PAME I-2020: Agenda item 4.1

Modelling Arctic oceanographic connectivity to further develop PAME's MPA toolbox

Progress report

Project objectives

The project aims to further develop PAME's toolbox for Marine Protected Areas (MPA) by mapping oceanographic connectivity in the Arctic region using biophysical modelling, and to use this data resource to identify major barriers to dispersal, gene flow and efficient design of MPA networks.

The project should assist PAME to promote an 'ecologically connected, representative and effectively-managed network of protected and specially managed areas'. The project could further inform the scoping process that is planned in the Conservation of Arctic Flora and Fauna's (CAFF) Circumpolar Biodiversity Monitoring Program (CBMP).

Methods

Connectivity in the Arctic Sea is estimated using biophysical modelling based on oceanographic circulation models and individual-based biological dispersal models. Dispersal stages like free-drifting spores and larvae are modelled as particles released in multiple locations and at multiple time points and allowed to drift with ocean currents at a set of different depths for up to 100 days. Modelling is repeated for 10 to 25 years depending on model used. Each particle will show a dispersal trajectory between release and end locations, and the data for millions of particles are summarised in connectivity matrices stating the probability of connectivity between all areas in the included domain (areas with a depth less than 500 m). Separate connectivity matrices are calculated for combinations of release time, drift depth and drift duration. From the connectivity matrix a number of metrics can be calculated, e.g. the presence of dispersal barriers, and to assess the efficiency of MPA networks.

Progress of the project

After two thirds of the project period the following milestones have been achieved:

- Data from two oceanographic circulation models (TOPAZ 4 and ROMS Arctic 4) have been accessed and organised
- Biological information about dispersal traits of marine invertebrates and fish have been reviewed and used as input to parameter selection in the biological dispersal model
- Meetings have been held with reference persons, e.g. within CAFF and WWF
- Biophysical modelling of connectivity is completed in the Arctic Sea domain with a depth above 500 m (Fig. 1) for all parameter combinations using a specific workflow implemented on a computer cluster.

Remaining tasks in the project

The final phase of the project will include:

- Quality control of modelled connectivity patterns
- Summarising data into connectivity matrices
- Provide an analysis of connectivity barriers

- Give examples of applications in the design of MPA networks
- Submit a technical report
- Submit a scientific report

Input from the Reference group

Input from the Reference group can improve the quality of deliverables in the project and also suggest interesting applications of the connectivity information produced within the project. Example of inputs can be:

- GIS information about seabed characteristics (e.g. distribution of rocky reefs)
- Biological studies of larval occurrence of dispersal traits in the grey literature
- Specific questions, e.g. source-sink issues and local MPA initiatives, that would benefit from connectivity information, e.g. network properties
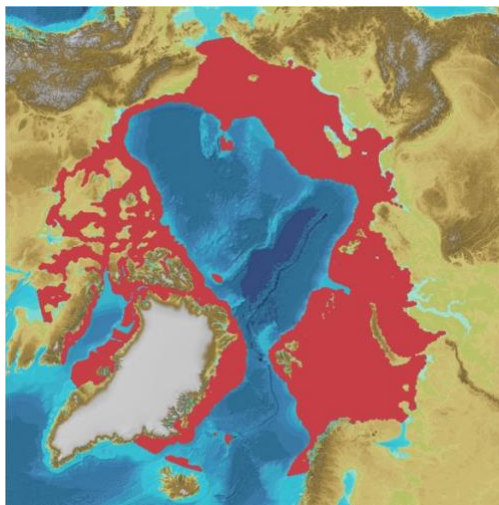- How to make data produced within the project available

Figure 1. The domain (depth≤500 m) where particles are released consisting of 40893 grid cells is shown in red.
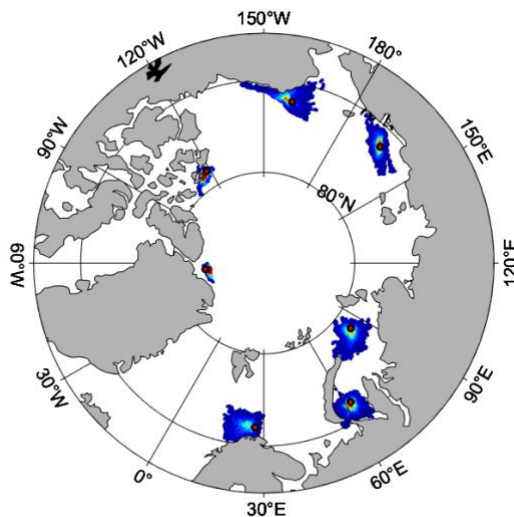

Figure 2. Examples of dispersal from seven release points of simulated larvae in surface waters. The red circular markers indicate starting positions and the colour code shows the dispersal probability after 30 days (from blue to red).