



**EU-H2020 MEESO**  
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# Modelling Mesopelagic fish with the “StrathSpace” approach


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## The Modelling Challenge

- Physiologically and spatially explicit demographic model
- Ocean-basin scale – advection plus diffusion
- Hypothesis tests require wide parameter exploration
- Need exceptional computational efficiency



$$g(w) = A w^n - \epsilon_a w - \epsilon_r \psi_m(w) w$$

$$N(w) = \frac{R}{g(w) w_r} \exp \left( - \int_{w_r}^w \frac{\mu(x)}{g(x)} dx \right)$$

$$\frac{dg(w)N(w)}{dw} = -\mu(w)N(w)$$

$$\mu(w) = aA w^{n-1} + F\psi_F(w) \quad S(a) = \exp \left[ - \int_0^a \delta(x) dx \right]$$

$$\frac{\partial f}{\partial t} = - \frac{\partial f}{\partial a} - \delta(a, t) f \quad \int_0^\infty \beta(a) S(a) e^{-\lambda a} = 1$$

## Our Solution

- Focus on single species
- Computationally efficient discrete-space and discrete-time approach
- In space the population is divided in a grid of horizontal cells.
- Vertically, there are two layers – the surface (top 100m) and a deep layer (c. 400m) for adults.
- Separate computation of physical (movement) and biological (growth) components
- The probability of moving between cells is calculated by Lagrangian particle tracking using a General Circulation Model (GCM).
- Gives  $\sim 10^4$  speed-up relative to Lagrangian ensemble

## Representing Physical Transport

Update at regularly spaced times:  $T_i$

$$C_{q,x,T_i}^+ = \sum_y \Psi_{x,y,T_i} C_{q,y,T_i}^-$$

$C_{q,x,T_i}^- \equiv$  Class abundance just before update

$C_{q,x,T_i}^+ \equiv$  Class abundance just after update

$\Psi_{x,y,T_i} \equiv$  Transfer matrix element from y to x for period to  $T_i$ . Determined by particle tracking in flow fields from GCM plus random (diffusive) component.

## Updating the Biological Model

At each spatial cell and length class

- Calculate the increase in body length that occurs in a time-step and according to the von Bertalanffy growth equation

$$\Delta L = (L_{\infty} - L)(1 - e^{-\gamma\Delta t})$$

$$L_{\infty} = L_{max}F/(F_h + F)$$

$$\gamma(T) = \gamma_0 Q_{10}^{(T-T_0)/10}$$

- For each source length class move surviving individuals (after applying a mortality rate) to destination length class
- If in spawning period calculate the eggs produced and add to the egg class

## Updating the system state

For each spatial cell, in turn:

- Grow (increase in length) the population over all length over a growth time-step
- Remove individuals by applying mortality over the time-step
- If the time is greater than the next transport time-step then stop

Do next transport update, output state variables and repeat.

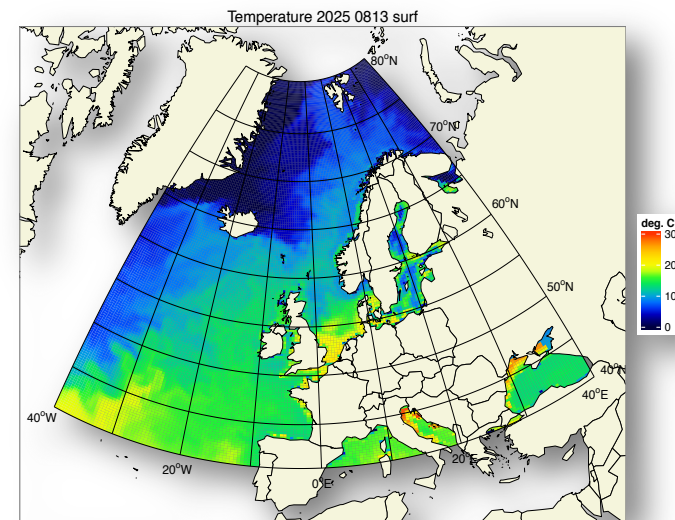
Produces model realisations in good agreement with PDE and Lagrangian ensemble solutions, but MUCH faster.

## The StrathSPACE model of *Benthosema glaciale*

- Discrete time and space closed life-cycle population model
- Length structured population
- Von Bertalanffy growth
- Planktonic larvae
- Biodiffusive adults
- Temperature-dependent growth and mortality
- Transport and temperature from NEMO model, National Oceanography Centre (NOC), Southampton, for 1980-2099, with RCP 8.5 for forward run, for the whole Atlantic.
- Population model very fast (1-5 seconds per model year).



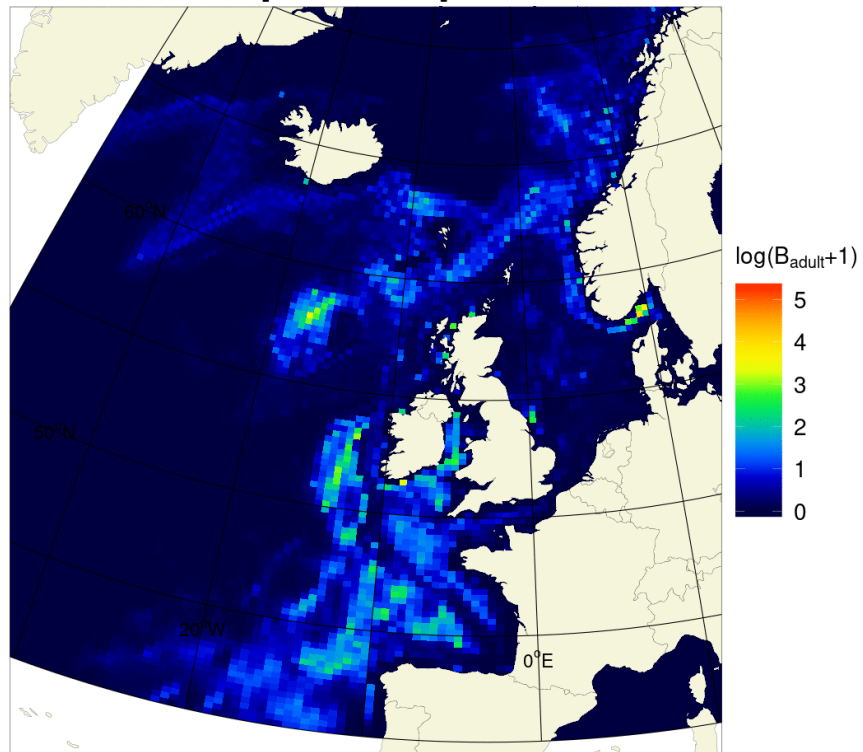
*Benthosema glaciale*



Projected (2025) surface temperature from the NEMO model

## StrathSPACE *Benthoosema* model outputs – spatial distribution

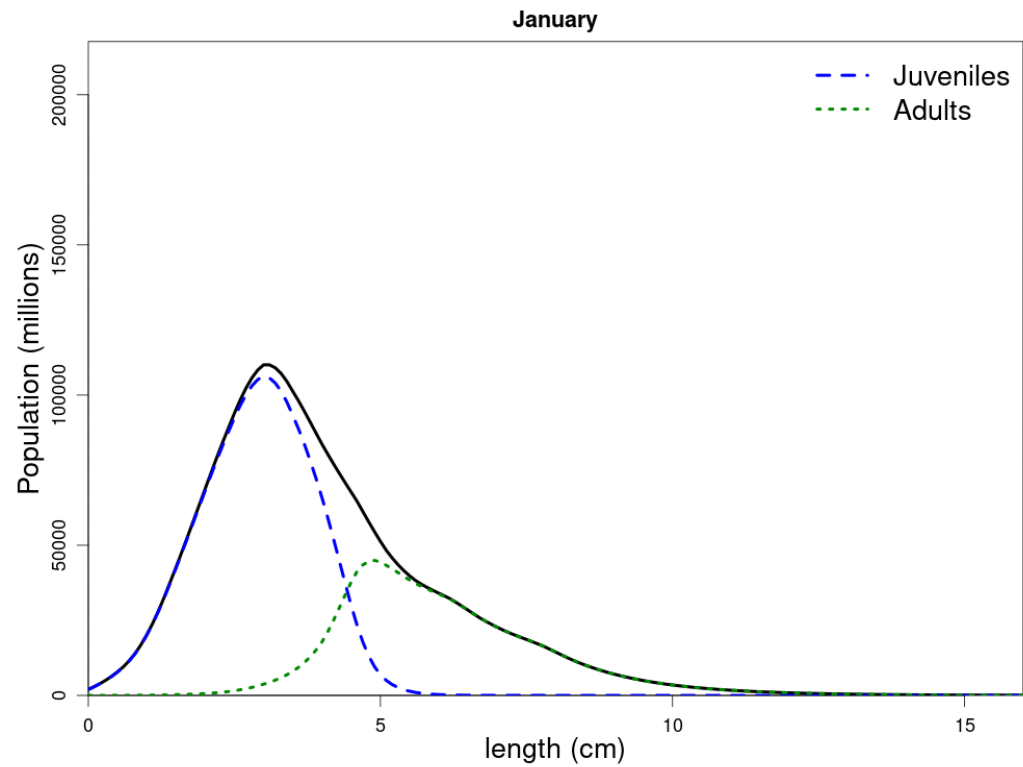
Adult distribution [tonnes/km<sup>2</sup>] - 1988



StrathSPACE *Benthoosema* model hindcast  
and forward run 1988-2050

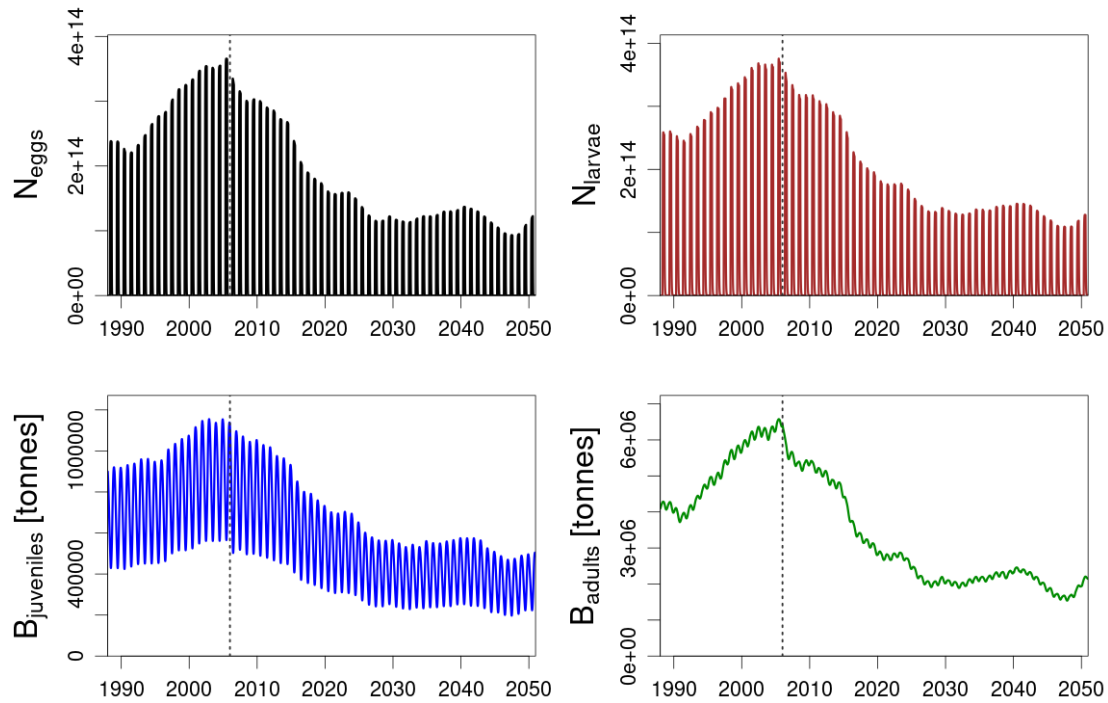


## StrathSPACE *Benthoosema* model outputs – length distribution



Modelled seasonality of *Benthoosema*  
length distribution

## StrathSPACE *Benthoosema* model outputs – abundance time series



Forward run *Benthoosema* model