	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
1.5.2 Habitat extent	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models

Table 7 (*continued*)

1.6.1 Habitat: Condition of the typical species and communities	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
1.6.2 Habitat: Relative abundance and/or biomass	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
1.6.3 Habitat: physical, hydrological and chemical conditions	Temperature	✗	✓	✓	✓	✓	✓	✓	e.g. coupling to hydrodynamic model
	Salinity	✗	✓	✓	✓	✓	✓	✓	e.g. coupling to hydrodynamic model
	pH	✗	✓	✓	✓	✓	✓	✓	e.g. adding carbonate system to the model
	Oxygen penetration depth	✓	✓	✓	✓	✓	✓	✓	
	Denitrification layer depth	✓	✓	✓	✓	✓	✓	✓	
1.7.1 Composition and relative proportion of ecosystem components	-	✗	✗	✗	✗	✗	✗	✗	
2.1.1 Trends in abundance, temporal occurrence and spatial distribution of invasive non-indigenous species	-	✓	✓	✓	✓	✓	✓	✓	new group/PFT representing a single invasive species
2.2.1 Ratio between invasive non-indigenous species and native species	-	✓	✓	✓	✓	✓	✓	✓	new group/PFT representing a single invasive species
2.2.2. Impacts of non-indigenous invasive species	-	✓	✓	✓	✓	✓	✓	✓	new group/PFT representing a single invasive species
4.1.1. Performance of key predator species or trophic groups	Primary production	✓	✓	✓	✓	✓	✓	✓	
	Secondary production	✓	✓	✓	✓	✓	✓	✓	
4.2.1 Proportion of large fish at the top of food webs	Cod biomass	✓	✓	✓	✓	✓	✓	✓	e.g. coupling to HTL model
4.3.1 Abundance trends of functionally important selected groups/species	Phytoplankton biomass	✓	✓	✓	✓	✓	✓	✓	
	Zooplankton biomass	✓	✓	✓	✓	✓	✓	✓	
	Bacterioplankton biomass	✓	✓	✓	✓	✓	✓	✓	e.g. new group/PFT
	Zoobenthos biomass	✓	✓	✓	✓	✓	✓	✓	e.g. new group/PFT
	Sea ice algae biomass	✓	✓	✓	✓	✓	✓	✓	e.g. new group/PFT
	Sea ice fauna biomass	✓	✓	✓	✓	✓	✓	✓	e.g. new group/PFT
	Sea ice bacteria biomass	✓	✓	✓	✓	✓	✓	✓	e.g. new group/PFT
	Herring biomass	✓	✓	✓	✓	✓	✓	✓	e.g. coupling to HTL model
	Sprat biomass	✓	✓	✓	✓	✓	✓	✓	e.g. coupling to HTL model
	Cod biomass	✓	✓	✓	✓	✓	✓	✓	e.g. coupling to HTL model
	Grey seals biomass	✓	✓	✓	✓	✓	✓	✓	e.g. coupling to HTL model
6.1.1. Type, abundance, biomass and areal extent of relevant biogenic substrate	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
6.1.2. Extent of the seabed significantly affected by human activities	Oxygen penetration depth	✓	✓	✓	✓	✓	✓	✓	
	Denitrification layer depth	✓	✓	✓	✓	✓	✓	✓	e.g. new state variable
6.2.1. Presence of particularly sensitive and/or tolerant species	-	✓	✓	✓	✓	✓	✓	✓	e.g. new group(s)/PFT(s) representing (a) single species
6.2.2. Multi-metric indexes assessing benthic community condition and functionality	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models
6.2.3. Proportion of biomass or number of individuals in the macrobenthos	Zoobenthos biomass	✓	✓	✓	✓	✓	✓	✓	e.g. new group/PFT
6.2.4. Parameters describing the characteristics of the size spectrum of the benthic community	-	✗	✗	✗	✗	✗	✗	✗	e.g. habitat suitability models

as capable, potentially capable or not capable of addressing the biodiversity-related *indicators*, aims to provide support for both the modelling community, suggesting research areas where more effort is needed, but also for policy makers and stakeholders to enable a better understanding and direction for funding requirements.

The analysis here described is biased by the high representation of coupled hydrodynamic-biogeochemical models versus other type of models that are not described here. However, there is no doubt that, when describing the marine food web from microbes to top predators, the increasing interest is towards end-to-end models, which combine LTL and HTL models in a single quantitative tool that can be used for ecosystem-based management since capable of handling multiple impacts, such as those expected under climate change [35]. The main challenge is to fill the gaps between the biomass-based representation of the widely developed and used LTL biomass-based models and the *descriptors*, *criteria*, *indicators* and *pressures* defined in the MSFD, which only partly correlate to biomass. While the development of new indicators, better linked to the type of outputs that current available models generate, is highly encouraged, new or revised models specifically targeted to inform on MSFD are to be implemented. The first step towards better addressing marine biodiversity is certainly increasing the ecosystem complexity in terms of functional groups to a meaningful level. One approach is the use of a cost function to assess among differently complex models (e.g. in terms of functional groups) the one that score the highest skills, and that not necessarily is the most complex model e.g. [36]. A further step is to move from PFT diversity to species diversity. An example is the one of Artioli et al. [37] that modifies a LTL model with the addition of phytoplankton diversity to simulate invasion from phytoplankton, and thus directly addressing non-indigenous species (D2) of the MSFD, which none of the Baltic models is currently doing. With such a toll, the assessment of the likelihood of success of an invasion and the estimate of the potential impact on ecosystem structure would become possible. In general, a tighter link between the political ground of the MSFD and the quantitative marine ecosystem models is urgently needed and the development of innovative tools in terms of models and indicators that can be used to that end is strongly encouraged.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.marpol.2016.04.021.

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