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A Prototype Decision Support Tool for Ballast Water Risk Management using a Combination of Hydrodynamic Models and Agent-Based Modelling

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NORTH SEA BALLAST WATER

European Union The European Regional Development Fund

The Interreg IVB
North Sea Region
Programme



*Investing in the future by working together
for a sustainable and competitive region*

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July 2013



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A PROTOTYPE DECISION SUPPORT TOOL FOR BALLAST WATER RISK MANAGEMENT USING A COMBINATION OF HYDRODYNAMIC MODELS AND AGENT-BASED MODELLING

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1 ABSTRACT

We report the development of a prototype Decision Support Tool (DST) for modelling the risks of spreading of non-indigenous invasive species via ballast water. The DST constitutes of two types of models: A 3D hydrodynamical model calculates the currents in the North Sea and Danish Straits, and an agent-based model estimates the dispersal of selected model organisms with the prevailing currents calculated by the 3D hydrodynamical model. The analysis is concluded by a post processing activity, where scenarios of dispersal are combined into an interim estimate of connectivity within the study area. The latter can be used as a tool for assessment of potential risk associated with intentional or unintentional discharges of ballast water. We discuss how this prototype DST can be used for ballast water risk management and outline other functions and uses, e.g. in regard to ecosystem-based management and the implementation of the EU Marine Strategy Framework Directive.

2 INTRODUCTION

Transfers of non-indigenous species potentially may pose a threat to the receiving ecosystem and to the society. Organisms that mass-reproduce when they are transported and released in new environments by humans are 'non-indigenous invasive species', sometimes referred to as 'alien species'. Ultimately they may cause serious impact on ecosystems both ecologically and economically. Ship's ballast water is a main source of non-indigenous marine organisms and, when released, some of these species have caused dramatic and permanent damage to coastal ecosystems around the world (e.g.: Bax et al. 2003, Leppäkoski et al. 2003). Since it in practise has been impossible to control and mitigate the spreading of established invasive species in 'new' marine environments, efforts should focus on the prevention of introductions.

The trend in biological invasion shows an exponentially increase during the last 200 years (e.g. see: Leppäkoski & Olenin 2000,), nevertheless the problem of marine bio-invasion and the resulting environmental consequences has taken time to be realised. One of many reasons is that unlike terrestrial ecosystems, bio-invasions in the marine environment are poorly understood since their consequences may be difficult to observe by the eye. Many bioinvasions are a threat to the ecosystems, to human health as well as to the economy. The invaded ecosystems are also threatened as exotic species may alter ecosystem functions and community structure. In some cases, non-indigenous species cause a dramatic decline in important marine resources by competing with the native species for food, habitat, by predation/parasitism, or due to a number of indirect reasons.

Biological invasions may also interact in combination with other natural and anthropogenic environmental factors such as climate change, habitat destruction and pollution to jeopardize the integrity of the ecosystem. This means that the impacts of future introductions are uncertain as well as unpredictable and current invasions may evolve into unforeseen intricate patterns. More challenges are forecast to come in handling introductions and efforts should be focused on preventing new establishments in order to protect the native biota and its diversity by means of managing human activity.

The scope of this work is to demonstrate the usefulness of the combination of hydro-dynamical (HD) and agent-based models (ABM) as a tool for understanding the ecological connectivity of marine areas of the North Sea, Kattegat and the inner Danish straits and its application for risk assessment of invasive species brought to the region (or transported with-in the region) by ballast water from sea vessels. Ecological connectivity mapping is proposed to provide a theoretical basis for identifying areas where ballast water could be released with the least potential risk for species to spread extensively within the region. In addition connectivity mapping can provide knowledge on how well each specific part of the region is connected with other parts of the region.

3 METHODS

Study area - The study area is the North Sea, located on the continental shelf of north-western Europe and bordered by England, Scotland, Sweden, Norway, Denmark, Germany, the Netherlands, Belgium and France. It opens out to the Atlantic Ocean, the English Channel, and towards the less saline Baltic Sea.

The Greater North Sea (as defined by OSPAR) has a surface area of 750,000 km² and a volume of 94,000 km³ and is separated into various areas, the relatively shallow southern North Sea (the Southern Bight and the German Bight), the central North Sea, the northern North Sea, the Norwegian Trench and the Skagerrak, which is a shallow transition zone between the Baltic and the North Sea (OSPAR 2010).

The eastern part of the North Sea, along the coasts of Denmark and Germany, mean winter sea surface temperature (SST) is usually less than 3°C. The summer SST mean is 18°C and declines to 13°C northwards along eastern Britain (Hayward & Ryland 1995). The annual freshwater river input is ca 300 km³, about one-third of that comes from the snow-melt waters of Norway and Sweden and the rest from major rivers while the main source of fresh water supply is through the Baltic Sea (Hayward & Ryland 1995).

The most prominent current circulation of the North Sea is a roughly anti-clockwise flow where residual currents moves southwards along the east coast of the UK and northwards along the Western European coast. Saline water enters the Baltic Sea through Kattegat at depth while surface flow of brackish water from the Baltic Sea enters the Kattegat and North Sea. (OSPAR 2010).

The North Sea, which is an economically and ecologically important marine region, is sensitive to a range of human activities. Key issues are nutrient enrichment and eutrophication, contamination with hazardous substances, overfishing, physical modification and an unfavourable biodiversity status (OSPAR 2010, HELCOM 2010). Introduction of non-indigenous species has been identified as an emerging issue.

Many areas in the North Sea are valuable habitat for marine life as well as of economic importance for the surrounding states. The shallow and productive North Sea while being one of the busiest seas in the world in seaborne trading, it is also heavily exploited for its natural resources. Activities such as fishing, dredging, oil and gas exploration, shipping, discharges of nutrients and contaminants have polluted as well as depleted reserves in the area. Increases in awareness for the protection of the environment and resource management in the North Sea have surged during the last decades (Misund & Skjoldal 2005), and one significant issue that has been identified relatively recently is the ramifications of species introduction via ship transportation and aquaculture mishaps.

The most up-to-date inventory of alien species in the North Sea region lists alien aquatic species of 167 taxa (Gollasch et al. 2009). This calls for a precautionary approach to prevent future arrivals of new species. One of the key vectors in moving aquatic alien species is shipping, e.g. ballast water-mediated species introductions from ships prevail in many regions world-wide.

Hydro-dynamic model - The applied hydrodynamic model is based on the MIKE 3 modeling system developed by DHI. The MIKE 3 model is a dynamic time-dependent 3D baroclinic model for free surface flows. The mathematical foundation of the model are the Reynolds-averaged Navier-Stoke's equations in three dimensions, including the effects of turbulence and variable density, together with conservation equations for mass, heat and salt, an equation of state for the density, a turbulence module and a heat exchange module. The equations are solved on a Cartesian grid by means of the finite difference techniques. In another version of MIKE 3 (the MIKE 3 FM version) the equations are solved on an unstructured (flexible) mesh by means of finite volume/finite element techniques. The hydrodynamic model provides a full 3D model representation of the water levels, flows, salinity, temperature and density within the modeling domain. For more information on the MIKE 3 modeling system reference is made to DHI (2009) and DHI (2011).

Model setup - A 3D North Sea hydrodynamic model is applied as the basis for the agent-based modelling (ABM) and subsequent connectivity modeling. A period of a full year (2005) has been modeled in order to capture the seasonal and higher frequency variability of the North Sea circulation. The model represents the overall circulation patterns in the North Sea and the Belt Sea comprising of tide, meteorologically and density driven circulation, freshwater inputs and stratification. A local 3D hydrodynamic model resolving the Belt Sea in a higher resolution has also been applied.

The model domain includes the major part of the North Sea, the Belt Sea and the Baltic Sea. The model applies a Cartesian grid in UTM-32 projection with a horizontal resolution of 3 nautical miles. In the vertical dimension a 2 m resolution is used, with a maximum of 110 layers depending on the local water depth. However, the surface layer with surface elevation varying with the actual tide has a typical thickness of 5 m. For areas with depths under level -223 m the rest of the water column is included in the lowest layer. The model domain is shown in Figure 1.

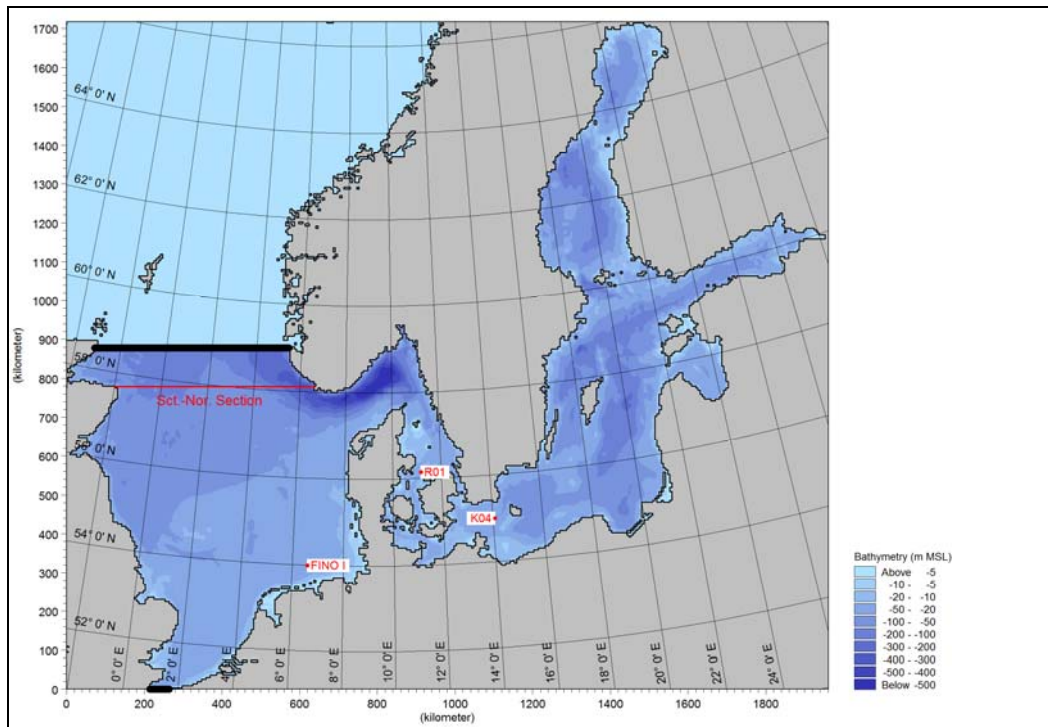


Figure 1. Model domain and location of selected measurement stations. The thick black lines indicate the open boundaries of the model

The model has been run for the period 2000-2008, but the period applied for the present purpose is the year 2005. The model runs with a hydrodynamic time step of 300 seconds. The model results in terms of 3D fields of for example current, salinity and temperature are saved every 1 hour.

The forcings on the open boundaries towards the Norwegian Sea and the English Channel include: (1) Astronomical tide along boundary (actual values for 2005), (2) salinity distribution in vertical sections (monthly climatologic from ICES), and (3) temperature distribution in vertical sections (monthly climatologic from ICES). Atmospheric forcings such as wind, air pressure, air temperature, cloudiness and precipitation (actual 2D maps with 1 hour resolution) were originally delivered by Vejr2, a former meteorological company. The wind and air pressure are incorporated in the momentum equations, and the precipitation is used in the mass equation. Wind is also included in the turbulence module. The heat exchange module, which calculates the sea-air heat exchange, makes use of wind, air temperature and cloudiness. The runoff in terms of discharges of freshwater from land to the model domain is represented in the model by 85 source points. The runoff is based on data from SMHI's operational HBV-model and on data from Global Runoff Data Centre (GRDC). It is important to note that the applied sources are lumped sources, which means that they represent the main rivers at each location as well as the non-resolved rivers/inflows in the vicinity of the location. This means that the total runoff to the Baltic Sea/North Sea is correctly represented in the 85 model sources. Initial fields of salinity and temperature, i.e. 3-D fields of salinity and temperature within the model domain, have been established based on previous model runs. The present hydrodynamic model setup is an updated version of the model used for the BANSAI project (SMHI 2005).

Since the North Sea hydrodynamic model is relatively coarse in the Belt Sea (3 nautical miles cell size), a local hydrodynamic model covering the Belt Sea and the Baltic Sea was also applied. This model has a finer resolution (down to 1km cell size) in the Belt Sea as illustrated in **Figure 2** and thus represents the flow here in more detail. The model was developed for another purpose, but has been made available for the present purpose (FEHY 2012).

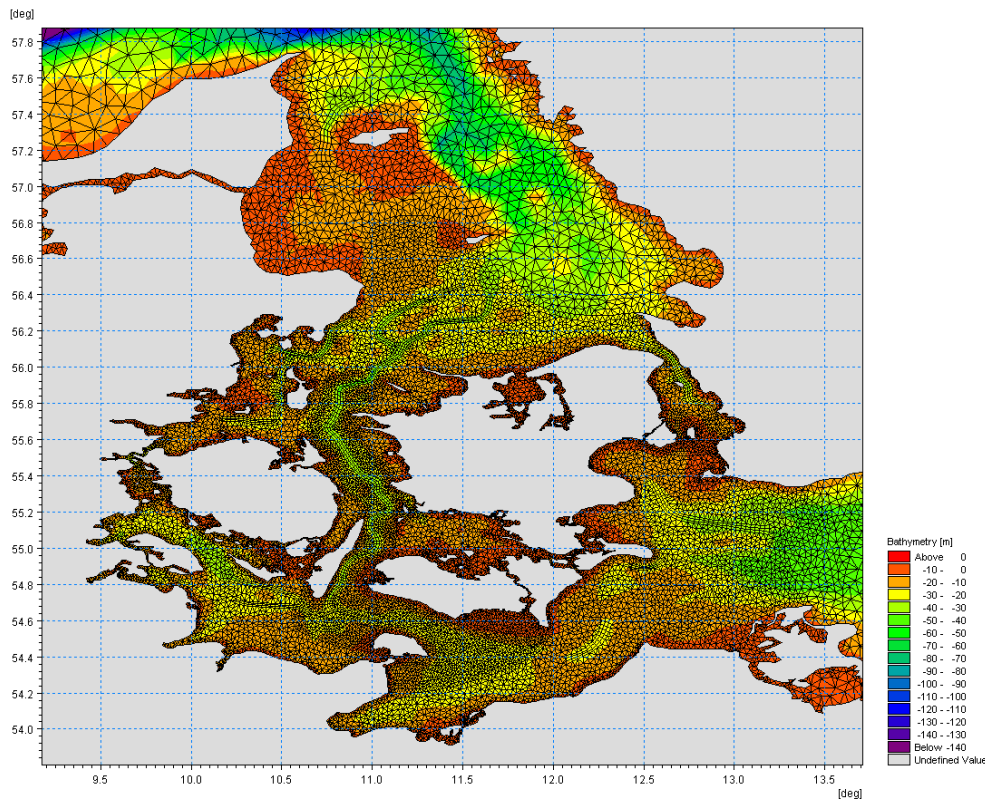


Figure 2. Section of the computational mesh for the hydrodynamic model covering the inner Danish waters. Colors indicate depth intervals in meters.

Agent-Based Modeling – Agent-Based Models (ABM) have been widely applied in recent years for simulating a variety of phenomena within very diverse disciplines such as biology and ecology, social sciences, industrial process optimization, traffic infrastructure planning and the financial sector just to mention a few examples. In ecology ABMs aim at describing the behavior and state of discrete entities such as individual organisms or groups of organisms (~superindividuals). One key element of ABMs is the ability to simulate how individuals respond (in terms of behavior and state) to a spatially and temporarily varying environment. When studying the aquatic environment and how small aquatic individuals spread within an aquatic system, information on water movement is a fundamental need. Here 3-dimensional hydro-dynamical models describing the water currents in high temporal and spatial resolution can provide a very detailed basis for these types of studies. By defining agents as discrete entities with an explicit x-y-z coordinate at any given point in time it is possible to link this type of ABM with a hydro-dynamical model and thus combine the current driven movement of agents (= advection/dispersion) with biological movement behaviour processes such as horizontal swimming, vertical migration and age induced settling. This type of ABM is often referred to as a Lagrangian type ABM which has been applied frequently e.g. in studies examining the spreading and migration of pelagic larvae and fish (e.g. Goodwin et al. 2001, Humston et al. 2004, Cowen et al. 2006).

To simulate the potential spread of marine invasive species deriving from ballast water an (Lagrange type) ABM was developed and applied in combination with the hydro-dynamical model as described in the previous section. The ABM framework applied is an integrated part of the ecological modeling software ECO Lab, which is an open equation solver for building and executing biological and ecological models of aquatic systems. ECO Lab may be applied as an add-on module to the MIKE 3 FM hydro-dynamical modeling system.

The developed ABM is here applied to simulate the spread of agents (or organisms) in the entire model area primarily driven by advection processes predicted by the hydro-dynamical model. Three model organisms are chosen to represent examples of major groups of marine organisms likely to be introduced as invasive species through the release of ballast water within the North-sea region. Here 'groups of marine organisms' refer to organisms which exhibit common behavioral characteristics. The groups of organisms considered here include representatives of a: (1) Planktonic species (purely passive drifters), (2) pelagic larvae of a benthic invertebrate species (passive drifters in combination with settling), and (3) fish species (passive drifters in combination with active swimming activity)

We mimic the spread of these three types of model organisms in a very simplistic way by: (1) Simulating passive drift in combination with a constant mortality rate, (2) simulating passive drift in combination with active settling activity triggered as a function of age, and (3) simulating passive drift in combination with active horizontal swimming behavior including mortality rate. In addition to these three simulations as a reference we simulate passive drifting only subject to advection/dispersion processes.

It should be emphasized that the approach described here is an attempt to address the spreading mechanisms and potential of small marine organisms in a general way. The approach is deliberately not addressing species specific spreading. Also when considering the risk of introducing invasive species in the marine environment species specific habitat preferences, life histories and environmental tolerances are essential to understand and predict the ability of introduced species to establish a sustainable population. These issues are not addressed here. However, species specific traits and the implication for establishing sustainable populations can be simulated by extending the current approach combining hydrodynamic modeling and ABM with habitat maps and/or classical concentration based (Euler type) ecological modeling. The latter describing any necessary dynamical parameter affecting the organism such as salinity, temperature, dissolved oxygen, food abundance etc.

Unlike the hydro-dynamical modeling, due to the nature of the phenomena modeled neither calibration nor validation of the ABM is being considered. This means that the modeling exercise here apart from the hydro-dynamical modeling is predominantly theoretical. The ABM approach can be seen as an interpreter to describe how common behavioral characteristics and traits may, or may not, result in significant deviations from passive drift. The results of the model approach should be evaluated as such.

ABM formulation

Selected simplistic functional behaviors and life histories used for formulation of the ABM include: (1) Movement in terms of dispersion and active swimming, (2) settling, (3) mortality, and (4) longevity. The background for and the ABM formulations used in this study are described in Appendix 1 in the Online Supplementary Material. Please note that this appendix includes additional reference not cited in this paper.

Connectivity mapping - The combination of HD modeling and ABMs (or particle tracking models) has been applied in several studies addressing the degree of connectivity between specific habitats or sub-regions within marine regions (Cowen et al 2002, 2006; Paris et al 2005; Christensen et al 2008, Berglunda et al. 2012) However, in most cases the studies have focused on specific species and connectivity between the species specific habitats, or in more general connectivity in terms of e.g. dispersal of passively drifting larvae between specific habitats such as coral reefs, spawning sites etc. A more general approach applying a combination of hydro-dynamical modeling and simple particle tracking has been proposed to establish a framework for identifying connectivities of any sub-region within the South-Western shelf region of Australia (Condie et al. 2006). In short the particle trajectories from the simulations are treated statistically and translated into probability maps describing the 'probability of any two regions within the model domain being connected by the modeled circulation'. Probabilities were 'computed for a range of dispersion times on a 0.1 degree geographical grid' covering the model domain. The connectivity statistics addresses connectivities in discrete points in time and space as well as statistics aggregated for longer periods (months or quarters). As part of the project a web-based service was developed where users can select a 'source area' from a Map interface, select start time and dispersal duration, and as a result get a connectivity probability map for the selected source area and dispersal duration.

In this study the above outlined approach has been further developed, e.g. by (1) including not only passive particle tracking but also biological processes by applying ABM techniques and by (2) developing an overall connectivity index or indices compiling all connectivity statistics of each local area into a single value.

In order to define 'connectivity' we discriminate between two types of connectivities: downstream-connectivity and upstream-connectivity (**Figure 3**).

Downstream connectivity we define as connectivity between donor areas (or source areas), and surrounding areas (or receiving areas). Here 'areas' does not necessarily refer to computational grid cells but rather any areal division of the model domain into e.g. a regular grid or a number of management units. During a simulation each agent 'visiting' an area at any time will have a distinct trajectory forward in time visiting other areas in the model domain. When simulating a large number of agents the equivalent large number of trajectories forward in time can be statistically analyzed revealing the probability of areas to supply agents to other areas. This we refer to a downstream connectivity probability. Downstream connectivity answers questions such as 'where do the agents go from here?'

Upstream connectivity we define as connectivity between receiving areas and source areas. Again 'areas' can refer to any areal division of the model domain. During a simulation each agent 'visiting' an area at any time of the simulation will have a distinct trajectory backwards in time having visited other areas in the model domain prior to the registration of the agent in the area analysed. When simulating a large number of agents the equivalent large number of trajectories backwards in time can be statistically analyzed revealing the probability of areas to receive agents from other areas. This we refer to as an upstream connectivity probability. Upstream connectivity answers questions such as 'where do the agents come from?'

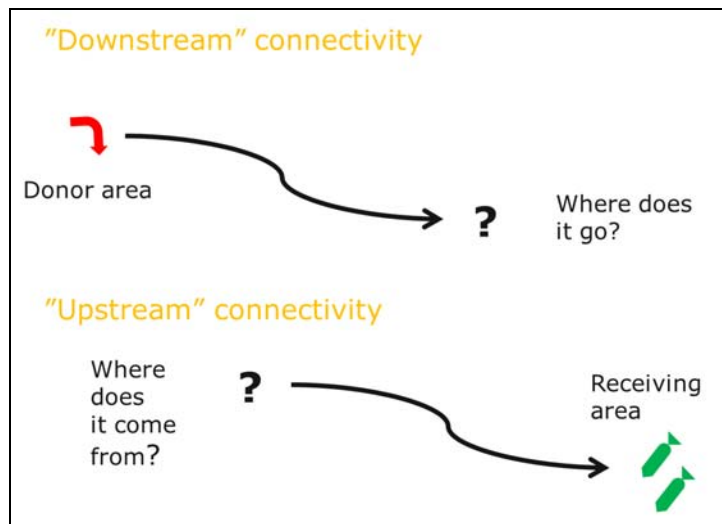


Figure 3. Sketch of the differences between the concepts of downstream connectivity and upstream connectivity.

Both upstream and downstream connectivity probabilities can be evaluated at any dispersal time ranging from seconds to years depending on the organism and dispersal phenomenon considered.

Connectivity probability - All agent trajectories stored every 6 hour of the 1 year simulation period are analyzed statistically. The model domain is divided into 25×25 km quadratic grid cells resulting in approximately 1000 local areas covering the sea area. This is the spatial resolution at which connectivities will be evaluated. For each agent registered in an area the future and previous location of each agent is registered/tracked considering four dispersal times (forward and backwards in time). This is repeated for every 6 hour. For details on the selection of dispersal times see the next section.

To calculate downstream connectivity for the whole simulation period the numbers of agents remaining in the area and appearing in other areas at each of the four dispersal times are counted. Downstream connectivity probabilities are calculated simply by dividing these numbers for each area by the total number of agents registered in the area analyzed. The outcome is a distribution map for each area showing the distribution of probabilities, i.e. the probability of an agent in an area to be registered sometimes in the future in the same area and in each of the surrounding areas. In cases where mortality is included in the scenario probabilities are weighted according to the likelihood that an agent survives each of the four dispersal times.

To calculate upstream connectivity for the whole simulation period for an area the numbers of agents originating from the same area and each of the surrounding areas at each of the four dispersal times backwards in time are counted. Upstream connectivity probabilities are calculated by dividing these numbers by the total number of agents registered in the area analyzed. Also here the outcome is a distribution map for each area showing the distribution of probabilities, i.e. the probability of an agent in an area having visited each of the surrounding areas including the probability of agents that have remained in the area analyzed during the dispersal times considered.

For scenario 1 (passive drifting), scenario 2 (planktonic organism) and scenario 3 (juvenile fish) these procedures are repeated for all 25×25 km areas.

For scenario 4 the combination of mortality and settling was not simulated in one simulation. Since mortality is high (0.1 per day) and mean settling age is 30 days, only a very little fraction of introduced agents will reach settling age. To achieve sufficient statistical basis for the connectivity analysis this would require a very large number of agents in the model simulation. For technical reasons this was not desirable. Instead mortality was taken into account as part of the post-processing of the model results.

For each agent registered in an area every 6 hours the future location where it settles is registered. For all agents registered in each area at any time for the whole simulation period the numbers of agents settled in each of the surrounding areas, including the area analysed, are counted and the probabilities are calculated by dividing these numbers by the total number of agents registered in the area analyzed. To account for mortality (0.1 per day) the number of agents settled in an area is adjusted using the following equation:

$$N_{adj} = N \times (1 - k)^t \quad (2)$$

Where:

- N_{adj} is the adjusted number of settled agents
- N the number of agents settled in an area
- k the mortality rate per day (=0.1 per day ~ 0.1 daily mortality probability)
- t time between the time an agent is registered until it settles

Similar to the downstream dispersal probabilities, prior to calculating the upstream dispersal probabilities for each area in scenarios 4 numbers of agent originating from each of the surrounding areas are adjusted according to the equation above, N_{adj} now being the adjusted number of agents at the point in time where agents are discharged into the water, and 't' is the time between the time of discharge until the agents is settled.

For downstream connectivity probabilities in scenario 4 since agents are registered every 6 hours the same agent will be registered every 6 hour starting at the time of its introduction to the model domain until it settles somewhere (in average 30 days after introduction). Every consecutive 6 hour time step that the same agent is registered, the time remaining until settling decreases by 6 hours. This way all the registrations of an agent, each time representing a time and location of release of ballast water, will correspond to the assumption that the distribution of larvae age-classes is uniformly distributed in the ballast water at the time of release.

Notice that for scenario 4 while downstream connectivity probabilities reflect the assumption that all age classes are evenly represented in the ballast water at time of discharge, upstream connectivity probabilities reflect the case where organisms are age class zero at the time of discharge.

The outcome of the connectivity probability mapping for all scenarios as described above consists of connectivity probability matrices equivalent to distance matrices applied e.g. as a look up table for distances in km's between major cities or locations in Road atlases. Instead of distances in km's the connectivity matrices include numbers representing probabilities of, in case of downstream connectivity, agents in area A ending up in area B and agents in area B ending up in area A. In contrary to a distance matrix either direction has different probabilities. A conceptual example is shown in Table 1.

The resulting connectivity matrices will consist of approximately two 1000 × 1000 matrices for downstream and upstream connectivities respectively, for each set of dispersal times. Connectivity probabilities for each area can be extracted from the two matrices to produce connectivity probability maps for downstream and upstream connectivities respectively. These approximately 2000 maps can be referred to a multilayer connectivity maps or MCMs and are available as Online Supplementary Material.

Table 1. Example of a downstream connectivity matrix for 4 areas (1-4). Table values represent probabilities of agents in one area (=source area) ending up in another area (=receiving area).

Source area	Receiving area				Sum
	1	2	3	4	
1	0.92	0.04	0.00	0.04	1.00
2	0.01	0.31	0.08	0.60	1.00
3	0.07	0.50	0.29	0.14	1.00
4	0.00	0.15	0.63	0.22	1.00
Sum	1.00	1.00	1.00	1.00	

Ideally in cases where all agents simulated as passive drifters (as in scenario 1) and where agents are not subject to mortality the sum of probability values within each probability map will be 1. However when mortality is included as part of the ABM the sum of probabilities will be less than 1 all probabilities (in case of downstream connectivity) representing the probability of an organism being distributed to other areas a specific point in time ahead.

Since connectivity probabilities are expected to vary spatially depending on the dispersal time considered, 4 dispersal times were selected for each analysis in order to cover a range of dispersal situations for a given organism. These four dispersal times were selected for each analysis from three criteria: (1) Ecological relevance, (2) a minimum of 10% of agents at t=0 remaining at any dispersal time, and (3) seasons evenly reflected in calculation results. Here 'ecological relevance' refers to e.g. that the dispersal time should lie within the expected life duration and/or the duration of the pelagic stage.

For scenario 1 (passive drifting) upstream and downstream connectivity probabilities are calculated for different sets of four dispersal times: 2, 4, 6, and 8 days, 3, 9, 15, and 21 days, and 7, 14, 21, and 28 days. The different sets of dispersal times are used for comparison with scenarios 2, 3, and 4 (see below), and in order to evaluate how selections of different dispersal times may influence the calculated connectivities. A maximum of 28 days were applied primarily to ensure that months and seasons were evenly reflected in calculation results.

For Scenario 2 (planktonic species) upstream and downstream connectivity probabilities are calculated for four dispersal times: 3, 9, 15, and 21 days. These were selected for the following reasons. Since a mortality of 0.1 d⁻¹ is applied 10% of the agents at t=0 remains approximately 24 days later. The 24 days were divided evenly into four time periods (0-6 days, 6-12 days etc.) and the mean day numbers of each of four 6-days periods were selected as the four dispersal time (~3, 9, 15 and 21 days).

For scenario 3 (fish) upstream and downstream connectivity probabilities are calculated for four dispersal times: 1, 2, 3, and 4 weeks. These were selected for the following reasons: Since juvenile fish typically has much lower mortality (here 0.003 d^{-1}) 10 % of agents will remain after approximately 2 years. Thus to cover the entire time span this will require a much longer simulation than the 1 year simulation for the current study. In addition the need to reflect months and seasons evenly a maximum of approximately 1 month dispersal time were selected. Based on these considerations four weekly dispersal times were selected.

For scenario 4 (pelagic larvae of benthic invertebrate) upstream and downstream connectivity probabilities are calculated for the same four dispersal times as for scenario 2.

Connectivity indexes - The primary strength of the connectivity probability matrices described in the previous section is to give detailed information on how connected any two areas are within the modeling domain integrated over time. However more than 1000 maps require some kind of simplification in order to provide a more overall measure on how well connected areas are in general without necessarily providing any information on precisely which areas are interconnected. Within ballast water risk assessment there is need to distinguish between areas more likely to export organisms far away and/or to a larger area than other areas (~ through downstream connectivity). These areas with high dispersal potential can be perceived as high risk zones where the release of invasive species through ballast water may have an increased potential of reaching optimal habitat conditions thereby increasing the likelihood for establishing a population successfully. Here we propose a methodology to compile all information from the downstream connectivity probability maps into one single map using a simple and transparent approach.

Similarly, in terms of upstream connectivity, it is important to identify areas more likely to receive invasive species than others, i.e. acting as sinks. These areas can be identified from upstream connectivity probability matrices as areas with high probabilities of receiving agents from far away and/or from a large area.

It is clear that the proposed simplification of connectivities through the development of connectivity indexes assumes that agents are distributed randomly within the entire modeling domain which is not the case when it comes to invasive species from ballast water. However indexes will give indications on where release of ballast water may be more likely to result in a significant spread of organisms, and which areas will be more likely to receive invasive species than others. This type of information is important from a management point of view.

For calculation of connectivity indexes the term 'momentum' (M) is introduced. Momentum can be calculated in several ways. The momentum can be calculated for each area and its probability map by simply summing the products of connectivity probabilities of each surrounding area and the distances to the areas.

$$M(\text{area } i) = \sum \text{Prob}(\text{area } j) \times D(\text{area } j) \quad (3)$$

This approach weights the probabilities with distance only. The results presented in this report apply this formula. However alternative definitions of Momentum may be applied to including multiplication of probabilities with areal coverage instead of distance, or a combination of areal coverage and distance, where areal coverage refers to the size of the area covered by say the 90 % fractile of probabilities.

4 RESULTS

The hydrodynamic model has been validated in terms of water level, salinity and temperature in a number of stations. The comparisons generally show a fairly good comparison between measurement and model. A few examples of this validation are given in Appendix 2 (see locations in **Figure 1**). The comparisons demonstrate that the model is able to reproduce the water temperatures well within the model domain. Both the variability and the absolute values are captured by the model. The annual cycle of the thermal stratification is described well by the model. Also the salinity conditions are described well by the model. The model captures the salinity stratification and the intrusions of saline North Sea water through the Belt Sea to the Arkona and Bornholm basins and further into the Gotland Deep in the Baltic Proper. The vertical structure of the water column in the northern North Sea is illustrated in Figure 4 (panel B), which shows the annual mean salinity and water temperature in a vertical section between Scotland and Norway. The lower salinities of surface waters along the Norwegian coast represent the outflowing brackish Baltic water.

The model includes the tidal currents as well as the meteorologically induced and the baroclinic currents. The modeled annual mean surface currents are shown in Figure 4, panel A. The mean current may be regarded as the residual currents, which may be expected to be important with respect to connectivity. Significant northward and northeastward residual current is observed in the southeastern and eastern part of the North Sea, whereas the western part displays relatively lower residual currents. In the Belt Sea an outward (northward) residual surface flow is observed, which transports the brackish Baltic water out into Skagerrak. In Skagerrak an anticlockwise gyre is observed and a residual flow along the Norwegian coast brings the Baltic surface water into the North Sea and further into the Norwegian Sea. All these features are in accordance with the literature. In the vertical, Figure 4 (panel C) shows a marked outward residual current in the upper water column along the Norwegian coast. This represents the outflow of mixed, brackish Baltic water and is consistent with the vertical salinity distribution mentioned above. In other parts of the vertical cross-section a relatively low, southward residual current is observed.

Because the calculation procedures are repeated for each 6 hour time step of the 1 year simulation time each agent will be included multiple times as part of the statistical basis for the analyses. Thus the total number of agents being analyzed results in a large amount of agents as the basis for the statistical probability maps.

The statistical analyses of connectivity were done based on results from the ABM simulations carried out for both a regional model for the entire model domain and a local model for the Kattegat, the Belts and the western part of the Baltic Sea. The statistical basis for the downstream connectivity of scenario 1 is shown in **Figure 5** and **Figure 6** for the two models. For the vast majority of the model domain the statistical basis for each area is more than 1000 agents. Smaller numbers are found close the shorelines and in the inner Danish straits. This is partly because a part of the 25 × 25 km squares along shorelines include land and thus the area covered by water is smaller than 25 × 25 km. In addition the smaller numbers may be a result of more agents being excluded from the simulation because agents closer to land and in shallow areas more likely hit land or seafloor boundaries.

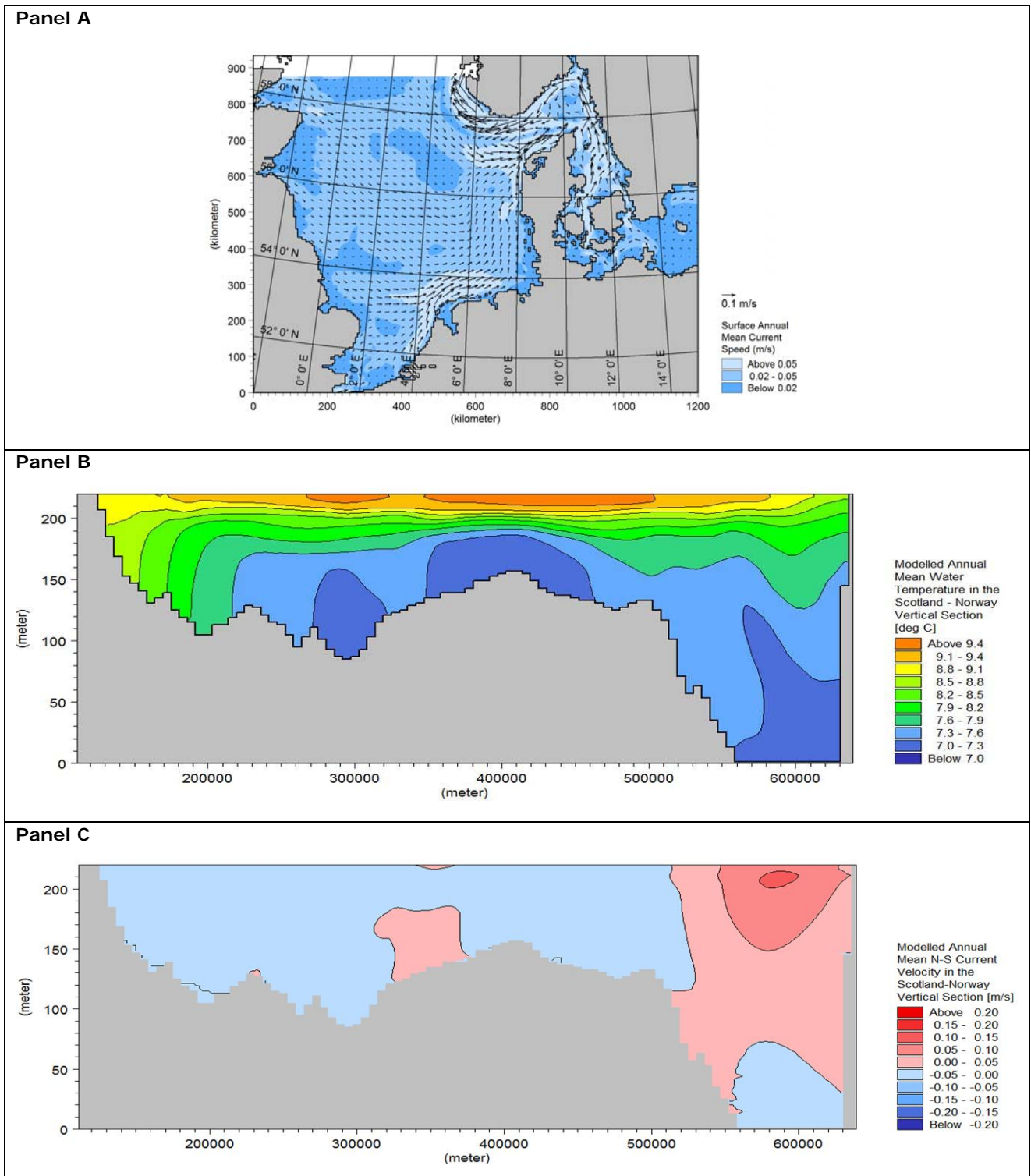


Figure 4. Panel A: Modeled annual (2005) mean surface currents. Panel B: Modelled annual mean water temperature in a vertical section from Scotland to Norway. Panel C: The north-south current component in the same vertical section. See Figure 1 for the location of the vertical section.

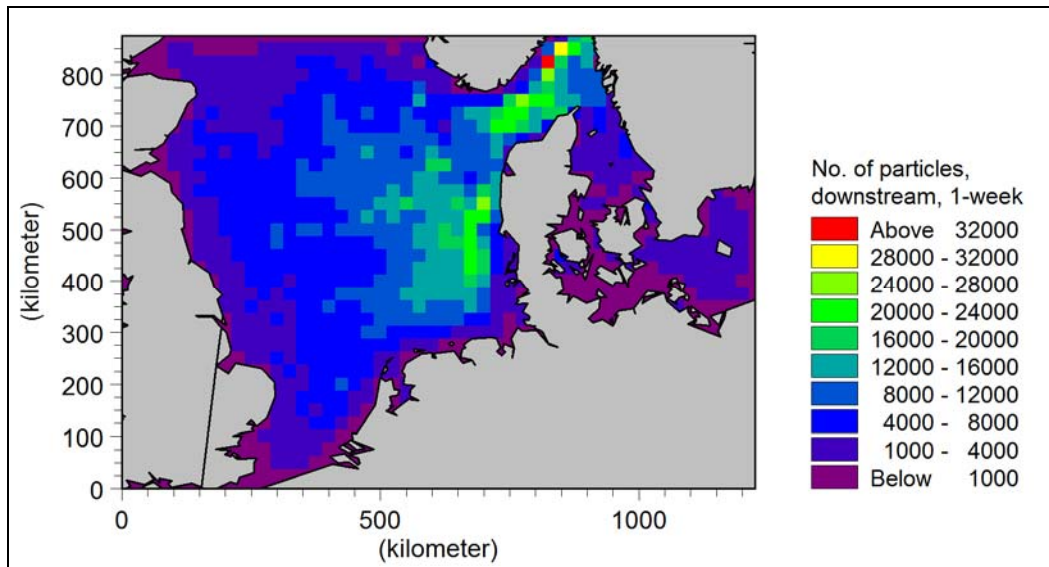


Figure 5. Statistical basis for the downstream connectivity probability mapping of scenario 1. Numbers are numbers of agents available for the statistical analysis of the downstream connectivity using the regional model.

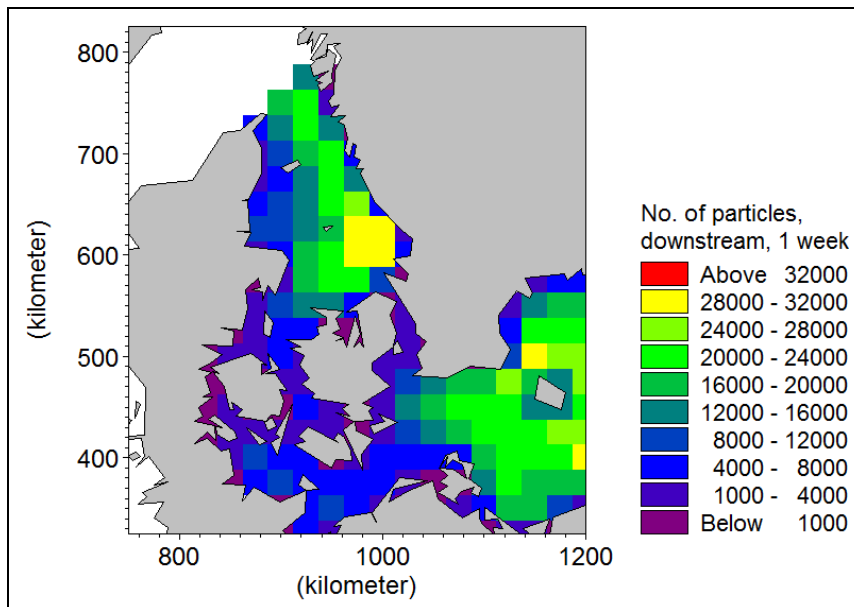


Figure 6. Statistical basis for the downstream connectivity probability mapping of scenario 1. Numbers are numbers of agents available for the statistical analysis of the downstream connectivity using the local model.

As described in the previous sections these coastal areas are discarded from the statistical analyses. Also in areas located close to the open boundaries of the model domain the statistical basis is low because of many agents crossing the open boundaries and subsequently not available for statistical analyses. Because of these issues the robustness of the methodology based on the current simulations is strongest in the open waters of the North Sea, Kattegat and the eastern Baltic Sea, and may be less robust in some parts of the coastal and shallow waters, and close to the open model boundaries. Robustness can be improved by applying more agents in the inner Danish straits, by improving the model describing the agent trajectories more correctly close to land and seafloor boundaries, and by extending the model domain further out so that open model boundaries reduces their impact on connectivity statistics. The statistical basis shown in **Figure 5** and **Figure 6** is for scenario 1 for 1 week dispersal time. Similarly data on statistical basis can be shown for scenarios 2-4 and for each dispersal time.

Connectivity probability maps - Below in Figure 7 is shown an example of downstream connectivity probability maps of scenario 1 (simple drifting) for one selected area in the North Sea (indicated by red arrows) for four different dispersal times: 1, 2, 3, and 4 weeks. Values are probability values between 0 and 1, and the sum of probabilities in each map is 1 since no mortality is considered. Only values larger than 0.01 are shown. In all maps the probability distributions are highly influenced by a north going currents along the west coast of Jutland showing that probability values larger than 0.01 are dominating in the northern and north-eastern directions. Maps also indicate that there are significant differences in probability maps depending on the dispersal time considered: - the longer the dispersal time considered the further away agents move.

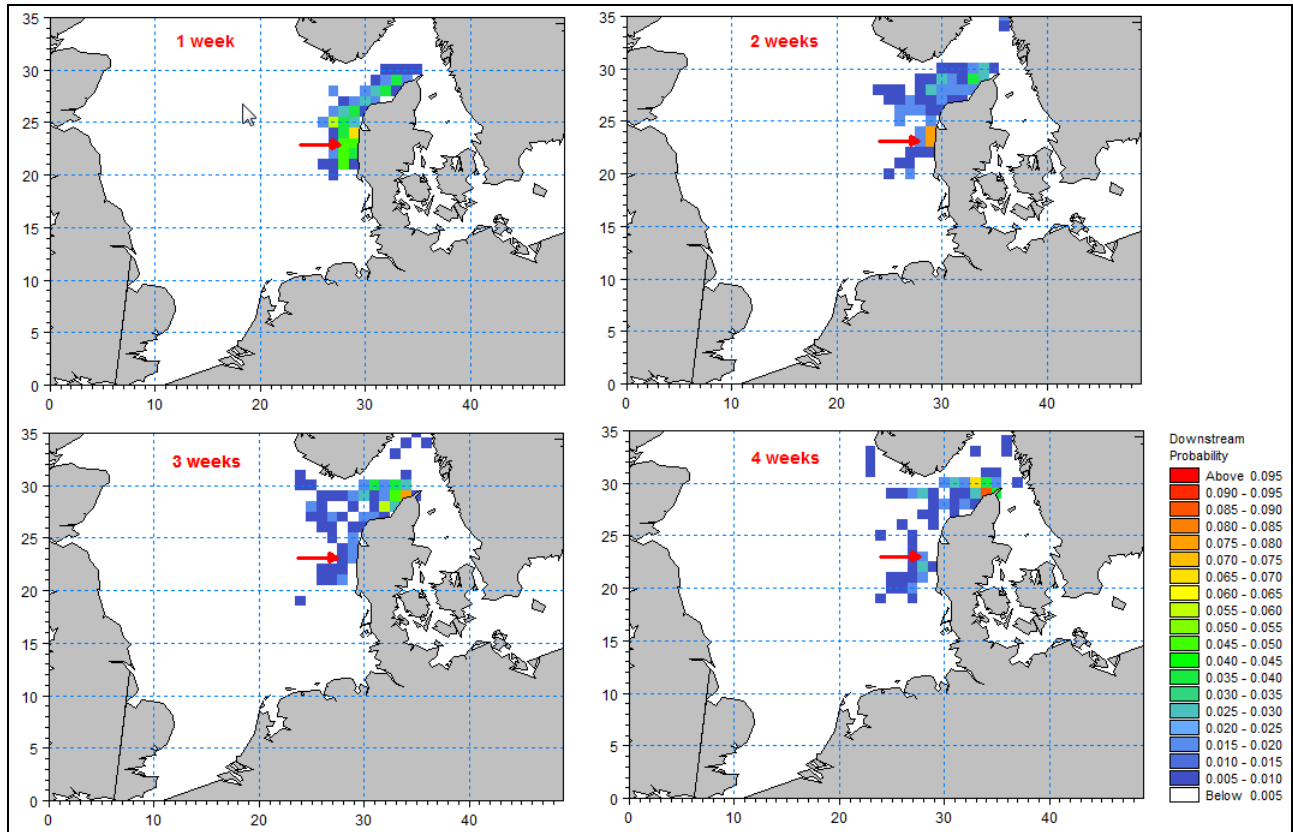


Figure 7. Downstream connectivity probability maps for one selected area in the North Sea (indicated by red arrows) for 4 dispersal times: 1, 2, 3, and 4 weeks.

Only probability values larger than 0.01 are shown.

Four probability maps of the four different dispersal times are combined into one probability map (**Figure 8**). Because no mortality is included each dispersal time weighted equally and probabilities for the four dispersal times are simply averaged.

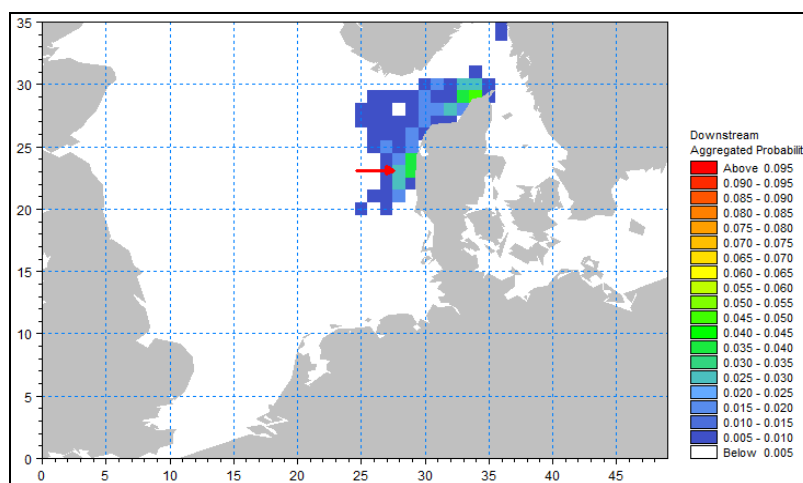


Figure 8. Downstream connectivity probability map for one selected area (the same as in Figure 7) in the North Sea (indicated by red arrow) with aggregated probability values for 1, 2, 3, and 4 weeks dispersal times.

All probability maps presented in **Figure 7** and **Figure 8** reflect the hydro-dynamical variations during 2005 for scenario 1 where simple drifting is simulated. Similar maps for any area within the model domain can be extracted from the downstream connectivity matrices for each scenario 1-4 representing a given dispersal time or a combination of dispersion times. For scenarios where mortality are included the connectivity probability maps of the combination of the four dispersal times are weighted according to the probability of agents to survive to each of the four dispersal times. This will result in an aggregated probability map where e.g. 1 week dispersal probabilities will be weighted more than 2, 3 and 4 weeks probability values. Other dispersal times e.g. 2, 4, 6, and 8 days, will show probability maps with a much narrower distribution of >0.01 probabilities around each area. These are not presented here.

Likewise similar maps for upstream connectivity probabilities can be extracted for each area representing the probability of agents registered in an area having come from other areas. Results for the upstream analyses are not presented here.

Both upstream and downstream probability connectivity maps for scenario 1 aggregated over time for every 25 × 25 km blocks are available on Online Supplementary Material.

Connectivity indexes - Downstream momentum were calculated for the 4 scenarios based on the aggregated connectivity probabilities (=probabilities evaluated based on multiple dispersal times). Notice that momentums for scenarios 3 are based on combined 1, 2, 3, and 4 week dispersal times, while for scenario 2 and 4 momentums are based on combined 3, 9, 15, and 21 days dispersal times. For comparisons scenario one will be evaluated at each of these set of time scales.

Downstream momentum for scenario 1 for 1-2-3-4 weeks dispersal times are shown in Figure 9 Figure 10.

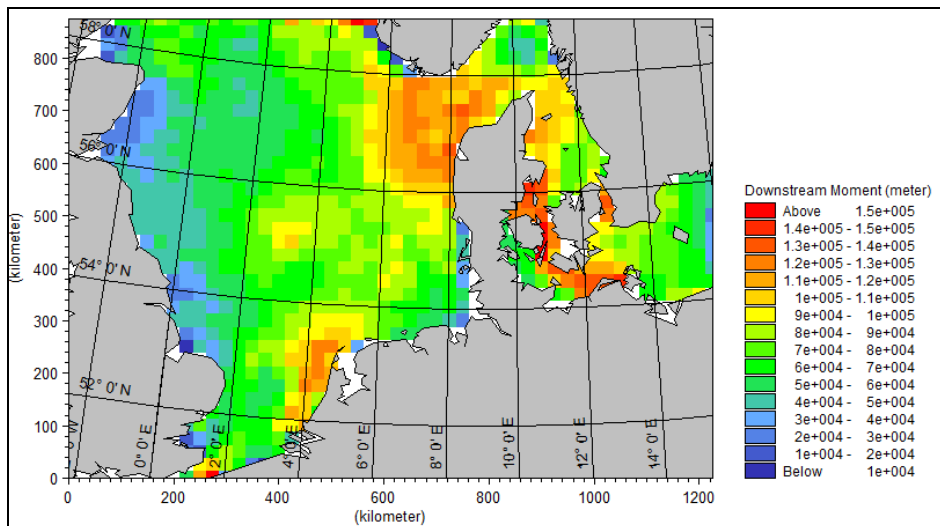


Figure 9. Downstream connectivity indexes (momentums) for scenario 1 (passive particle tracking). Indexes are based on combined 1, 2, 3, and 4 week dispersal times.

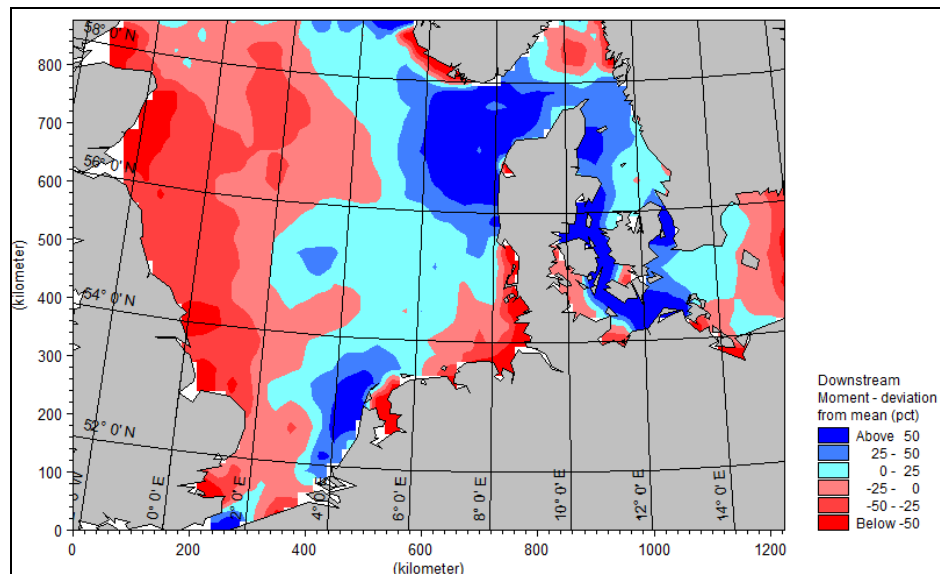


Figure 10. Downstream connectivity indexes (momentums) for scenario 1 (passive particle tracking) presented as deviation from mean value in percentages for 1, 2, 3, and 4 weeks dispersal times.

Downstream momentum values show the highest values found in the north eastern part of the North Sea between the Danish and Norwegian coasts, along west coast of the Netherlands and in Kattegat and the Danish belts, while large parts of the western part of the North Sea, German Bight and the Baltic sea east of Bornholm have low connectivities.

Downstream momentum for scenario 2 for 3-9-15-21 days dispersal times are shown in **Figure 11** and **Figure 12**.

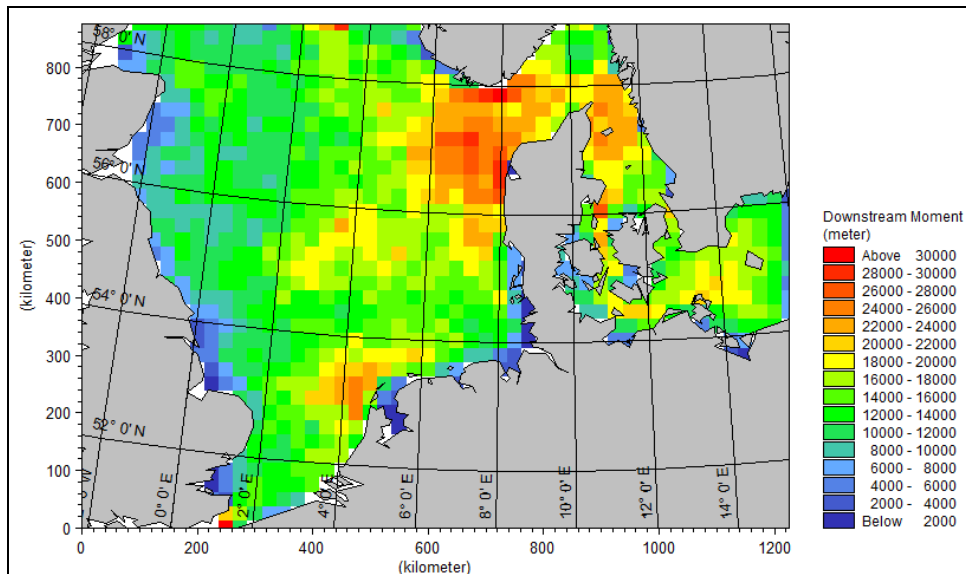


Figure 11. Downstream connectivity indexes (momentums) for scenario 2 (planktonic organisms). Indexes are based on combined 3, 9, 15, and 21 days dispersal times.

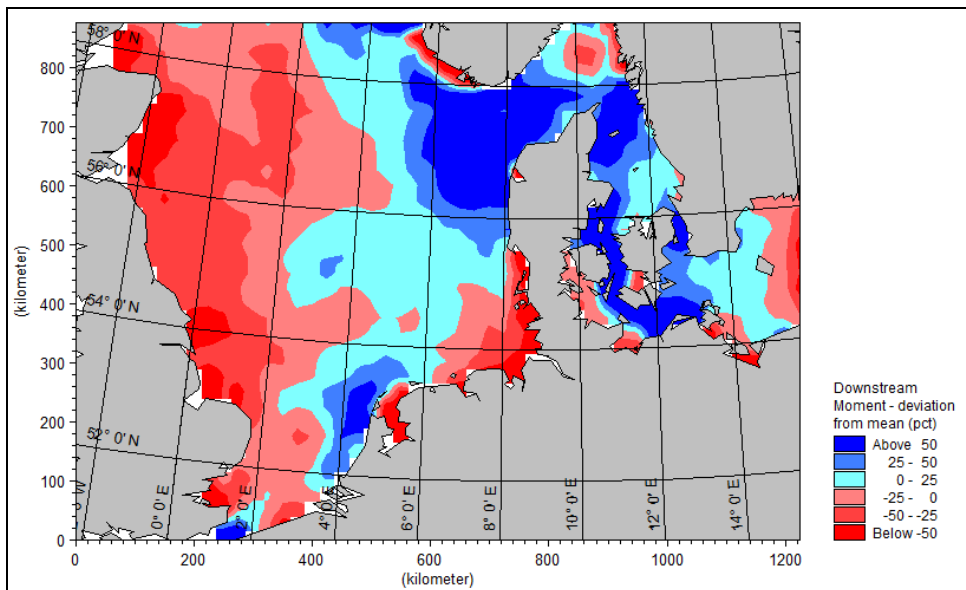


Figure 12. Downstream connectivity indexes (momentums) for scenario 2 (planktonic organism) presented as deviation from mean value in percentages for 3, 9, 15, and 21 days dispersal times.

Downstream momentum values of scenario 2 show the similar distribution pattern as in scenario 1. Notice that dispersal time applied for scenarios 1 and 2 are different. For more accurate comparison see the preceding section.

Downstream momentum for scenario 3 for 1-2-3-4 weeks dispersal times are shown in **Figure 13** and **Figure 14**.

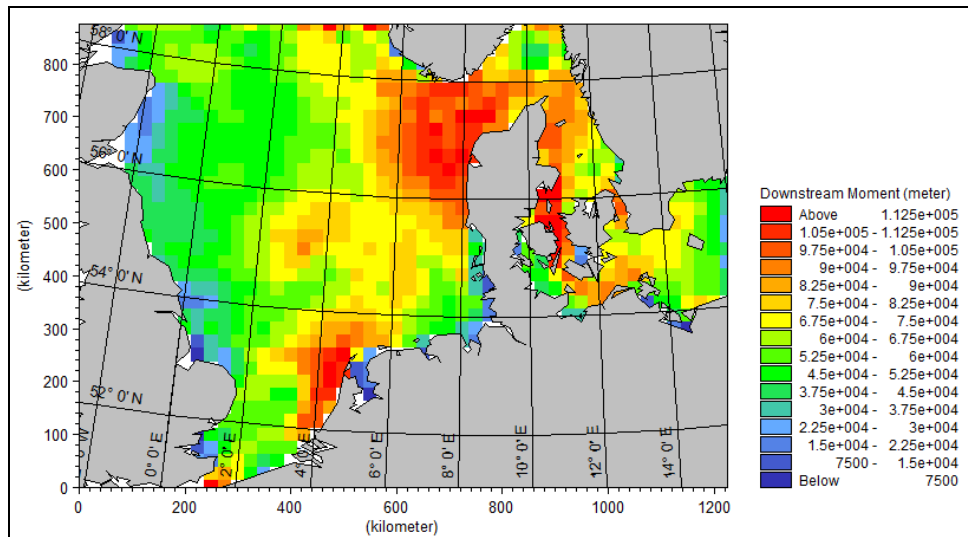


Figure 13. Downstream connectivity indexes (momentums) for scenario 3 (juvenile fish). Indexes are based on combined 1, 2, 3, and 4 weeks dispersal times.

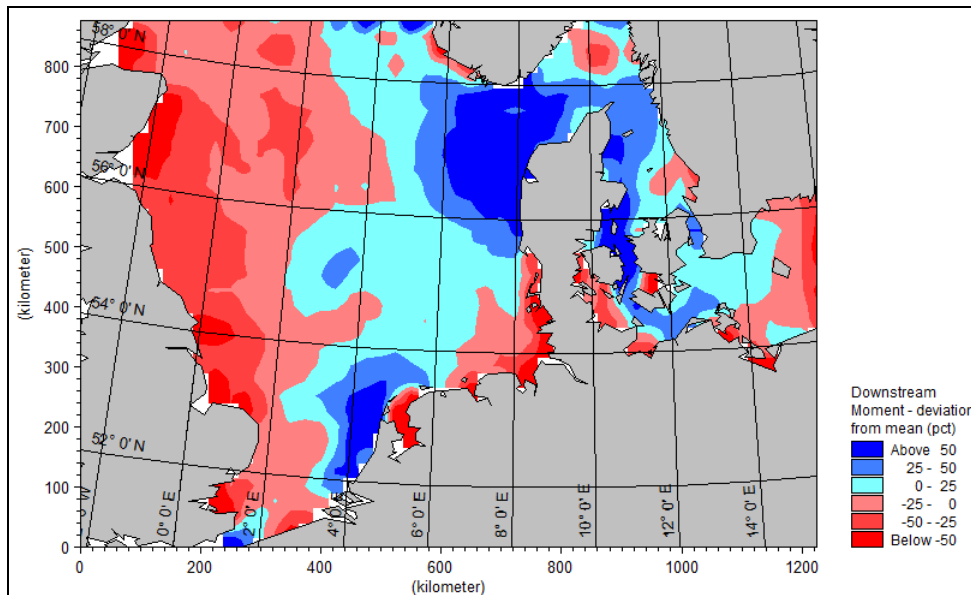


Figure 14. Downstream connectivity indexes (momentums) for scenario 3 (juvenile fish) presented as deviation from mean value in percentages for 1, 2, 3, and 4 weeks dispersal times.

Downstream momentum values for scenario 3 show the similar distribution pattern as in scenario 1. For more accurate comparison see the preceding section.

Downstream momentums for scenario 4 for dispersal times corresponding to the time duration of the time between the registration of each organism until it settles are shown in **Figure 15** and **Figure 16**.

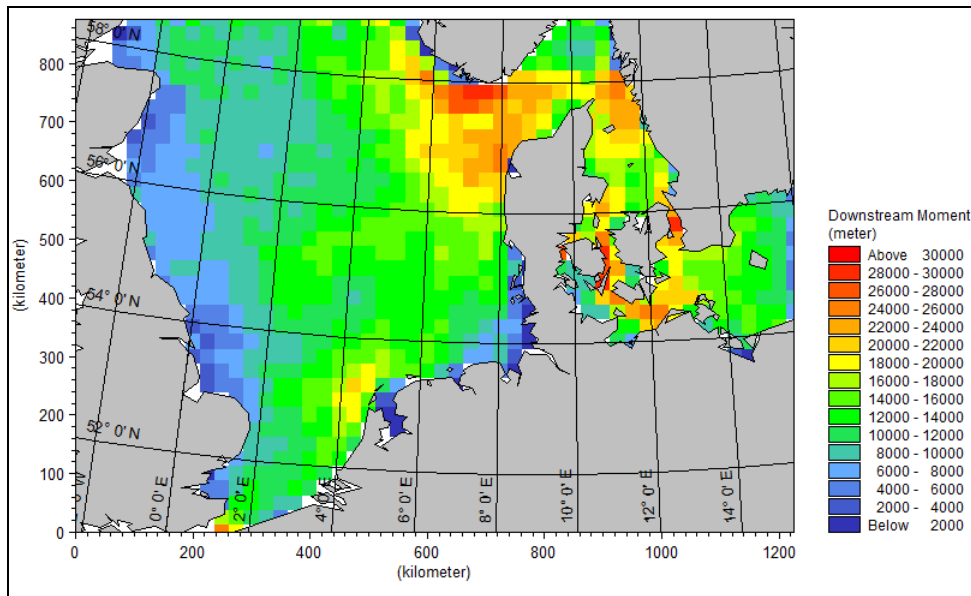


Figure 15. Downstream connectivity indexes (momentums) for scenario 4 (pelagic larvae). Indexes are based on dispersal times corresponding to the time duration until each individual settles.

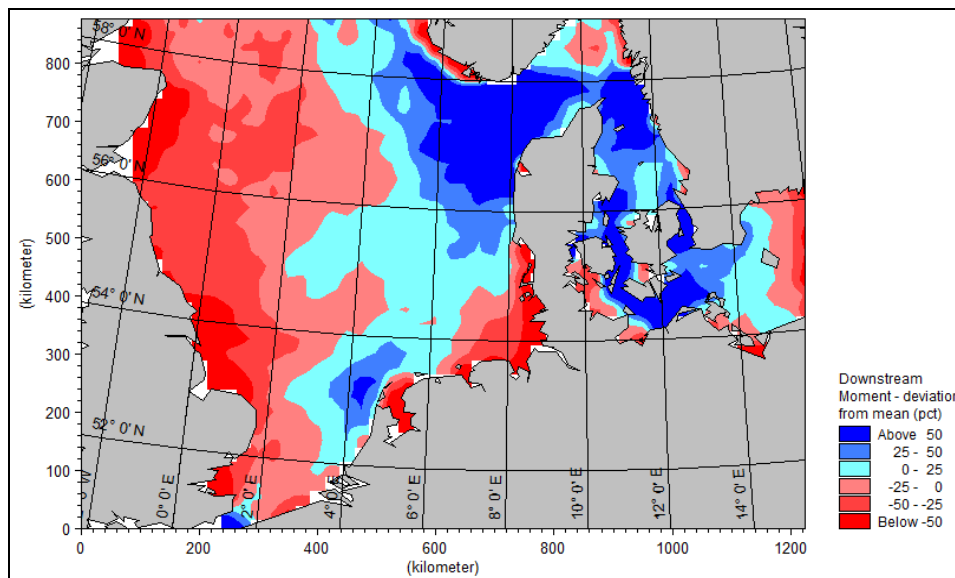


Figure 16. Downstream connectivity indexes (momentums) for scenario 4 (pelagic larvae) presented as deviation from mean value in percentages for dispersal times corresponding to the time duration until each individual settles.

Downstream momentum values for scenario 4 show the similar overall distribution pattern as in scenario 1, 2 and 3, however with some deviation. For more accurate comparison see the previous section.

Importance of dispersal time - The selection of dispersal time for evaluating connectivity between marine areas is important simply because the longer time we 'follow' the dispersal of an organism the longer distance the organism is likely to travel, as long as the organism is still alive. In terms of connectivity indexes this implies the longer the dispersal times evaluated the higher the connectivity index. However in addition to the magnitude of the connectivity indexes the spatial pattern of connectivity indexes may change. As an example connectivity indexes were calculated for scenario 1 for two sets of dispersal times: 2-4-6-8 days, and 7-14-21-28 days and deviation from the overall mean value were plotted, see Figure 17. Although the overall patterns of the two plots for the two sets of dispersal times are similar some discrepancies are evident. Some areas show larger deviation from the mean value when evaluated on a longer time span, while others show smaller deviation from the mean value.

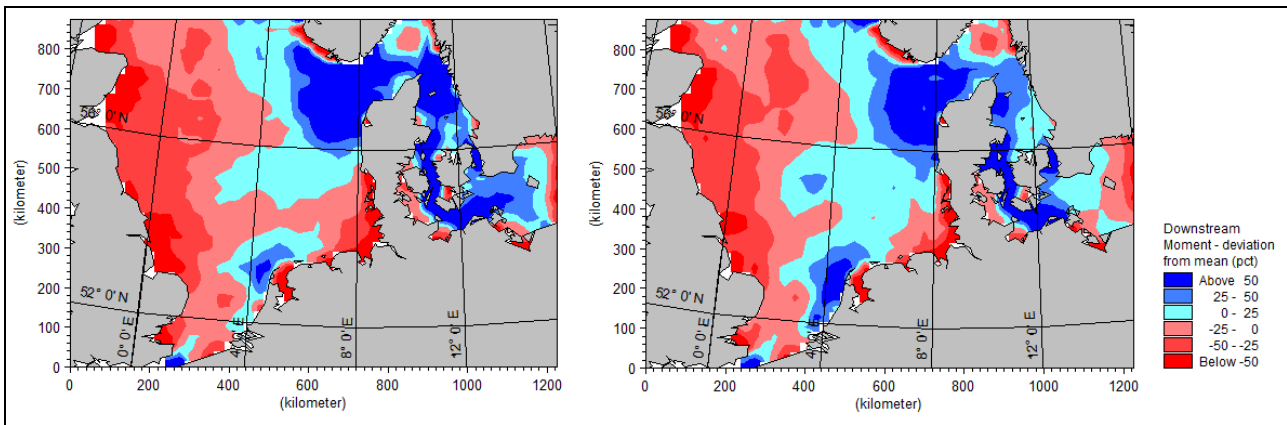


Figure 17. Downstream connectivity indexes (momentums) for scenario 1 (passive particle tracking) presented as deviation from mean value in percentages for 2, 4, 6 and 8 days (left) and 1, 2, 3 and 4 weeks (right) dispersal times.

Importance of biological factors - As for the selection of dispersal time when evaluating connectivity between marine areas biological factors including mortality, settling etc. are important because e.g. the longer an organism lives the longer we can 'follow' the dispersal of an organism and the longer distance the organism is likely to travel if flow conditions are suitable. Thus, when applying connectivity probability maps to predict, for instance, the likelihood that an introduced organism in an area will spread to other specific areas biological factors are important.

Biological factor may also have an effect when comparing the connectivities between areas. In **Figure 18** and **Figure 19** are shown the comparisons for scenarios 1 and 2, and scenarios 1 and 3 respectively for the calculated deviation from the mean value of the connectivity indexes. Comparisons between scenarios 1 and 2 are done for 3-9-15-21 days dispersal time, and comparisons between scenarios 1 and 3 are done for 7-14-21-28 days dispersal times.

Both comparisons show the similar overall pattern in the variability of connectivity indexes. However scenario 2 shows some differences compared to scenario 1. For instance, connectivity indexes in the Danish belts show significantly lower deviation from mean than in scenario 1. This indicates when evaluating the connectivity of specific marine areas for organisms with high mortality, mortality may be important to consider when simulating the spread of organisms. Scenario 3 on the contrary shows only very little deviation from scenario 1 indicating that swimming behavior simulated as random walk has not major effect on the spatial variability in connectivity.

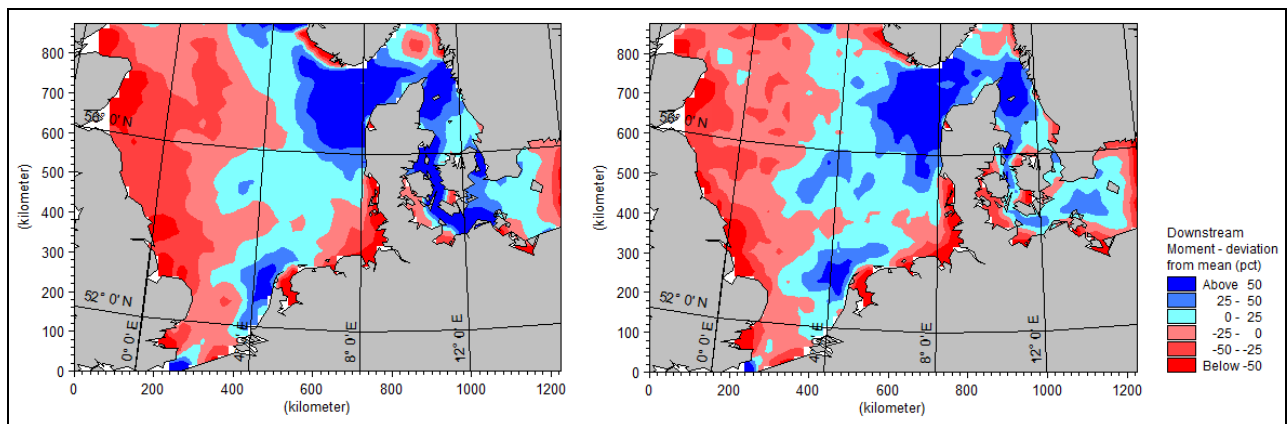


Figure 18. Comparison of Downstream connectivity indexes (momentums) for scenario 1 (passive particle tracking) and scenario 2 (planktonic organism). Left panel: Scenario 2 (planktonic organism). Right panel: Scenario 1 (passive particle tracking). Presented as deviation from mean value in percentages for 3-9-15-21 days dispersal times.

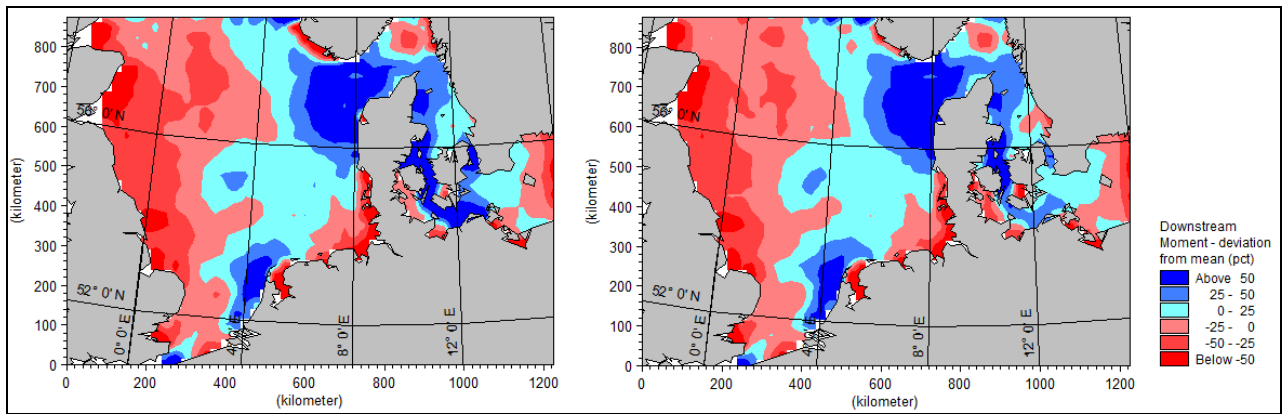


Figure 19 Comparison of Downstream connectivity indexes (momentums) for scenario 1 (passive particle tracking) and scenario 3 (juvenile fish). Left panel: Scenario 3 (juvenile fish). Right panel: Scenario 1 (passive particle tracking). Presented as deviation from mean value in percentages for 1-2-3-4 weeks dispersal times.

For scenario 4 comparisons are done with scenario 2, not scenario 1, since scenario 4 is not evaluated on selected dispersal time, but rather dispersal times corresponding to the time duration from the time of registration of an agent in an area until it settles. To get an idea how settling affects the momentum comparison of 'deviations from mean' between scenario 2 and 4 are shown in **Figure 20**. Differences between scenarios 2 and 4 are the settling introduced in scenario 4 and that momentums of scenario 2 are evaluated at discrete dispersal times (3, 9, 15 and 21 days).

Here as for scenarios 2 and 3 the main overall patterns in the variability of connectivity indexes are maintained with some deviations locally.

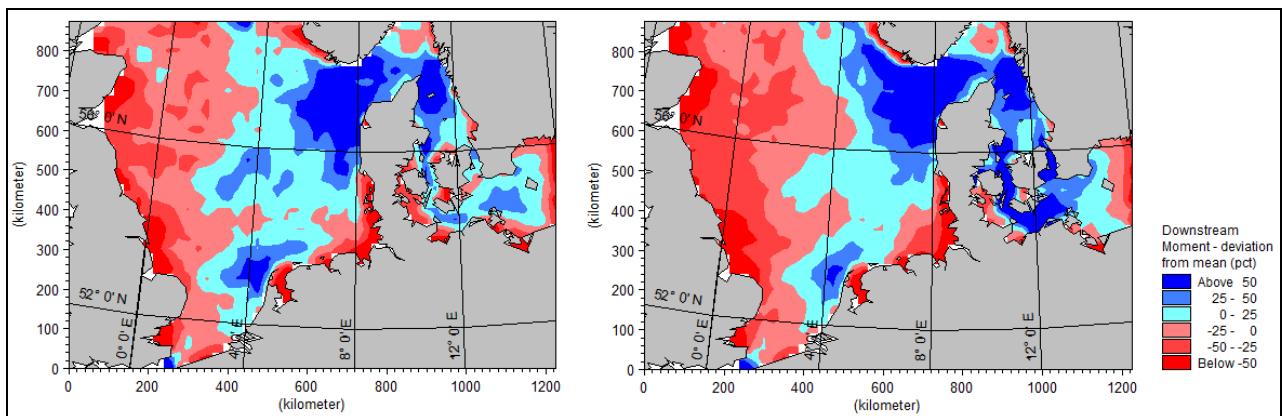


Figure 20. Comparison of Downstream connectivity indexes (momentums) for scenario 2 (planktonic organisms) and scenario 4 (pelagic larvae of benthic invertebrate). Left panel: Scenario 4 (pelagic species). Right panel: Scenario 2 (planktonic organism). Presented as deviation from mean value in percentages. Dispersal times evaluated for scenario 2 is 3-9-15-21 days and for scenario 4 the time duration until each individual settles.

Momementum – upstream: Upstream connectivity indexes are only shortly presented here since the main focus of the present study is to identify areas where the release of ballast water may have a high potential for spreading to other parts of the North Sea region. We will not go into details on how dispersal time or biological factors may affect the outcome of the upstream connectivity analysis. However as for the downstream connectivity analyses in general for all scenarios the overall patterns in terms of connectivity indexes the similar spatial variability between areas clearly identifies areas which more likely will receive ballast water derived organisms from far away. In Figure 21 shown the upstream connectivity indexes for scenario 1 (passive particle tracking) based on 1-2-3-4 weeks dispersal times.

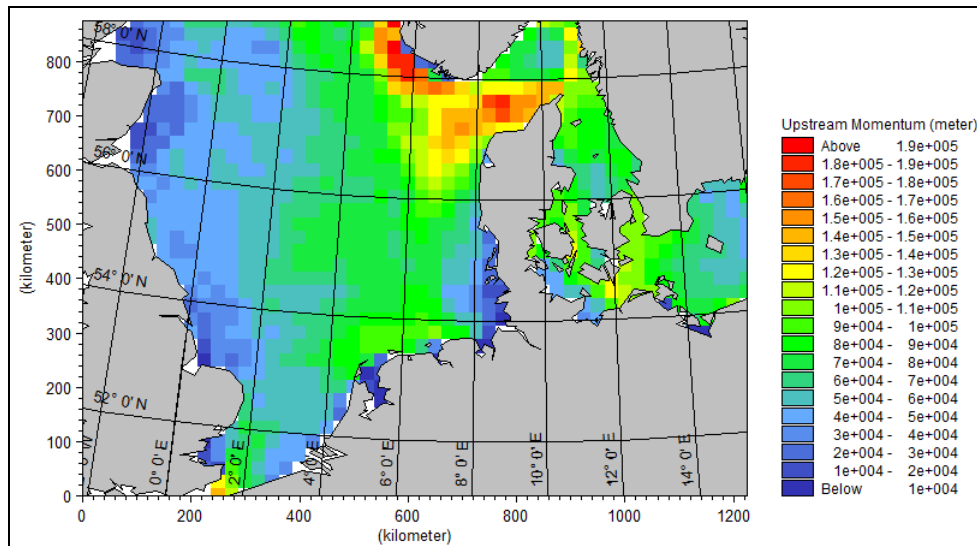


Figure 21. Upstream connectivity indexes (momentums) for scenario 1 (passive particle tracking). Indexes are based on combined 1, 2, 3 and 4 weeks dispersal times.

Areas with the highest values of upstream connectivity are primarily areas of the deeper part of the waters between North-western Jutland and Norway and along the south-western Norwegian coastline. The values are highly distinct from other marine areas and this indicate that these areas serve as major sinks or receiving water bodies of passively transported agents. Again as for the downstream connectivity lowest values are found in particular in the western part of the North Sea, in the German Bight and the Baltic Sea east of Bornholm. Intermediate values are found in the eastern part of the North Sea, in Kattegat, the Danish straits including Fermann Belt and in the western parts of the Baltic Sea.

5 DISCUSSION AND CONCLUSIONS

The analyses carried out for this demonstration project show that when evaluating the connectivity of marine waters of the North Sea region including Skagerak, Kattegat, the Danish belts and the western parts of the Baltic Sea, the hydrodynamics seem to play the most important role when considering small organisms with limited ability to perform a significant autonomic movement behavior. Despite some differences in calculated connectivities due to biological factors and the choice of dispersal time applied for the connectivity analyses the overall pattern of the variability of connectivity indexes show, at least at this preliminary stage of analyses and at a regional level, a rather unambiguous indication that biological factors and dispersal time are only of secondary importance when ranking areas according to their degree of connectivity. At local level however under some conditions biological factors as well as the choice of dispersal time applied may play an important role.

It is strongly recommended that additional biological factors that could have a potential impact on connectivity of marine areas should be identified and tested to sustain (or contradict) these conclusions. These may include: (1) Simulation of diurnal vertical migration of planktonic species, (2) simulation of oriented swimming behavior of juvenile fish, and (3) analyses of differences in connectivity between seasons.

Also the methodology proposed here for calculating connectivity (as momentums) solely depending on the distance travelled by each simulated organism during a number of dispersal time needs to be consolidated. As an example the inclusion of the area covered by e.g. a 90 % fractile of connectivity probabilities could be considered.

In addition to connectivity indexes the downstream connectivity probability maps for each individual area, only periferical commented in the result section, has a very high potential for predicting the probability of a ballast water derived organism ending up at a specific location, e.g. locations identified as being especially sensitive or at locations providing suitable habitat for specific species. Similarly upstream connectivity probability maps for a specific area (a given habitat, a MPA, etc.) predicts which areas may potentially contribute with ballast water derived organisms.

The primary aim of the methodology presented here is to demonstrate how to apply a combination of agent based modeling and hydro-dynamical modeling to describe and develop measures for the inter-connectivity of marine ecosystems systems and its potential application for ballast water risk assessment. During this work a number of issues have been identified on how to improve the methodology: (1) The hydro-dynamical model was not developed specifically to adressed these issues, in particular near-shore hydro-dynamics are important to avoid agents to be 'captured' in still water which in most cases may be a model resolution artifact rather than a true hydrodynamical phenomenon, (2) agent-based models may be further developed to be species specific including habitat preferences, environmental stresses and population dynamics, and (3) inclusion of water quality modeling will improve prediction of the effects on environmental stresses on agents.

In case the prototype DST is further developed, we foresee it might be useful for other purposes such as: (1) Production of pressure layers (i.e. the downstream connectivity map) for mapping of cumulative human pressures and impacts, (2) production of 'ecosystem component layers' (i.e. the upstream connectivity map) for mapping of cumulative human impacts, and (3) Marine Spatial Planning, including zoning and site selection, i.e. for future designation and design of Marine Protected Areas.

In conclusion, we have developed a prototype Decision Support Tool for modelling of risks of spreading of introduced alien species via ballast water. The prototype tool reported constitutes of two types of models and a post processing activity: Firstly, a 3D hydro-dynamical model calculates the currents in the North Sea and Danish Straits. Secondly, an agent-based model estimates the dispersal of selected model organisms with the current regime calculated by the 3D model. Thirdly, scenarios of dispersal are combined into an interim estimate of connectivity within the study area.

The prototype tool should in our opinion be regarded as a platform for further development and testing. However, it can in its present form be used for interim estimates of connectivity and hence as a tool for assessment of potential risk associated to intentional or unintentional discharges of ballast water. The tool can also be used for other purposes, e.g. in regard to ecosystem-based management and the implementation of the EU Marine Strategy Framework Directive.

6 ACKNOWLEDGEMENTS

This study is based on work done under The North Sea Ballast Water Opportunity project, which is co-funded by the INTERREG IVB North Sea Region Programme of the European Regional Development Fund (ERDF), the Danish Nature Agency and DHI. The authors would like to thank Johnny Reker, Flemming Møhlenberg and Ulrik Berggren for constructive discussions as well as Ciarán Murray for language checking.

7 SUPPLEMENTARY ONLINE MATERIAL

Appendix 1: ABM formulation in this study

Appendix 2: Comparison of measured and modelled salinity

Appendix 3: Maps of estimated downstream connectivity

Appendix 4: Maps of estimated upstream connectivity

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APPENDIX 1: ABM FORMULATION IN THIS STUDY

The selected simplistic functional behaviors and life histories used for formulation of the ABM include movement in terms of dispersion and active swimming, settling, mortality and longevity.

Dispersion represents primarily turbulence and water movement not resolved in the discretization of the hydrodynamic model. In principle molecular diffusion is also responsible for dispersion; however, when distances between computational grid cells are small (more than a few meters apart), diffusion is typically insignificant compared with the physical turbulence. This is not the case in the model applied, hence, molecular diffusion is ignored here. Dispersion is here calculated using a random walk method as a simple numerical solution to the Langevin equation which is typically applied for simulating dispersion processes:

$$\Delta X = X_n - X_{n-1} = A(X_{n-1}, t_{n-1}) \cdot \Delta t + \sigma_L \cdot N(0,1)$$

Where:

- A is a drift term
- σ_L is the standard deviation of the turbulent dispersion
- $\sigma_L = \sqrt{2 \cdot \Delta t \cdot D_L}$
- D_L is the dispersion coefficient ($m^2 s^{-1}$)
- $N(0,1)$ is the standard normal distribution: mean=0, variance=1.

Separate dispersion coefficients can be set for each of the three x, y, and z flow components.

The simulation of swimming behavior of marine organisms using Lagrangian type ABMs has been studied by a number of groups in the past. The connectivity of marine populations associated with coral reefs in the Caribbean have been studied using combined HD and ABM modeling including vertical and horizontal swimming capabilities^{1,2}. Larval transport pathways of Cuban snapper in the Caribbean including larval behaviour has also been studied³.

Three different Lagrange type ABM models for simulating (horizontal) movement of fish cohorts and their impact on spatial distribution and population dynamics of coastal fish stock have been studied and compared⁴. The three types of models types include:

- **Random walk models**, which assume no ability to respond to external stimuli.
- **Kinesis**, which describes movement as a simple response to the conditions at the exact location of the fish, i.e. no response to neighboring stimuli or ability to search within a certain area for optimal conditions and respond accordingly. Kinesis based movement is typically simulated as a velocity equal to the previous time step plus a change in direction and a speed. When conditions are good speed are reduced and the likelihood of maintaining the heading (or orientation) is increased. When conditions are bad speed increases and the likelihood of maintaining the heading decreases approaching random walk.
- **Restricted area search**, which describes movement in response to conditions in the neighborhood defined as within a specific search radius. Orientation and speed can be adjusted towards areas where conditions are better.

¹ Cowen, R.K, C.B. Paris & A. Srinivasan (2006): Scaling of Connectivity in Marine Populations. Science 311:522

² Cowen, R.K., C.B. Paris, D.B. Olson & J.L. Fortuna (2003): The role of long distance dispersal versus local retention in replenishing marine populations. Gulf and Caribbean Research Supplement, Gulf and Caribbean Research 14(2):129-138

³ Paris, C.B., R.K. Cowen, R. Claro & K.C. Lindeman (2005): Larval transport pathways from Cuban snapper (*Lutjanidae*) spawning aggregations based on biophysical modelling. Marine Ecology Progress Series 296:93-106

⁴ Humston, R., D.B. Olson & J.S. Ault (2004): Behavioral assumptions in models of fish movement and their influence on population dynamics. Transactions of the American Fisheries Society 133:1304-1328

Random walk models in general proved to be inefficient for locating preferable habitats, while both kinesis and "restricted area search" showed comparable success in identifying preferred habitats for a sample group of fish. Kinesis was recommended by the authors because its simplicity especially suitable when knowledge on how fish respond to neighboring conditions is unknown.

Three swimming behaviors for fish are relevant to the BWO project:

- Random walk: I - To reflect distribution of fish with no response to specific environmental preferences.
- Kinesis: II - To reflect distribution of fish in response to specific environmental preferences (e.g. salinity, temperature and/or dissolved oxygen)
III - To reflect distributions of fish in response to availability of suitable habitat (e.g. food availability) considering mortality linked to a simplistic bio-energetic model.

The random walk method is selected to reflect simple swimming behavior of fish despite the models inability to mimic the population distribution in some case studies. Our selection is based on the intent of analysing the expansion of potential invasive fish species in general without considering species specific habitat preferences. Random walk as a swimming process in the ABM will merely give an indication on the magnitude of the impact of swimming behavior (~swim speed) on the deviation from passive drift, but not the true or the most likely migration trajectories of the model organisms. Instead we recommend applying the kinesis movement in future studies of juvenile fish dedicated specific species with known habitat preferences.

Random walk in the ABM is implemented using a uniform random distribution $N(0,1)$ to sample from $N(e,v)$ where "e" is the average sustained swimspeed and "v" is the variance of the swim speed. Vertical swim behavior will not be considered^{5,6}.

Many benthic organisms have pelagic larvae stages that last from a few hours to several weeks. The pelagic stage ensures a high dispersal of the reproductive outcome. The pelagic stage is followed by a sessile stage and this transition between the two stages is typically referred to as "settling". Settling can be triggered by several factors such as age, development stage and/or environmental cues. In ABMs settling can be modeled as an onset of the settling process followed by vertical movement towards the bottom. In literature, settling velocity of e.g. mussel larvae is described following Stokes law⁷. However, it is generally assumed that settling velocities of pelagic larvae of benthic invertebrates are quite fast when settling starts⁸ and that variation in settling velocities have an insignificant impact on the resulting distribution of settled larvae in general. More important is the age at which settling begins (i.e. the duration of the pelagic stage) which varies significantly between species and also within species⁹. For some pelagic larvae it has been shown that the larvae can register or "taste" the quality of the substrate and this way select among settling locations¹⁰. This stage is relative short up to a few days and may certainly affect the distribution of settled larvae at small scales, in some cases possibly also at larger scales.

In the ABM we describe the initiation of settling by a uniform random sampling from a normal distribution defined by an average age of initiation of settling and associated variance. We assume that larvae settle with a constant vertical settling velocity. The ability of larvae to sense whether settling conditions are suitable or not is not included in the ABM formulation.

Mortality in general is important to consider when attempting simulating the spreading of marine organisms, in particular for organisms with a relatively high mortality, i.e. of organisms with expected life duration of days or a few weeks. The mortality among individuals, and in particular when designing ABMs, is often defined as the risk of dying in terms of a probability value within a certain time range (e.g. as day^{-1}). In nature and in many ABMs mortality rates varies among agents within the same species depending on age, condition, habitat etc.¹¹. However, for simplicity and in order to comply with the generality of the current approach we introduce

⁵ Humston, R., J.S. Ault, M. Lutcavage & D.B. Olson (2000): Schooling and migration of large pelagic fishes relative to environmental cues. *Fish. Oceanogr.* 9(2):136-146

⁶ Humston, R., D.B. Olson & J.S. Ault (2004): Behavioral assumptions in models of fish movement and their influence on population dynamics. *Transactions of the American Fisheries Society*, 133:1304-1328

⁷ Morales, Y., L.J. Weber, A.E. Mynett & T.J. Newton (2006): Mussel dynamics model: A hydroinformatics tool for analyzing the effects of different stressors on the dynamics of freshwater mussel communities. *Ecological Modelling* 197:448-460

⁸ Flemming Møhlenberg, DHI, pers. comm.

⁹ Shanks, A.L. (2009): Pelagic larval duration and dispersion distance revisited. *Biol. Bull.* 216:373-385

¹⁰ Rodriguez, S.R., F.P. Ojeda & N.C. Inestrosa (1993): Settlement of benthic marine invertebrates. *Mar. Ecol. Prog. Ser.* 97:193-207

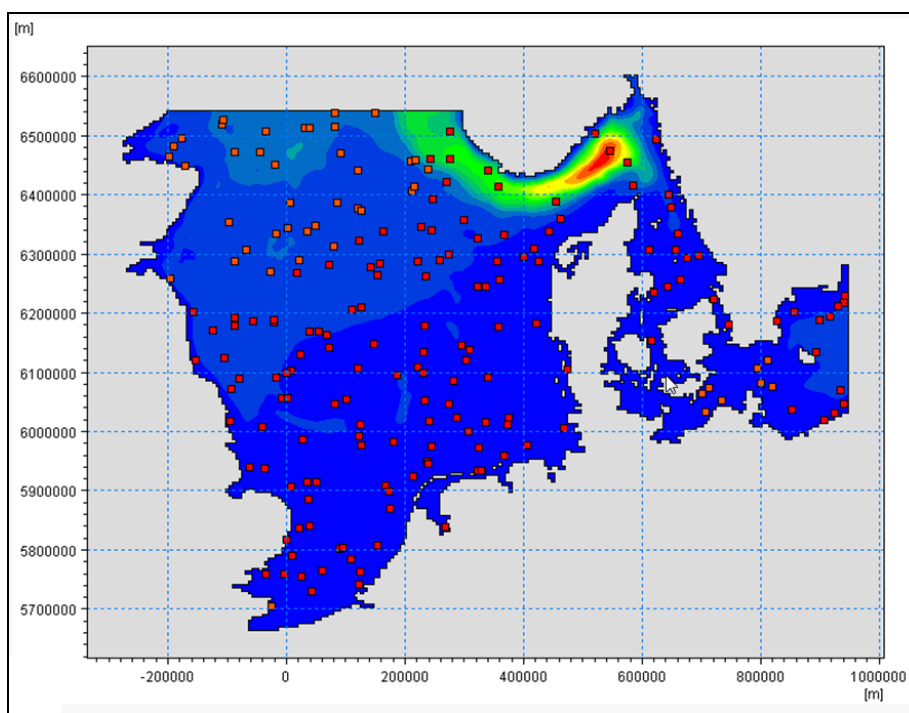
¹¹ Grimm, V., & S.F. Railsback (2005): Individual-based modeling and ecology. Princeton SERIES in Theoretical and Computational Biology. Princeton University Press, Princeton. 428 pp

mortality as a simple constant mortality rate independent of any factor that may have negative or positive effects on the mortality risk of the individual. However, in case the current approach will be extended to consider specific species mortality rates should be simulated as a function of known internal (= within-organism) and external (= environmental) factors.

Longevity is typically referred to as the life expectancy of an organism and deviates from a mortality rate by referring to an absolute age rather than a probability. Maximum longevity can be included in an ABM to ensure that unrealistic outliers of life duration controlled by the mortality rate are ignored. In order to minimize the number of agents in the simulation a maximum longevity can be included so that agents are discarded from the simulation when an agent reach a threshold beyond which it is no longer relevant for the purpose of the simulation.

For each simulation a fixed number of agents are introduced to the model area repetitively throughout the simulation period with a fixed time interval. Between 100 and 400 agents are introduced every second day and randomly distributed in the model area (see Figure next page). Agents are introduced to the surface layer of the model and the simulation covers an entire year (~ 2005) to make sure that both seasonally as well as day to day variations in hydrography are represented. For the ABM a time step of 6 minutes is used and track records of each unique agent are stored every 6 hours.

Dispersion coefficients are difficult to quantify and often require very detailed monitoring data on concentration profiles with high temporal and spatial resolution. The coefficients were estimated as this type of data was not available for the present study. A constant vertical dispersion coefficient of $10^{-6} \text{ m}^2 \text{ s}^{-1}$ with horizontal dispersion coefficients of $0.5 \text{ m}^2 \text{ s}^{-1}$ are applied, equivalent to an average horizontal current velocity of approximately 0.04 m s^{-1} in the x- and y-directions in the horizontal plane, respectively.



Example of agents introduced to the model area every second day randomly distributed in space.

Typical swimming speeds of marine organisms covering orders of magnitude of body lengths are shown in the table below. For example, herring larvae display values between $0.02 - 0.5 \text{ m s}^{-1}$. According to studies of nine species of late stage larvae of marine reef fish, maximum sustainable swimming speed (MSSS) was found to be between 6 and 34 cm s^{-1} . MSSS of juvenile herring and sprat varies between $10-12 \text{ bl s}^{-1}$ while other studies have reported 2 and 7 bl s^{-1} . Juvenile herring larvae studied were of 3 and 6 cm . MSSS for sprat and herring larvae of a body length of 5 cm may range between 10 and 60 cm s^{-1} . To mimic random swimming behaviour, an average swimming speed in the x- and y-directions of 0.25 m s^{-1} is applied with a variance of 0.01 m s^{-1} .

¹² Videler, J.J. (1993): Fish swimming. Chapman & Hall, Fish and Fisheries Series 10

¹³ Fisher, R., & D.R. Bellwood (2002): The influence of swimming speed on sustained swimming performance of late-stage reef fish larvae. Marine Biology 140:801-807

¹⁴ Turnpenny, A.W.H. (1983) Swimming performance of juvenile sprat, *Sprattus sprattus* L., and herring, *Clupea harengus* L., at different salinities. Journal of Fish Biology 23(3):321-325

Typical swimming speeds amongst a range of swimming organisms¹².

8.1.1.1	Species	8.1.1.2	Velocity	8.1.1.3	Length
8.1.1.4		8.1.1.5	($m s^{-1}$)	8.1.1.6	(m)
8.1.1.7	Blue whale	8.1.1.8	10	8.1.1.9	30
8.1.1.10	Tuna	8.1.1.11	10	8.1.1.12	3
8.1.1.13	Human	8.1.1.14	1.7	8.1.1.15	1.8
8.1.1.16	Mackerel	8.1.1.17	3.3	8.1.1.18	0.3
8.1.1.19	Herring, adult	8.1.1.20	1	8.1.1.21	0.2
8.1.1.22	Heering, larvae	8.1.1.23	0.5	8.1.1.24	0.04
8.1.1.25	Heering, larvae	8.1.1.26	0.16	8.1.1.27	0.02
8.1.1.28	Heering, larvae	8.1.1.29	0.06	8.1.1.30	0.01
8.1.1.31	Copepods	8.1.1.32	0.002	8.1.1.33	0.001
8.1.1.34	Sea urchin sperm	8.1.1.35	0.0002	8.1.1.36	0.00015

A typical average age at initiation of settling of pelagic stages of benthic invertebrates is approximately 30 days¹⁵. However, it is highly variable between and within species. As an example of a typical settling age this value is applied in the ABM together with a variance of 100 (SD=10). Settling velocity is set to $1 m s^{-1}$ representing an instantaneous settling within the time step applied.

Reported values of typical mortality rates of various marine organisms vary enormously. Applying a constant mortality rate for selected functional groups of marine organisms reveals the importance of mortality processes for the spreading of marine organisms: the longer the average life expectancy the larger the spreading potential. A few examples on reported and applied mortality rates are given below. Mortality rates of $0.2 d^{-1}$ for copepods have been applied when simulating population dynamics in upwelling regions¹⁶, while daily mortality for Pacific Oyster larvae (*Crassostrea gigas*) of $0.07-0.23 d^{-1}$ have been recorded. For marine fish larvae, natural daily mortality rates values between $0.05 - 0.78 d^{-1}$ have been reported¹⁷. Mortality rates for juvenile fish are typically found to be negatively correlated to size in terms of actual body length or weight. A recent study including a compilation of natural mortality of marine juvenile fish from the literature reported mortality rates (y^{-1}) for juvenile fish (4–10 cm) of $0.35-5 y^{-1}$. To mimic mortality of planktonic organisms we apply a mortality rate of $0.1 d^{-1}$ and of juvenile fish a mortality of 0.003 . For pelagic larvae of benthic organisms we apply the same mortality rate as for planktonic organisms.

For all model organisms longevity of maximum 90 days is applied. For planktonic species and pelagic larval stages of benthic organisms, this is done to ignore unrealistic outliers in life expectancies. For fish longevity of 90 days is not realistic since fish typically has a much longer max longevity. The purpose for applying the short longevity is to obtain an even distribution of agents in the simulation throughout the year. A max longevity of more than a year will result in the build-up of the number of agents in the simulation. For an optimal outcome of the simulation, the ABM should be run for a long warm up period prior to the selected simulation year so that the number of agents introduced systematically will balance with the number of agents dieing. However, this method was not possible within the scope of this project. The same maximum longevity is employed for the simulation of pure conservative transport or simple drifting.

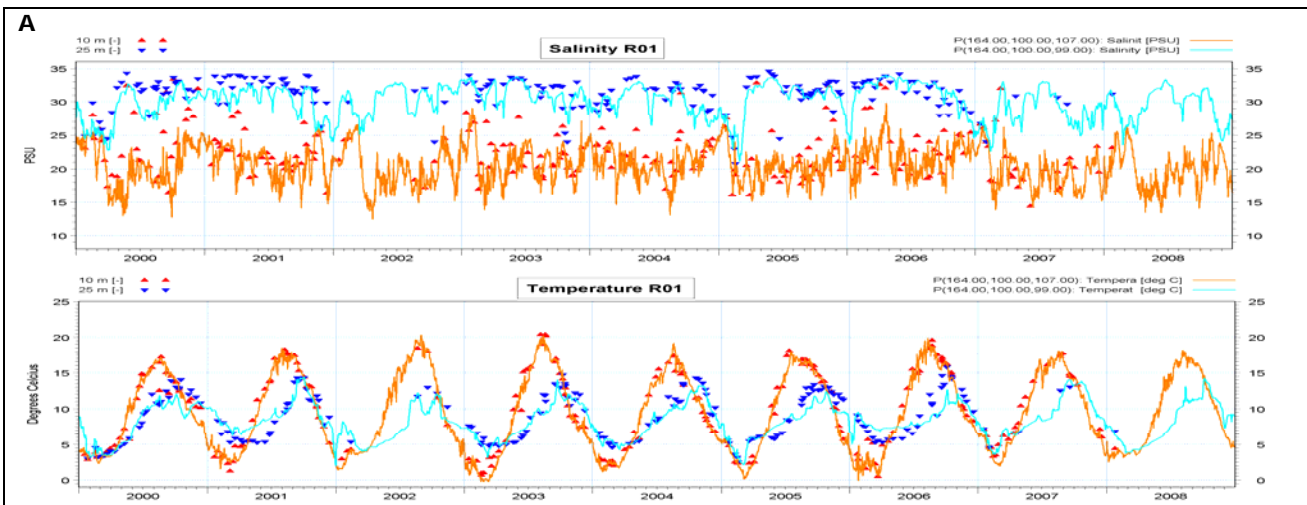
All agents impacting land or sea-floor boundaries were discarded from the simulation.

¹⁵ Flemming Møhlenberg, DHI, pers. comm.

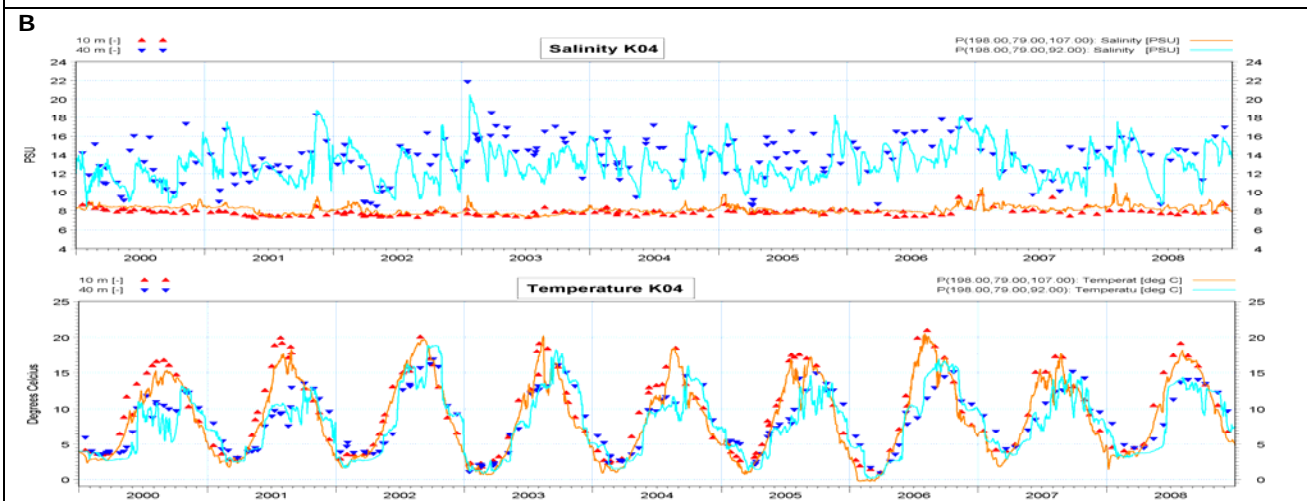
¹⁶ Batchelder, H.P., C.A. Edwards & T.M. Powell (2002) Individual-based models of copepod populations in coastal upwelling regions: implications of physiologically and environmentally influenced diel vertical migration on demographic success and nearshore retention. *Progress in Oceanography* 53:307-333

¹⁷ McGurk, M.D. (1986): Natural mortality of marine pelagic fish eggs and larvae: role of spatial patchiness. *Mar. Ecol. Prog. Ser.* 34:227-242

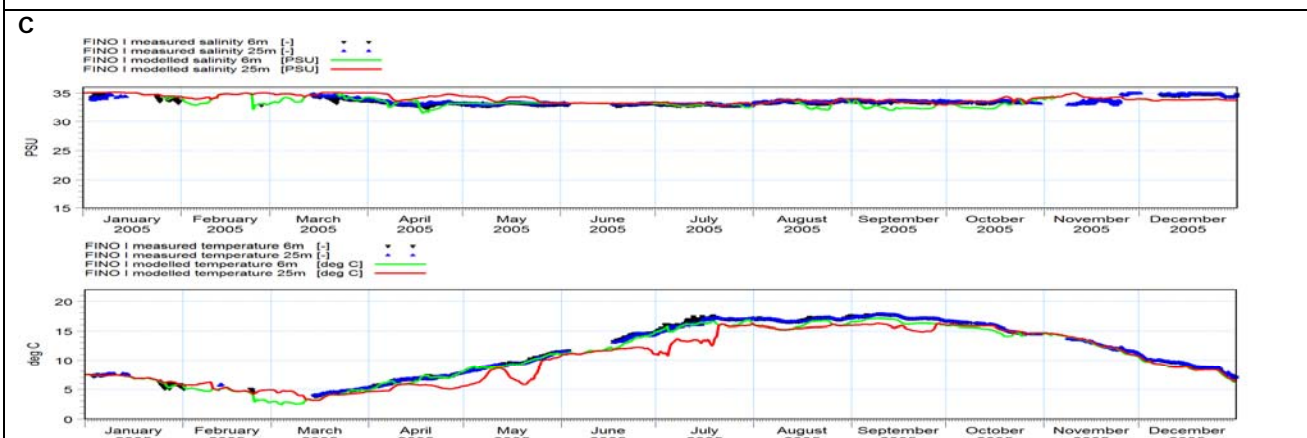
APPENDIX 2: COMPARISON OF MEASURED AND MODELLED SALINITY AND TEMPERATURE



Comparison of measured and modeled salinity (upper) and temperature (lower) in Station R01 in Kattgat. The two depths (10 m and 25 m) represent the surface layer and the bottom layer.



Comparison of measured and modeled salinity (upper) and temperature (lower) in Station K04 in Arkona Basin. The two depths (10 m and 40 m) represent the surface layer and the bottom layer.

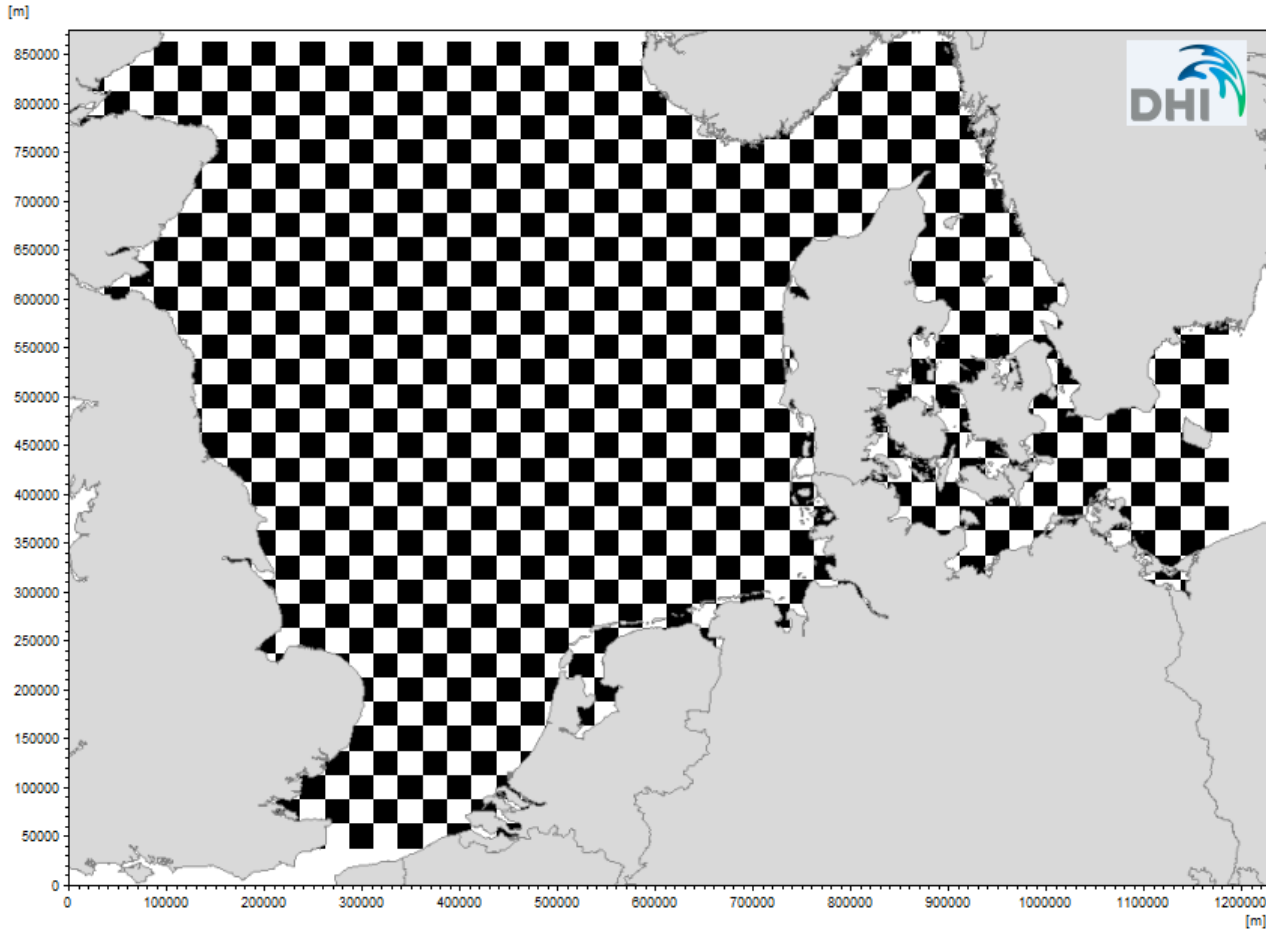


Comparison of measured and modeled salinity (upper) and temperature (lower) in Station FINO I in German Bight. The two depths (6 m and 25 m) represent the surface layer and the bottom layer.

APPENDIX 3: DOWNSTREAM CONNECTIVITY MAPS

This catalogue of downstream connectivity maps is a product of the BWO project and an appendix to the paper “A Prototype Decision Support Tool for Ballast Water Risk Management Using a Combination of Hydrodynamic Models and Agent-Based Modelling” by F.T. Hansen, J.H. Andersen, M. Potthoff, T. Uhrenholdt, H.D. Diem Vo and O. Linden in the WMU Journal of Maritime Affairs (submitted 2013).

Maps have generally been produced for areas shown below represented by checkerboard pattern:

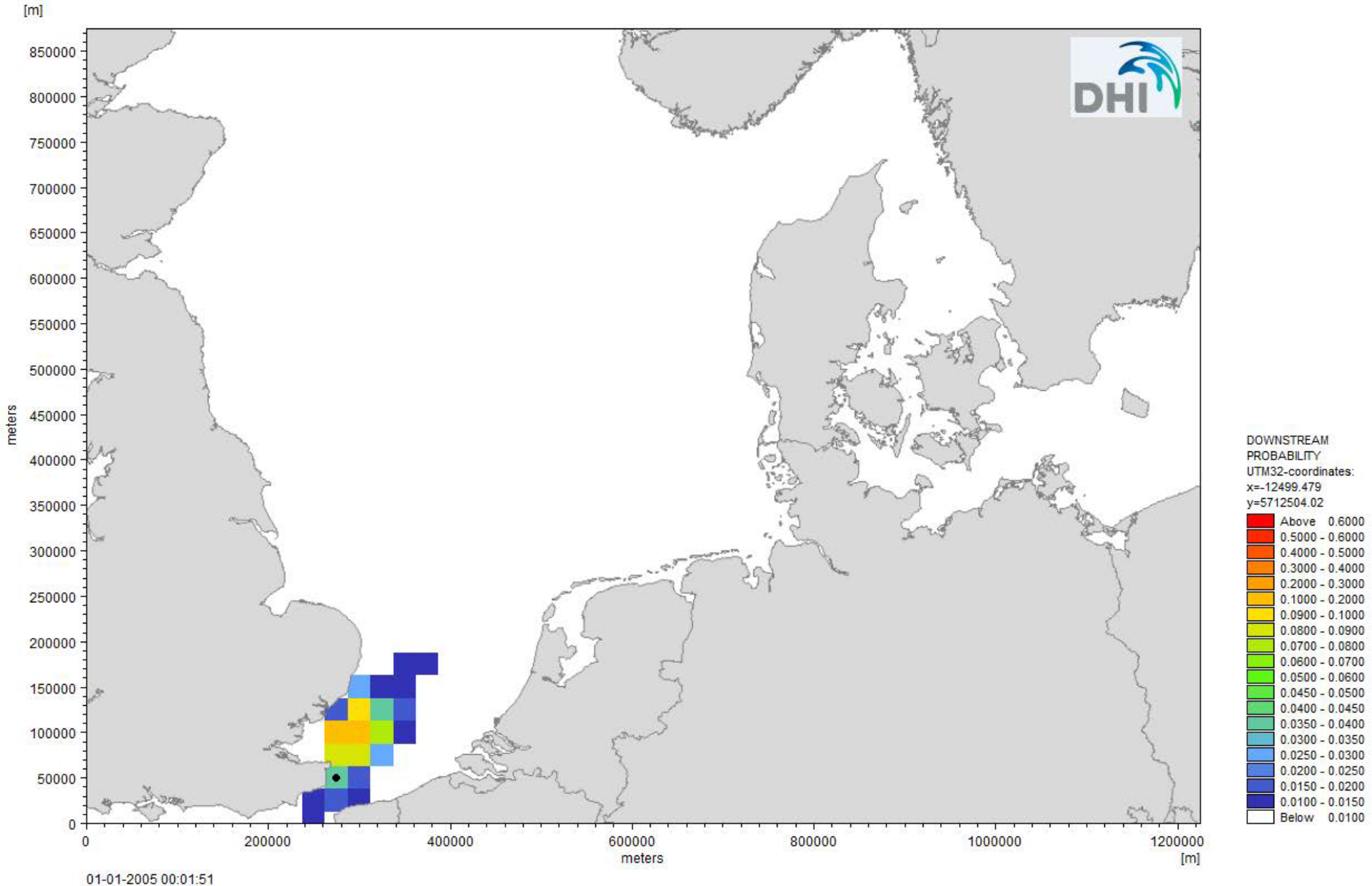


There may be some limitations in the interpretation of the maps along the coastlines, and close to open model boundaries (e.g. towards the North Atlantic, the Eastern Baltic Sea, and the English Channel).

Caution should be exercised in such areas. The probability distributions may be biased due to the lack of connectivity extending outside the open model boundaries. Limited statistical basis (number of agents) and/or due to limitation of the resolution of hydro-dynamical model may also render bias calculations.

As a result a number of areas along the coastline have been excluded from the catalogue of downstream connectivity probability maps.

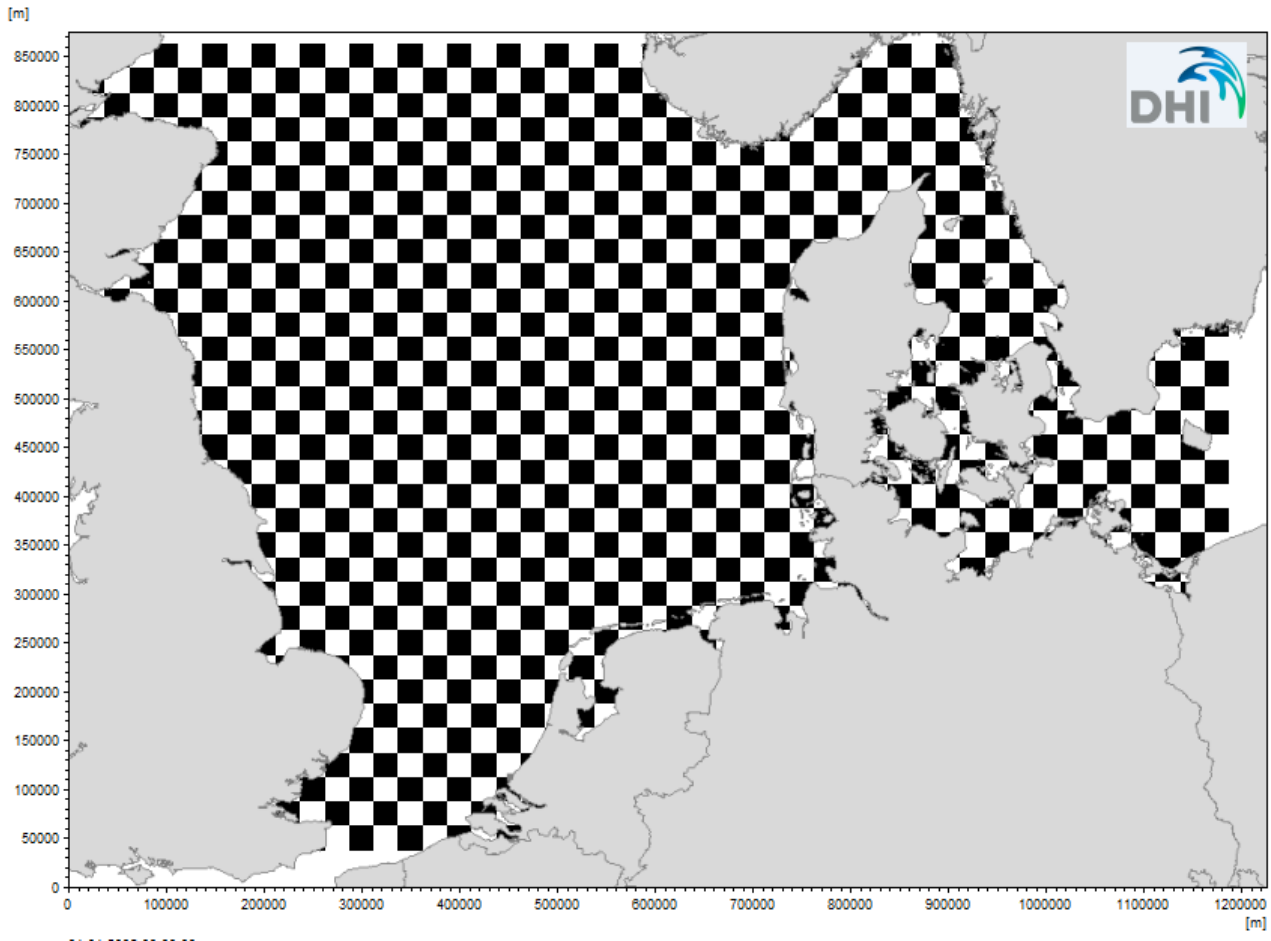
Below is shown one of the maps produced for downstream connectivities. All maps can be downloaded from <http://www.northseaballast.eu/inorthseaballast/1912/7/0/82>



APPENDIX 4: UPSTREAM CONNECTIVITY MAPS

This catalogue of upstream connectivity maps is a product of the BWO project and an appendix to the article "A Prototype Decision Support Tool for Ballast Water Risk Management Using a Combination of Hydrodynamic Models and Agent-Based Modelling" by F.T. Hansen, J.H. Andersen, M. Potthoff, T. Uhrenholdt, H.D. Diem Vo and O. Linden in the WMU Journal of Maritime Affairs (submitted 2013).

Maps have generally been produced for areas shown below represented checkerboard pattern:

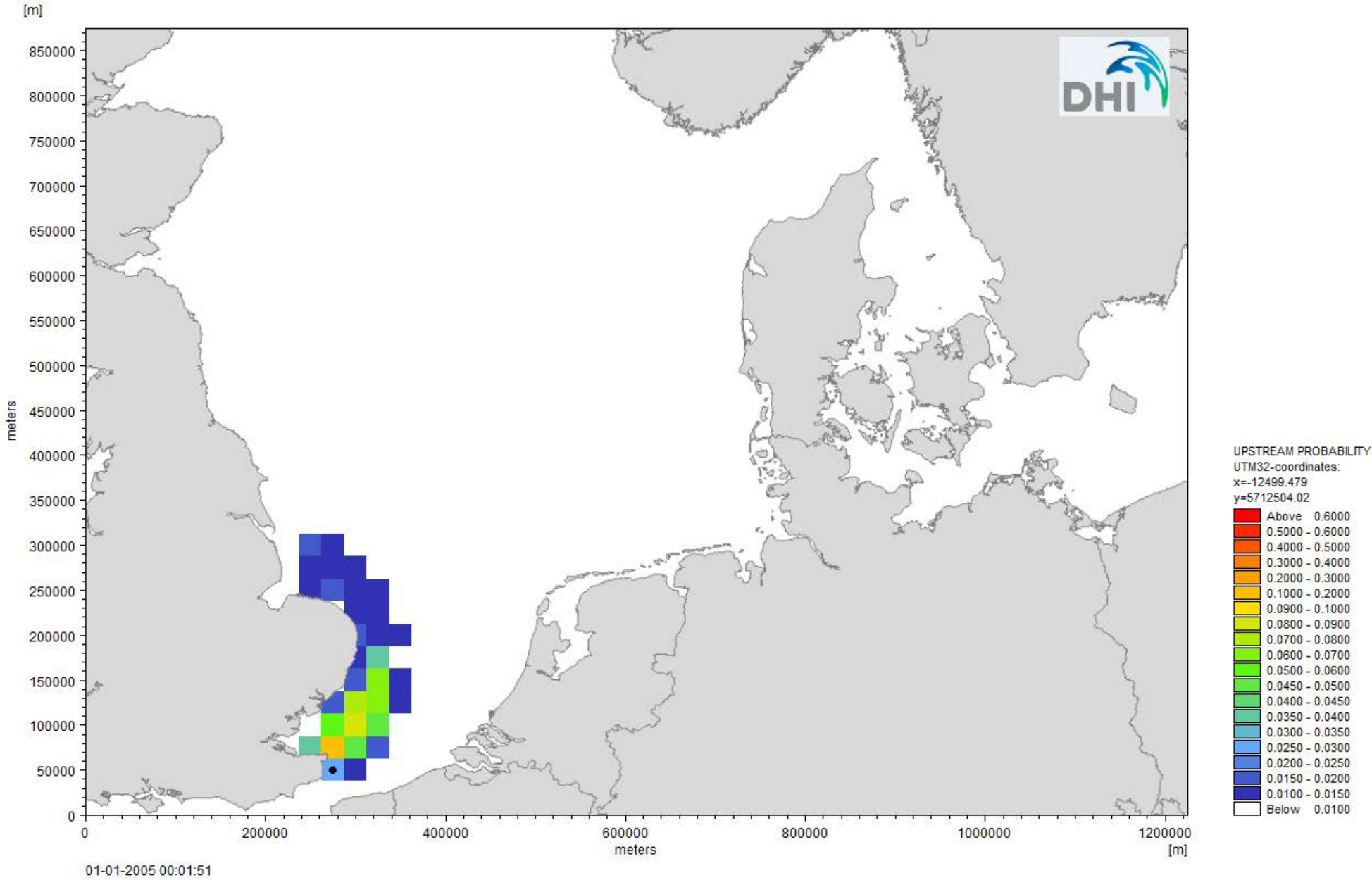


There may be some limitations in the interpretation of the maps along the coastlines, and close to open model boundaries (e.g. towards the North Atlantic, the Eastern Baltic Sea, and the English Channel).

Caution should be exercised in such areas. The probability distributions may be biased due to the lack of connectivity extending outside the open model boundaries. Limited statistical basis (number of agents) and/or due to limitation of the resolution of hydro-dynamical model may also render bias calculations.

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