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### D2.11 Sub-model Library of IBM submodels including user guide

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## **D2.11 Sub-model Library of IBM submodels including user guide**

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#### **Note on Code Access:**

**Section A.** The model code can be requested from either Marc Hufnagl ([marc.hufnagl@uni-hamburg.de](mailto:marc.hufnagl@uni-hamburg.de)) or Wilfried Kühn ([wilfried.kuehn@zmaw.de](mailto:wilfried.kuehn@zmaw.de)).

**Section B.** The model code can be requested from Asbjørn Christensen ([asc@aqu.dtu.dk](mailto:asc@aqu.dtu.dk))

## Section A. IBM Model

### A.1 Model description

#### A.1.1 General characteristics

The model consists of two parts: an individual-based model (IBM) for simulating the growth and development of larval fish (eggs, non-feeding and feeding stages) and a 3D dispersion model based on a Lagrangian approach.

The IBM has general parameterization depicting the temperature-dependent development rate of endogenous feeding stages (eggs and yolk sac larvae) and the foraging and growth of feeding larvae of marine fish (e.g., Peck and Daewel 2008, Peck et al. 2009). Specific parameter sets have been derived for herring (*Clupea harengus*), (Hufnagl & Peck, In Prep), sprat (*Sprattus sprattus*), (Daewel et al. 2008) and Atlantic cod (*Gadus morhua*) (Daewel et al., submitted).

The Lagrangian model uses the 3D fields for velocities, temperature and vertical eddy diffusion coefficients delivered by the hydrodynamic model HAMSOM (Hamburg Shelf Ocean Model). The two models have been coupled to examine characteristics of larvae (passive particles) in the southern North Sea (Kühn et al., 2008)

#### A.1.2 Individual-based model

In the IBM, eggs and larvae were treated as passive particles that develop and grow with time and have specific time-varying traits (e.g., weight, length, amount of ingested food, etc.). The list of traits can be increased. Within a 3D framework, further characteristics which can be assigned to individual particles (larvae) are daily spatial positions or temperature history.

The IBM was structured as an i-state configuration model, treating individuals as explicit entities (Caswell and John 1992). Although the egg and yolk-sac phases were parameterised based on empirical relationships, the formulation for exogenous feeding larvae was based on a balanced bioenergetics approach that accounted for energy gain (ingestion: represented by food consumption  $C$  and assimilation efficiency  $\beta$ ) and energy loss due to metabolism ( $R$ ) and specific dynamic action (SDA):

$$G = C\beta(1 - SDA) - R.$$

The IBM parameterisations were species-specific and based on previously published models for both sprat (Daewel *et al.* 2008), Atlantic cod (Lough *et al.* 2005) and herring (Hufnagl and Peck, In Prep). The cod model was previously employed for short-term feeding and growth of cod larvae on Georges Bank and needed to be slightly modified for use in longer-term simulations. In the following, we describe and compare the IBM parameterisations used for cod and sprat eggs and larvae. IBM-parameterisation.

An endogenously-feeding subroutine (for egg and yolk-sac larvae) includes temperature-dependent utilization of yolk reserves and concomitant somatic growth of larvae. The effects of temperature on the duration of the egg stage ( $H_{egg}$ ) and yolk sac larval stage ( $H_{ys}$ ) of various larval fish species were recently published by Peck et al. (2009). Based on these functions, the duration of endogenously-feeding life stages (egg and yolk-sac larvae) is longer in some species at (constant) temperature, but upper and lower temperature limits are species-specific and should be included in the model (Peck et al. 2009).

In exogenously-feeding marine fish larval, foraging and growth can be depicted using subroutines having the same structure but with species-specific parameter estimates. The majority of the parameters and functions are similar to those previously published in physiologically-based foraging and growth models for larval fish (e.g., Letcher et al., 1996; Lough *et al.* 2005; Daewel et al. 2008) including the effect of individual dry weight ( $M_D$ ) and temperature on metabolic rates ( $R_S$ ) as well as parameterisations needed for the foraging and growth sub-module (activity multiplier ( $k$ ), specific dynamic action (SDA), maximum gut content ( $GC_{max}$ ), and length-weight relationship). One parameter that prevented overfeeding (gut evacuation rate, GER) was adapted from a generalized formulation published by Peck and Daewel (2007) and included a  $Q_{10}$  factor and a second factor that increases

GER during feeding. Such temperature and feeding adjustments in GER are well justified based upon the data collected for a number of different species (see Peck and Daewel 2007).

The IBM includes mechanistic foraging subroutines that depict a number of different processes including prey encounter and handling time. A pause-travel predator formulation was used allowing larvae to search for prey during pauses between swimming events. In some species, information is available to modify foraging parameters based upon prey density ( $p_i$ ), reactive distance ( $RD$ ), pause frequency ( $P_f$ ) and pause duration ( $P_d$ ) (see MacKenzie and Kiørboe 1995) as well as the velocity component of contact rate ( $V$ ) with prey (Browman and O'Brien 1992). Example values of  $P_d$  and  $P_f$  for small and large cod larvae are  $\sim 1.7$  s and  $30/60$  s $^{-1}$ , and  $1.4$  s and  $32/60$  s $^{-1}$ , respectively (see Lough et al. 2005). Maximum prey sizes consumed at different larval body sizes can be determined from measurements of the prey in gut contents (e.g., Voss et al. 2003). An important parameter is the maximum prey length ( $pl_{i,max}$ ) and how that increases with increasing length ( $L_S$ ). An example of this type of formulation for cod was provided by Daewel et al. (2008) who used a sigmoidal function:

$$pl_{i,max} = \frac{1.2936}{\left(1 + e^{-(L_S - 2.8579)/1.2758}\right)}$$

The effect of body size on both the lower threshold and preferred prey sizes can be calculated using a profitability weighting formulation (see Letcher et al. 1996). A comparison between the species indicated that the larvae of some species are able to profitably feed on larger prey items and on a larger prey size spectrum compared to other marine fish larvae of the same length.

Finally, potential larval survival ( $PLS$ ) was included in the IBM and was calculated as a percentage of larvae remaining above a critical, minimum weight ( $W_{min}$ )-at-age ( $t$ ). Larvae that lose weight ( $W < W_{min}$ ) are considered to have died due to starvation and are removed from the simulation. The critical weight of different larvae can be taken from known weight-length relationships (generally, larvae less than 65% of mean weight-at-length are considered to have died due to starvation (e.g., see Lough et al. 2005 and Peck et al. 2005). However, that threshold is species-specific. Mortality due to predation can also be included by assuming length-dependent mortality rates published for the larvae of various species (e.g., Houde 1989 and references therein).

### A.1.3 Particle Tracking Model

In a Lagrangian approach the temporal and spatial dispersion of a particle or an ensemble of particles under the influence of (horizontal and vertical) currents and (horizontal and vertical) turbulent diffusion can be studied. These particles can represent oil spills as well as zooplankton and also fish larvae.

The horizontal and vertical displacements the particles experience under the influence of advection are determined by linear interpolating the 3D grid velocities (obtained from the hydrodynamic model as hourly or daily means) to the current particle (subgrid) position  $x$  and calculating the 3D displacement during the time step  $\Delta t$  :

$$\Delta x_{adv} = w(x) * \Delta t .$$

Additionally, due to the (vertical and horizontal) turbulence the particles accomplish random movements  $\Delta x_r$  the maximum distance of which is determined from the calculated eddy diffusion coefficient  $A_v$  by a random-walk algorithm. The turbulent diffusion coefficients also have to be interpolated to the current position of the particle. In the literature, two different versions of random-walk approaches have been used, so both of them have been implemented and tested:

- 1) 'naive random walk' (Maier-Reimer, 1975):

$$\Delta x_{diff} = P_x \Delta t ,$$

$$\text{with } P_x \in \text{random}[ - P_{x,max}, P_{x,max} ] .$$

The maximum random velocity of a particle  $P_{x,max}$  is given by the eddy diffusion coefficient  $A_v$ :

$$P_{x,max} = (6 A_v / \Delta t)^{1/2} .$$

It follows:

$$\Delta x_{\text{diff}} = \text{ran} [-(6 A_v \Delta t)^{1/2}, (6 A_v \Delta t)^{1/2}] .$$

2) ,diffusive random walk' (Visser, 1997):

$$\Delta x_{\text{diff}} = dA_v/dx \Delta t + [6 A_v (z + dA_v/dx \Delta t/2) \Delta t]^{1/2} .$$

It has been shown (Visser, 1997) that the ,naive random walk' algorithm leads to accumulation of particles in regions of low turbulence – which is excluded by physical reasons. Only for homogeneous turbulence both algorithms give the same result. Consequently, in our simulations only the 'diffusive random walk' approach has been used.

The total displacement of a particle equals the sum of the advective and random displacements:

$$\Delta x_{\text{tot}} = \Delta x_{\text{diff}} + \Delta x_{\text{adv}} .$$

The other relevant physical parameters (temperature, salinity) have also to be interpolated to the current particle position for further use within the IBM.

## A.2 Running the Model

The relevant model codes are available as the following two subroutines:

```
subroutine GENERIC(parameterlist)  
subroutine TRAORT(parameterlist),
```

which have to be included into a main program frame. The latter has to supply the 3d fields of horizontal and vertical velocities, temperature, salinity (optional) and horizontal and vertical eddy diffusion coefficients.

The program code is written in FORTRAN90 and can be run on a PC (Windows environment) or on a main frame.

### A.3 Example Parameters

Variable	units	Generic
Dw: dry weight	µg	$dW = aI \cdot L^{bI}$
L: length	mm	Size range feeding larvae
R: respiration rate		$R = k \cdot R_s$
$R_s$ : routine respiration	µg	$R = a \cdot DW^{0.6} \cdot e^{(c \cdot T)} \cdot Y \cdot X$
k: activity multiplier	-	2 to 3
$\beta$ : assimilation efficiency	%	$\beta = 0.6 \cdot (1 - 0.3 \cdot e^{-0.001(DW - DW_{max})})$
SDA specific dynamic action	Dimensionless	0.10 to 0.30
$\gamma$ : oxycaloric equivalent	Cal·µl O <sub>2</sub> <sup>-1</sup>	0.00463
$\chi$ : conversion cal to dry weight	µg dw·cal <sup>-1</sup>	227
C: consumption	µg·s <sup>-1</sup>	$C = \frac{\sum pdw_i \cdot ER_i \cdot CS_i}{1 + \sum ER_i \cdot HT_i}$
CS: capture success	#·s <sup>-1</sup>	$CS = 1.0 - \left(1.0 \cdot \frac{pL_i}{pL_{max}}\right)$
pL <sub>i</sub> : prey length in class i	mm	
relative prey number in class i	%	$pc_{i,rel} = 77.898 \cdot e^{-0.0082pL_i}$
Prey dry weight	µg	$\log(pdW) = (5.544 \cdot \log(pL) - 7.476) \cdot 2$
maximum ingestible prey length	mm	$pL_{max} = L \cdot 0.08$
HT: handling time	s	$HT_i = e^{0.26410 \cdot \tan\left(\frac{pL_i}{L}\right)}$
ER: encounter rate	s <sup>-1</sup>	$ER_i = \left(\frac{2}{3} \cdot \pi \cdot RD_i^3 \cdot \frac{pc}{1000} \cdot PF\right) + \left(\pi \cdot RD_i^3 \cdot \frac{pc}{1000} \cdot PF \cdot PD \cdot V_i\right)$
PF: pause frequency	s <sup>-1</sup>	1.3
PD: pause duration	s	0.35
RD <sub>i</sub> : reactive distance for prey class i	mm	$RD_i = \frac{pL_i}{2 \cdot \tan\left(\frac{\alpha}{2}\right)}$
$\alpha$ : angle of visual acuity	°degrees	$\alpha = 0.0167 \cdot e^{0.142 \cdot 4 \ln(1) + 0.229 \ln(1)}$
V <sub>i</sub> : velocity component of contact rate for prey class i	mm·s <sup>-1</sup>	$V_i = (v_{pi}^2 + v_L^2 + \omega^2)$
v <sub>pi</sub> : swim speed of prey class i	mm·s <sup>-1</sup>	$v_{pi} = 3 \cdot pL_i$
v <sub>L</sub> : swim speed of larvae	body lengths·s <sup>-1</sup>	$BL = 0.0593 \cdot L - 0.2253$
$\omega$ : turbulent velocity	mm·s <sup>-1</sup>	1.3
GC: maximum gut content	µg	$GC_{max} = 0.64 \cdot DW^{0.995}$
GER: gut evacuation rate	µg h <sup>-1</sup>	$GER = 1.792 \cdot L^{-0.828Q_{10} \frac{T-12}{10}}$

## A.4 Deliverable Update

UHAM (Partner 3) has contributed a larval fish IBM and user guide to this Deliverable, IMR (Partner 11) will further contribute to both Tasks T2.2.4 (Deliverable D2.10) and T2.2.5.1 (Deliverable D2.11) through delivery of the SYSTMOD model.

SYSTMOD was nominated as a fish model for the MEECE project. SYSTMOD was developed by Johannes Hamre, former chief scientist at Institute of Marine Research, together with Steinar Moen, Powersim (Hamre and Moen 2008) (<http://www.powersim.com/>). It has been presently applied on the cod-capelin-herring interactions in the Barents Sea, and with temperature as an environmental driver. The model is unique compared to other stock assessment models in the way that it is including three fish stocks and that temperature prediction enables us to simulate future development of the three fish species. The conceptual functional relationships formulated are sound and based on well established knowledge about species interaction under climate fluctuations. The model has, however, two limitations which has lead us to the conclusion that we want to develop it further before it should be applied in a trophic integrated MEECE model system:

1. The environmental driver, temperature, is a proxy for several other ecosystem factors that we want to implement in the model. Particularly, we consider the temperature as a proxy the abundance of productivity at trophic level 2. This should be included in the model.
2. The model needs to be more transparent with respect to definition and referencing of the data to be used in the modeling process (e.g., in verification/validation) and if possible, an indication of uncertainty connected with the data (Subbey 2010). Moreover, a description of how the model assimilates observation data is needed. This requires that data and model are separated.

Such improvements will both make it better accessible for linking it up with lower trophic levels models and as a tool in stock assessment and management strategies. IMR will work on these improvements during 2010.

Our second concept on fish models is newly developed by PhD student Kjell Rong Utne and chief scientist Geir Huse. It is a model concept for migration of pelagic fish feeding on zooplankton. The model is further linked to a phytoplankton model driven by a ROMS physical model system. It has been particularly developed for migration of blue whiting, mackerel and Norwegian spring-spawning herring feeding on the boreal zooplankton in the Norwegian Sea. In contrast to SYSTMOD, the pelagic fish model is more specifically process-oriented, and hence very well suited for linking up with other MEECE models on other trophic levels. Kjell Rong Utne is now fully funded by MEECE and he will submit his thesis consisting of 4 papers in early June. The model will be available for the MEECE community at that time. He will further be employed as scientist at IMR and continue with the development of the models systems and to make it available for MEECE.

Hence, our conclusion is that we will make available both the pelagic model system and a revised SYSTMOD for MEECE. The pelagic model system will be available in June 2010, while the revised SYSTMOD will be available toward the end of the year.

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## Section B. The SLAM+(ERSEM+POLCOMS) model coupling

### B.1 Introduction

This document contains a short description and user guide of the SLAM (Sandeel Larval Advection model) model, coupled offline with the POLCOMS+ERSEM model provided by Plymouth Marine Laboratory (PML) in the MEECE project. The SLAM model underlying this implementation is published mainly in Can. J. Fish. Aquat. Sci. 65: 1498-1511 (2008) by Christensen *et al.*

The SLAM in the present implementation is set up within the IBMlib (Individual based model library) framework maintained by DTU Aqua. The present code package, however, contains only a self contained subset of the IBMlib framework. The basic idea of IBMlib is sketched and is very well in line with the goal of MEECE to ease the traditionally cumbersome process of coupling biological models to arbitrary biogeochemical models. The present code package is a preliminary demonstration coupling of the SLAM and POLCOMS+ERSEM models; the production runs in MEECE WP 3+4 will be performed with an upgraded and extended version of the present code package, and interested MEECE participants are encouraged to obtain latest version before embarking on simulations on their own with the SPAM model setup.

### B.2 Functionality

SLAM+(POLCOMS+ERSEM) setup allows you to perform flexible individual- based modelling of early life stages within the space-time window covered by a supplied POLCOMS+ERSEM data set. Sandeel larvae and/or eggs can be released according to any space-time pattern specified in the input file. The model describes growth of egg/larvae in relation to local physical conditions obtained from the supplied POLCOMS+ERSEM data set. The model can easily be extended by alternative biological processes, e.g. alternative active larval behaviour.

### B.3 License and intellectual property rights

At some point it is planned to make the IBMlib public available, but this awaits the clarification of some the license issues of integrated external packages as well as code hosting and distribution issues; until then, the code is available to MEECE participants within the MEECE project under provisions specified in the MEECE consortium agreement and the intellectual property rights belong to DTU Aqua.

### B.4 Installation

#### B.4.1 Portability

The code is written in strict Fortran 90 and does not invoke operating system specific features nor does the code rely on non-standard compiler specific services. Therefore the code (possibly with some superficial preparations) should compile and execute on any platform; however, the code has only been applied on Linux platforms until now.

#### B.4.2 Requirements

In order to build the SLAM executable, the following resources must be available:

- A Fortran 90+ compiler and C++ compiler. The compiler and link flags in the Makefile applies to Intels *ifort* compiler, however the transcription of these flags should be straightforward by consulting the documentation of alternative compilers; most flags are standardized.
- NetCDF. The code assumes the Fortran 90 implementation (the fortran- only variant) is installed (at compilation time by use association of of the netcdf module - usually netcdf.mod, somewhere in the include path - and at link time by linking to libnetcdf.a and libnetcdf.a). The NetCDF is freely available at [www.unidata.ucar.edu/software/netcdf](http://www.unidata.ucar.edu/software/netcdf). It is recommended to use NetCDF 4+ (which requires HDF5 and zlib installed), but NetCDF 3.6+ should also work.

- GNU make. The current makefile is written for GNU make, however, with minor adaptation, it should also work with other implementations of make.
- tar and gzip. The code is packed with tar and compressed with gzip.

### **B.4.3 Code installation under Linux**

The code package comes as *SLAM4MEECE.tgz*. Put it in a suitable location and type the following commands

```
tar xvfz SLAM4MEECE.tgz
make tracker
```

This builds the SLAM executable tracker which you - on UNIX like systems - may place somewhere in the executable paths for convenience.

## **B.5 Running the code**

On UNIX like systems, the SLAM model is invoked from the command line simply as

```
tracker <inputfile> [ > <outputfile>]
```

(assuming tracker is somewhere in the executable paths). Here “<inputfile>” means the filename of an ASCII text file containing parameters for the simulation. The structure of inputfile” is outlined below. Optionally, an output file “<outputfile>” can be specified to capture the simulation output; if an output file is not specified, it is written to standard output.

## **B.6 Input files**

### **B.6.1 Simulation parameters**

The SLAM model code comes along with an input parser that reads input with minimalistic markup in the form

```
TAG = VALUE|SET OF VALUES
```

from the ASCII text input file specified on the command line above. *TAG* is a name of something (like starting time or a parameter) and *VALUE* is the value SLAM should use for *TAG*. *SET OF VALUES* means that this can also be a simple list (separated by spaces) of values. A small pieces of an input file could look like this

```
! --- Simulation parameters for ...
  y = 3445! an optional trailing comment
  x = 45.
  zvector = 1 56 99
  aname = whatever
```

A complete example of an input file is given below. Line order and white spaces does not matter. The following rules also apply for the markup:

- Comments: everything after (and including) “!” is skipped
- Empty lines: just ignored
- Malformed lines: just ignored (e.g. if you forgot “=“)
- Everything after “=” is considered part of the value for tag
- Required tag (or value) is missing. This will generate a runtime error, SLAM will stop, unless a default applied to the tag.

The input parser is given in the file *input\_parser.f* in the code package. An example of a minimal input file (i.e. the mandatory input tags) is given below (provided in file "input/test\_input.txt" in the code package *SLAM4MEECE.tgz*)

```

!-----
! Main simulation control file
!-----

start_time = 2005 03 01 0      !      year month day second_of_day
end_time = 2005 03 18 0      !      year month day second_of_day

hydroDBpath = hydroDB      !      file path to POLCOMS+ERSEM data set
grid_desc = grid_desc.txt  !      sub grid descriptor

advec_intg_method = euler    !      advection scheme: euler/rk27rk4
particle_time_step = 1800    !      in seconds for time integration of motion

! ----- biology spatial control -----
! r(1:4) start:   year month day sec_of_day
! r(5:8) end:     year month day sec_of_day
! r(9:11) lon_min lat_min z_min (z=0 -> surface)
! r(12:14) lon_max lat_max z_max (z=1 -> bottom)
! r(15) max_number_of_tracers
! r(16:) other input item to particle state

emitbox = 2005 03 02 0 2005 03 02 3600 2 54 1 3 55 1 100 e
emitbox = 2005 03 02 3600 2005 03 02 7200 4 54 1 5 56 1 100 | 9.66

! ----- biology growth -----
! parameters corresponds to Can. J. Fish. Aquat. Sci. 65: 1498-1511 (2008)

egg_hatch_begin = 78.484 0.10984 ! days since fertilization (A,k0 > 0)
egg_hatch_mid = 108.75 0.12488 ! days since fertilization (B,k1 > 0)
egg_hatch_end = 176.14 0.11358 ! days since fertilization (C,k2 > 0)

larvae_temp_coeff = -1.725 0.136142 0.00 ! mm/day/Celcius^n
larvae_temp_func = 1 ! 0: func=polynomial 1: func=exp(polynomial)
larvae_hatch_len = 7.7253 ! mm
larvae_length_expo = 0.315544 ! beta (small larvae growth exponent)
larvae_metamorph_len = 40.0 ! mm

```

- start\_time. The beginning of the simulation, specified as (year month day second of day)
- end\_time. The end time of the simulation, specified as (year month day second of day)
- hydroDBpath. File path to POLCOMS+ERSEM data set
- grid\_desc. The file name of the sub grid descriptor (see below).
- advec\_intg\_method. The integration algorithm for time forward integration of advected sandeel larvae (options Euler forward, Runge-Kutta 2 or 4)
- particle\_time\_step. Nominal time step for the integration algorithm in seconds.
- emitbox. Gives a window in space and time, where sandeel larvae/eggs are released. The may be specified as many emitbox entries as desired, in this way they may act in parallel

and quite complex release patterns can be set up. The first 4 integers are (year month day second\_of\_day) where the release begins (of that box); the next 4 integers are (year month day second\_of\_day) where the release stops (of that box). The next six numbers specify a spatial box (in latitude and longitude) where sandeel larvae/eggs are released. Dry (land-locked) sectors of the spatial box are omitted when releasing larvae/eggs. The first three numbers are the spatial lower SW corner of the release box given as (longitude,latitude,vertical position), the next three numbers are the spatial upper NE corner of the release box given as (longitude,latitude,vertical position). The vertical position can be specified as absolute depth (counted negative below the water surface) or as relative depth  $z: 0 < z < 1$ .  $z = 0$  corresponds to the sea surface,  $z = 1$  corresponds to the sea bed. Biological particles are released uniformly in time and space with in space-time window specified, so that the total number of particles released adds up to the integer given as number 15.

All other parameters following number 15 in emit box are passed to the biological module. There can be an "e", which means sandeel eggs are released by this emitbox; there can be an "l" which means sandeel larvae are released by this emitbox - in the latter case, a number giving the initial length (in mm) of the released sandeel larvae should be provided.

- stochastic egg growth parameters (egg\_hatch\_begin, egg\_hatch\_mid, egg\_hatch\_end), see Can. J. Fish. Aquat. Sci. 65: 1498-1511 (2008) for details.
- larval growth parameters (larvae\_temp-coeff, larvae\_temp\_func, larvae\_hatch\_len, larvae\_length, larvae\_metamorph\_len) see Can. J. Fish. Aquat. Sci. 65: 1498-1511 (2008) for details.

### **B.6.2 Sub grid descriptors**

The SLAM model allows to operate on a sub grid of the POLCOMS+ERSEM spatial domain in MEECE. The sub grid descriptors allow to cut out a subgrid, when the relevant biological habitat is smaller than the domain of the hydrodynamic model, to speed up calculations and run the simulation on a laptop. The sub grid descriptor is specified in same format as the simulation parameters above.

```
! -----
! ----- full grid definition -----
! -----
lambda_start_fullgrid = -19.833333333
lambda_end_fullgrid = 13.000000000
dlambda_fullgrid = 0.166666667
phi_start_fullgrid = 40.111111111
phi_end_fullgrid = 64.888888889
dphi_fullgrid = 0.111111111
nz = 40
! -----
! ----- subgrid definition -----
! -----

lambda_start_subgrid = -3.0
lambda_end_subgrid = 10.0
phi_start_subgrid = 52.0
phi_end_subgrid = 59.0
```

- (lambda\_start\_fullgrid, lambda\_end\_fullgrid) is the longitude range of the POLCOMS+ERSEM spatial domain in degrees East.
- lambda\_fullgrid is the longitude grid spacing of the POLCOMS+ERSEM spatial domain.
- (phi\_start\_fullgrid, phi\_end\_fullgrid) is the latitude range of the POLCOMS+ERSEM spatial domain in degrees North.
- dphi\_fullgrid is the latitude grid spacing of the POLCOMS+ERSEM spatial domain.

- (lambda\_start\_subgrid, lambda\_end\_subgrid) is the longitude range of the SLAM spatial sub domain in degrees East.
- (phi\_start\_subgrid, phi\_end\_subgrid) is the latitude range of the SLAM spatial sub domain in degrees North.

The sub grid will be coherent to the full POLCOMS+ERSEM grid (i.e. overlapping grid nodes) (provided in file "input/grid desc.txt" in the code package *SLAM4MEECE.tgz* )

## B.7 Output

The simulation writes logging information to standard output, and at the end of the simulation, the task example writes the state of the sandeel egg/larvae ensemble to standard output. It is normally highly specialized which output is desired, and therefore, to save disk space, it is most efficient to insert write statements in "main\_program.f" selecting exactly the information needed. The IBMlib features several writing subroutines.

## B.8 Programming

The IBMlib code is written in strict Fortran 90 and the coding style of IBMlib adheres to modern object-oriented programming principles to the extent they are supported by Fortran. IBMlib API will be provided later in MEECE. The most important interfaces in IBMlib are

- The physical interface: provided by physical\_fields.f. Here the biological modules can access the local physical/biological environment.
- The particle state interface: provided by physical\_state.f This interface lets IBMlib update the biological ensembles. All biological mechanisms are behind the particle state interface.
- The task interface: this is interface provided by IBMlib to the main program.

## Section C. Anchovy IBM Model for the Aegean

### An individual-based model of the anchovy full life cycle in the Eastern Mediterranean

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#### C.1 Overview

Understanding the growth, mortality, reproduction and transport patterns of small pelagic fish requires the coupling of hydrodynamics and lower trophic level dynamics to fish dynamics. The present biophysical model is an individual-based model (IBM), structured in a modular approach, composed by hydrodynamic, biogeochemical and fish modules to simulate the spatial and temporal variability of anchovy growth, abundance, movement and catches in the northern Aegean Sea (NAS).

For the representation of the fish population, the approach of “Super Individuals” (SI) was adopted (Scheffer et al., 1995), each one characterised by its position (x, y, z coordinates), age, length, weight, catch and growth rate. Physiological processes are resolved through a bioenergetics model, while population processes solved separately describe the evolution of the number of individuals in each age class, accounting for fishing and natural mortality. From the seven life stages included, the first two (eggs and early larvae) are considered as passive tracers. For the remaining stages in order to simulate fish movement to optimal areas, a dynamic programming method is used where food resources and processes are balanced in a memory and learning procedure. In addition to horizontal migration, a vertical movement is also incorporated as a combined function of the regular diurnal migration, prey concentration and water temperature provided by the coupled hydrodynamic-biogeochemical model.

#### C.2 Description of the individual-based anchovy model

##### C.2.1 Model domain

The North Aegean model domain extends from 38.7° N to 41.0° N and from 22.5° E to 27.0° E. Horizontal resolution is 1/10° (~10km) while 25 sigma-levels are resolved in the vertical, with logarithmic distribution approaching the surface. The U.S Navy Digital Bathymetric Data Base has been used to build the model bathymetry with bilinear interpolation into the model grid. The model domain and bathymetry are shown in Figure 1.

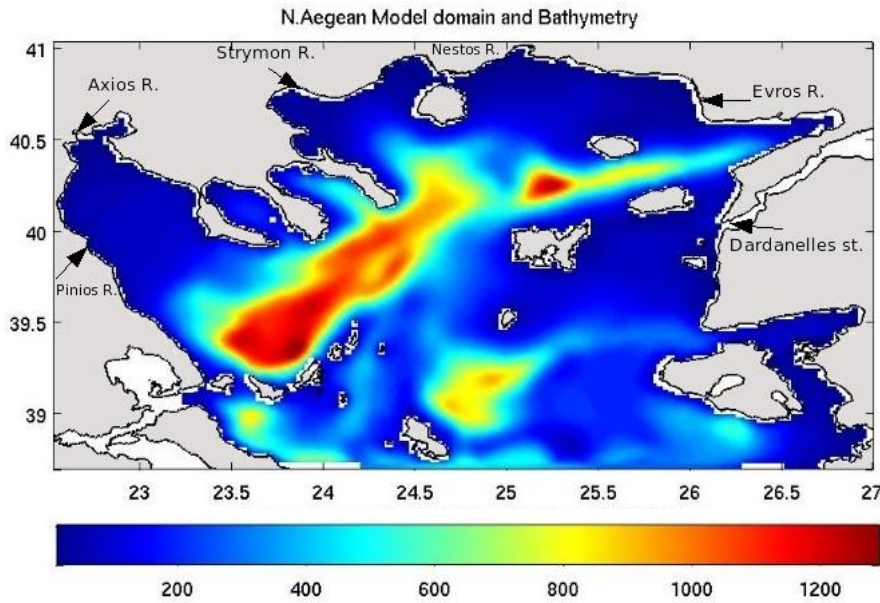


Figure 1. Study area: northern Aegean Sea. Model domain and bathymetry

### C.2.2 Modelling approach

The present model is structured in a modular approach synthesized by several modules: a physical, an ecological and a fish module (with other submodules within). The general structure of the model is shown in Figure 2. The main characteristics of each module are described below.

For the representation of the entire fish population, the super-individual (SI) approach is adopted (Scheffer et al., 1995; Kirby et al., 2003). Each SI is referred as “fish” which has certain characteristics (attributes).

The attributes that characterize each anchovy SI in the present module are: weight, length, position (x, y, z coordinates), number of individuals and age (explicitly related to its life stage).

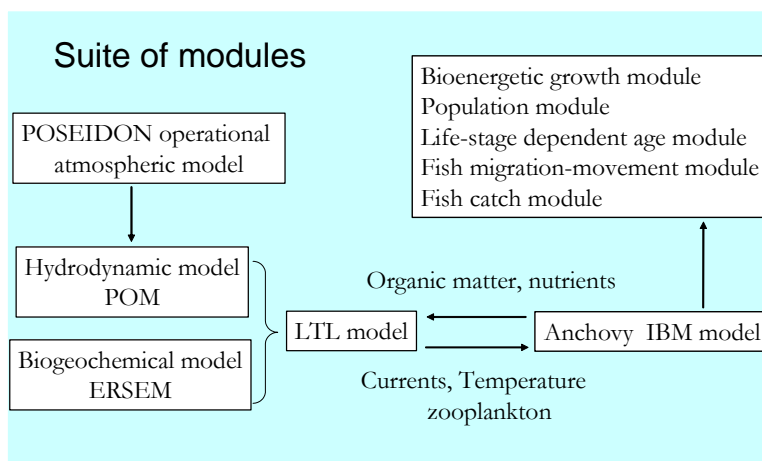


Figure 2. Suite of models which describe the IBM anchovy model.

### C.2.3 Abiotic and biotic environment as input for the anchovy IBM model

The abiotic environment is described with outputs from a hydrodynamic model. It provides the temporal and spatial three dimensional fields of physical variables (currents, temperature) as inputs to the IBM anchovy model.

The hydrodynamic model is based on the Princeton Ocean Model (Blumberg & Mellor 1983), which is a primitive equation, sigma-coordinate circulation model embedded with a Mellor-Yamada 2.5 turbulence closure sub-model (Mellor & Yamada 1982) that is used to compute vertical mixing coefficients. POM (<http://www.aos.princeton.edu/WWWPUBLIC/htdocs.pom>) is a widely spread community model with numerous applications. In the N. Aegean it has been applied by Kourafalou and Tsiaras (2007) while it is also implemented in the Aegean Sea as part of the operational "POSEIDON" forecasting system.

Regarding the association of the anchovy's growth processes with its environment, an ecological model provides three zooplankton densities (heterotrophic flagellates, microzooplankton and mesozooplankton) which serve as available energy via consumption for the anchovy module.

The ecological model is based on the European Regional Seas Ecosystem Model (ERSEM), (Petihakis et al. 2002). ERSEM uses a "functional" group approach to describe the ecosystem where the biota is grouped together according to their trophic level (subdivided according to size classes or feeding methods). The biological functional group dynamics are described by both physiological (ingestion, respiration, excretion, egestion etc.) and population (growth, migration, mortality) processes. Carbon dynamics are coupled to chemical dynamics of nitrogen, phosphate, silicate and oxygen. The pelagic state variables include 4 groups of phytoplankton (diatoms, nanoplankton, picoplankton, dinoflagellates), 3 groups of zooplankton (heterotrophic flagellates, microzooplankton, mesozooplankton), bacteria, dissolved organic matter and particulate organic matter. Each group (except mesozooplankton) has dynamically varying C/N/P ratios and is represented by their carbon, nitrogen, phosphorus and in the case of diatoms silicon, components.

#### **C.2.4 Bioenergetics growth module**

The Wisconsin bioenergetics framework (Ito 2004; Rose et al., 2007) is applied to simulate anchovy growth. The wet weight increment per unit weight of weight per day is calculated by the equation

$$\frac{1}{W_{SI}} \cdot \frac{dW_{SI}}{dt} = [C - (R + EG + SDA + EX + EGG)] \cdot \frac{CAL_z}{CAL_f},$$

where  $W_{SI}$  = fish wet weight (g) of the SI,  $t$  = time (days),  $C$  = consumption,  $R$  = respiration (or losses through metabolism),  $SDA$  = dynamic action (or losses because of energy costs of digesting food),  $EG$  = egestion (or losses because of faeces),  $EX$  = excretion (or losses of nitrogenous excretory wastes) and  $EGG$  = egg production (or losses because of reproduction). Components of the energy budget ( $C, R, EG, EX, SDA, EGG$ ) are in units of (g prey g fish<sup>-1</sup> day<sup>-1</sup>), which are converted to (g fish g fish<sup>-1</sup> day<sup>-1</sup>) by using  $CAL_z$  = caloric equivalent of zooplankton (cal g prey<sup>-1</sup>) and  $CAL_f$  = caloric equivalent of fish (cal g fish<sup>-1</sup>).

For the implementation of the bioenergetics model, the anchovy life span is divided into seven life stages: embryonic (egg+yolk sac larvae), early larval, late larval, juvenile, adult stage (age-1), adult stage (age-2) and adult stage (age-3). A full description of the structure and parameterization of the anchovy model can be found in Politikos et al. (2010).

#### **2.4 Population dynamic-reproduction module**

The rate of change of fish density (numbers of individuals) for each SI without including reproduction process is represented by the equation,

$$\frac{dN_{SI}}{dt} = -(M_{SI}(age, T, population\_density) + F_{SI}(age, \mathbf{x}, time))N_{SI},$$

where  $N_{SI}$  is the daily number of the SI,  $M_{SI}$  is the assigned natural mortality ( $\text{day}^{-1}$ ) based on the SI age, temperature (T), population density and  $F_{SI}$  is the corresponding fishing mortality ( $\text{day}^{-1}$ ) which depends on age, position  $\mathbf{x} = (x, y, z)$  of the SI and time.

Natural mortality rates applied in the model are age, density and temperature dependent. Specifically, for egg stage, natural mortality is modeled using a temperature dependent empirical relationship derived from Somarakis et al., (2010), while early-larval natural mortality is density egg dependent following Somarakis et al., (2007a). Constant natural mortality rates were imposed for late-larval, juvenile and adult stages, following Mantzouni et al. (2007) and Giannoulaki et al. (2007).

Fishing mortality has three components: an age-dependent part, a spatial and time dependent one. Differentiations on fishing parameter values for adult anchovies of age-1, age-2 and age-3 anchovy has been estimated by Somarakis et al. (2007b) and adopted in the modelling approach. Also, a spatially dependent mask has been formulated based on fishing effort grounds. The mask acts as a flag (takes the value zero every time that the SI is on a grid that is not considered as a fishing area and the value 1 when a SI is within the fishing area). Further elaboration of vessel monitoring systems (VMS) data is required to quantify the spatial part of fishing mortality.

The catch in numbers for each SI is calculated using a Baranov equation (Quinn and Deriso, 1999) including a spatial component,

$$c_{SI}(\mathbf{x}, t; \delta t) = \frac{F_{SI}(\text{age}, \mathbf{x}, \text{time})}{M_{SI}(\text{age}, T, \text{population\_density}) + F_{SI}(\text{age}, \mathbf{x}, \text{time})} N_{SI} \times (1 - \exp(-M_{SI}(\text{age}, \text{population\_density}, T) + F_{SI}(\text{age}, \mathbf{x}, \text{time}))\delta t),$$

where  $c_{SI}(\mathbf{x}, t; \delta t)$  is the catch in number of a SI in a time interval  $[t, t + \delta t]$  of length  $\delta t$  and position  $\mathbf{x}$ . The total yield  $CF_{SI}(t; \delta t)$  (in grams) at the time interval  $[t, t + \delta t]$  for each SI is calculated as the product of abundance with its weight,

$$CF_{SI}(\mathbf{x}, t; \delta t) = c_{SI}(\mathbf{x}, t; \delta t) W_{SI}.$$

Individual egg production (number of eggs per batch of a member of the SI) is modeled as a linear function of its weight,  $EGG_{Ind} = a \cdot W_{SI} + b$  following the estimations of Somarakis et al., (2010). The total amount of eggs per batch provided by a mature SI is calculated by the product  $EP_{SI} = EGG_{Ind} \cdot N_{SI}$ , where  $N_{SI}$  is the number of population in the SI. Considering the spawning period from May to September (Somarakis et al., 2007b), we assumed that each adult SI spawns 10 times during the spawning period with a mean frequency of reproduction, every four days.

### C.2.5 Fish movement module

At each time step, from the current position of the SI, we identify the surrounding points within the model grid that are used to calculate zooplankton, temperature and currents with bilinear interpolation. These values are provided to the SI to update its biological, population and movement processes.

The SI of eggs and early larvae stages are treated as passive tracers and the horizontal displacement of each SI due to advection is given by

$$L(x, y) = (u_{SI}, v_{SI}) \cdot dt + a \cdot dt,$$

where  $u_{SI}$ ,  $v_{SI}$  are the local current velocities at  $x$  and  $y$  directions (in  $m s^{-1}$ ),  $dt$  is the time step and  $a$  is a random component related to random movement due to other factors (e.g predation).

The swimming speed capability of late larval, juvenile and adult anchovies, are assumed to be proportional to their length (see also Lagr\_Move.F at Section 4). The SIs are assumed to move along a direction pointing to higher food resources while remaining within certain bathymetric ranges based on their known habitats. The SI actual swimming velocity is adjusted taking account of the current velocity in order to achieve the desired direction (Figure 3). Moreover, if there is enough food in its

current position it will only use swimming to compensate the currents by its flaps and maintain its position, or otherwise search for areas with more food. Schematically, Figure 3 shows the direction mechanism of fish movement.

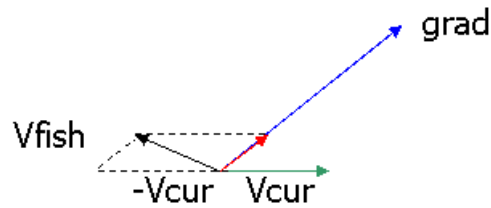


Figure 3. Direction mechanism of fish movement.  $V_{cur}$  is the current velocity,  $V_{fish}$  is the fish velocity so that it would direct along a gradient ( $grad$ ) towards optimal conditions (food resources and bathymetry).

### C.3. FORTRAN structure code

The two main fish routines are called within ERSEM ([www.meece.eu/library/ersem.html](http://www.meece.eu/library/ersem.html)) to implement the anchovy module:

- Ersem\_Fish.F routine which calculates all the biological characteristics of the SIs,, using AnchovyAge.F and AnchovyBio.F,
- Lagr\_Move.F routine which determines the position of the SIs following the modelled movement rules.

The biological attributes with the corresponding FORTRAN routines are summarized in Figure 4.

#### Ecology.F

```

. . .
. . .
IF (iswECOL$ .EQ. 1 ) THEN ! ERSEM routines
    CALL ox_dynamics
    CALL subpel
    CALL calc_sedimentation(delt)
    CALL subben
IF ( iswFISH$ .EQ. 1 ) THEN !IBM routines
    CALL ersem_fish(iyr,dt_fish)
    call lagr_move(dt_fish)
ENDIF
END IF
. . .

```

The biological calculations are made in Ersem\_Fish.F routine which are solved daily for all super-individuals, through a do loop:

```

c number of SIs: nsi
do 10 n=1,nsi
c age of the SI
  iage=age(n)
. . .
c position of the SI
  x=xsi(n)
  y=ysi(n)
  ii=int((x-alon(1,1))/xs)+1
  jj=int((y-alat(1,1))/ys)+1
. . .
c first see for Age shift and Egg production
  if(iage.eq.1)then
c egg->larvae
  call AnchovyAge(TTime,n,iage,1,dt1_eco,neweggs,ishiftdays)
  endif
  if(iage.eq.2)then
c larvae->juvenile
  call AnchovyAge(TTime,n,iage,2,dt1_eco,neweggs,ishiftdays)
  endif
  if(iage.ge.3.and.iage.le.5)then
c juvenile->adult0, adult0->adult1, adult1->adult2
  if(iyr1.gt.3)then
  call AnchovyAge(TTime,n,iage,3,dt1_eco,neweggs,ishiftdays)
  endif
  endif
  if(iage.eq.6)then
c adult 2
  call AnchovyAge(TTime,n,iage,4,dt1_eco,neweggs,ishiftdays)
  endif

c egg production
  if(iage.ge.4)then
  if(iyr1.gt.3)then
  call AnchovyAge(TTime,n,iage,5,dt1_eco,neweggs,ishiftdays)
. . .

c Now calculate fish weight and population
c -----
  call AnchovyBio(dt1_eco,TTime,n,iage,fisi,fjsi)

```

```

. . .
enddo

```

### Lagr\_Move.F

```

. . .
c fish velocity =0.5*fish length(m)
c the difference between fish and current speed determines the swimming
speed

fishspeed=1.7*0.001*bl(k)
curspeed=sqrt( (uloc+uwave)**2.+(vloc+vwave)**2.)
if(fishspeed.ge.curspeed)then
  ufish=(fishspeed-curspeed)*
&      (gradxi(k)*velsi(k)+gradxi_h(k)*toposi(k))
&      -(uloc + uwave)
  vfish=(fishspeed-curspeed)*
&      (gradyi(k)*velsi(k)+gradyi_h(k)*toposi(k))
&      -(vloc + vwave)
else
  ufish=0.
  vfish=0.
endif
. . .

```

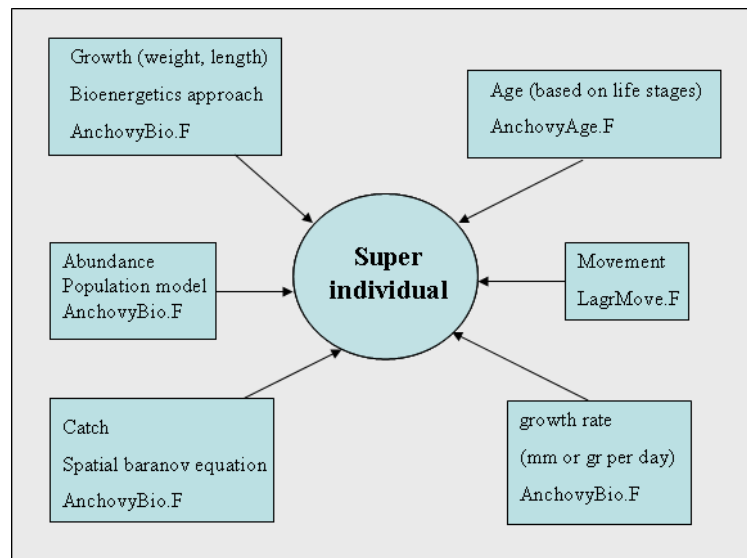


Figure 4. Attributes of the super-individual and the corresponding FORTRAN routines.

## C.4 Implementation of the model

Regarding the initialization of the model, the initial spatial positions for early life stages are determined by using data from observed egg and larval distribution surveys (Somarakis et al., 2010). For juvenile and adult stages, initial positions are set based on probability maps for anchovy potential presence in the North Aegean Sea (Giannoulaki et al., 2008).

A simulation from June 2003 to December 2004 period (starting at 1<sup>st</sup> June) was performed to simulate the basic features of anchovy spatial dynamics. The main outputs of the model, as well some preliminary results are presented below.

### C.4.1 Main outputs

The main outputs of the IBM anchovy model are:

- the spatial and temporal distribution of anchovy biomass ( $\text{gr/m}^2$ ) specified for each life stage (egg, larvae, juvenile, adults),
- the length frequency distribution of the anchovy population categorized in three nine size classes: <94mm, 94-104mm, 104-114mm, 114-124mm, 124-134mm, 134-144mm, 144-154, 154-164mm and >164mm.
- anchovy catches (spatially and summed over the whole area),
- anchovy weight and length of the SIs,
- dynamic and seasonal circulation patterns of all anchovy life stages,
- spatially explicit estimates of daily growth rates ( $\text{mm day}^{-1}$ ) of SIs as an index of habitat quality

### C.4.2 Model Results

The simulated egg distribution is shown to be in good relation with the observed distribution as shown in Figure 5. Increased concentrations are noticed in three subareas: Thermaikos Gulf, Strymonikos Gulf and Thermaikos Sea which constitute the major spawning and feeding grounds for anchovy (Somarakis et al. 2007b).

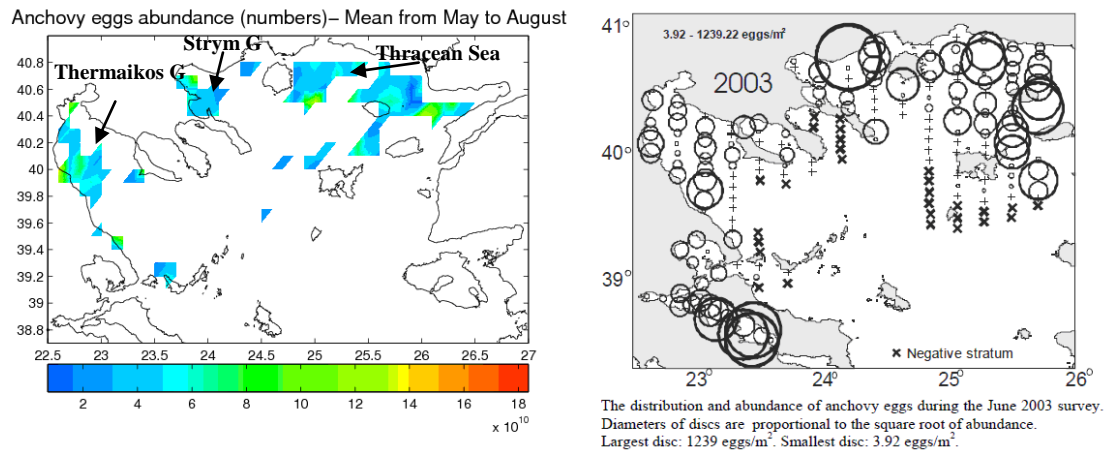


Figure 5. Simulated egg distribution (left) compared to the observed egg fields (right).

The cumulative catch distribution of adult SIs, (as shown in Figure 5a), follow the reported fishing grounds (Figure 5b). Although spatial catch data are not available for the entire validation of the model, we notice that by using an appropriate fish mask which represents the fishing grounds, the model captures adequately the spatial patterns of the fishing effort. In that way the model has the ability to explore the effects of alternative fishing management measures on the spatial dynamics of anchovy.

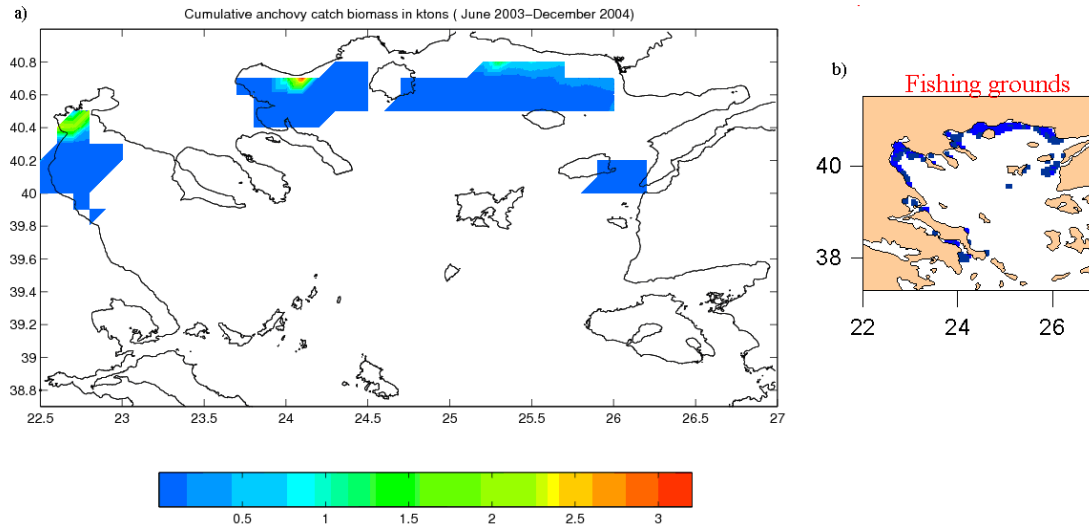


Figure 5. Cumulative catch distribution of a) adult SIs as simulated by the biophysical model over the period June 2003–December 2004, b) observed fishing grounds.

As it is shown in Figure 6, the model simulates the length frequency distribution (%) of the anchovy population (left panel) compared to the observed ones (right panel). The model shows an underestimation during its initialization in June 2003, but it captures the observed frequency distribution reasonably well in June 2004. Overall, results indicate that small and medium size fish are dominant, compared to bigger ones. For the long-term viability of the anchovy stock, it is important to investigate the factors (climatic, anthropogenic) that cause changes in anchovy’s length distribution and propose measures related to fisheries which would increase the mean length structure of the stock.

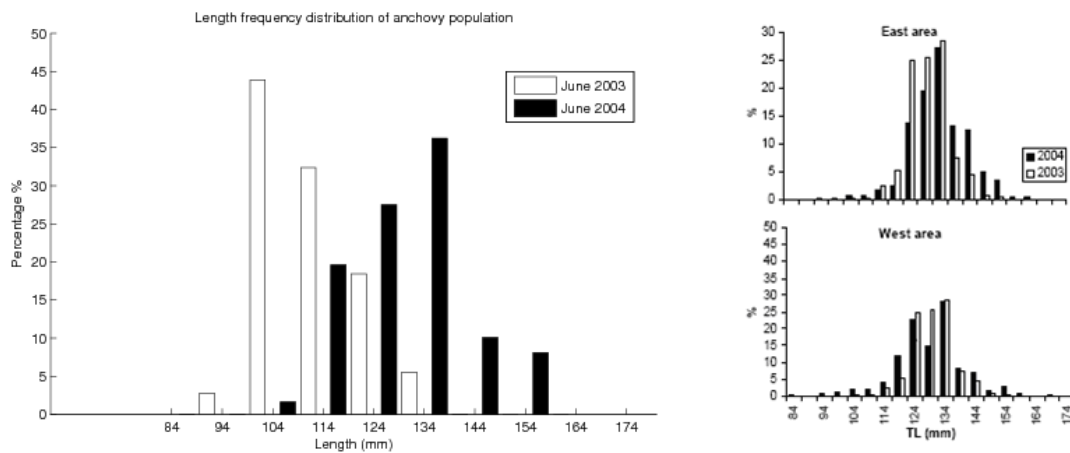


Figure 6. Length frequency distribution (%) of the anchovy population in June 2003 and 2004: simulated (left panel) and observed (right panel) for eastern and western area of Aegean Sea.

The daily positions of an SI are illustrated in the left side of Figure 7. The different coloured dots represent the propagated life stages of anchovy starting from egg stage. In addition, at the right part of the figure, the corresponding weight, length and biomass of the SI are simulated. Generally, anchovy weight is characterized by a seasonality being reduced during autumn where the zooplankton levels are low. Also, the adult SI moves towards coastal areas that are more favourable for growth as indicated in the left panel of Figure 7.

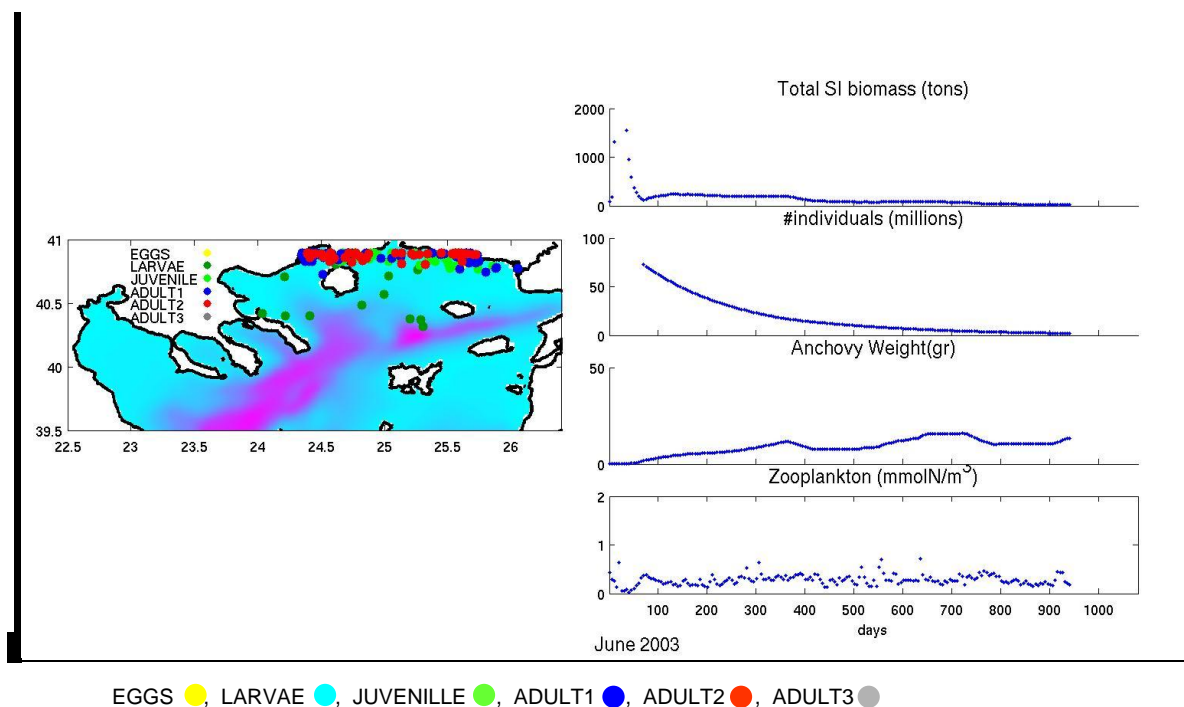


Figure 7. Daily positions of a SI during its lifetime starting from egg (yellow circle) and its corresponding weight, length and biomass.

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## Section D. An IBM (Individual Based Model) for *Calanus finmarchicus* in the Norwegian Sea

### An IBM (Individual Based Model) for *Calanus finmarchicus* in the Norwegian Sea

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#### D.1 Introduction

As part of the WP2 activities to create a library of plug and play type models, which can be coupled to existing coupled hydrodynamic and intermediate and complex NPZD type models, this report describes an IBM model for *Calanus finmarchicus* in the Norwegian Sea.

The model consists of three different modules:

- **calanus mod:** this module contains the main driver together with a number of subroutines that is specific for *Calanus finmarchicus*
- **zoo generic:** this module contains the generic part of a zooplankton IBM. In addition to the type definitions, there are a number of subroutines that operates on the types and that (with assumed only minor changes) could be used by similar IBMs
- **tools:** this module contains some additional routines that are used by the other modules. They are not specific for the IBM and are only included for completeness
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A short description of each module and the source code are given in Chapter 3-5. The IBM relies on input from an ocean circulation model and a two-way interaction with a biogeochemical model which produces phytoplankton fields. Consequently, the IBM takes as input a 3D phytoplankton field together with 3D fields for velocities and temperature that are included as external modules in the present code. The module will also need information about the grid (bottom depth, depth of layers, longitude, latitude, cell size) that should be supplied by the user in the call to the main routine. As outputs the module produces a 2D field (PMORT) for phytoplankton mortality together with the updated IBM. The module will need access to a routine computing the horizontal movement of particles. In the code this routine is named HORMOV, and assumed available from a module called LADIM (Lagrangian Advection and Dispersion Model). This module is not included. Within the IBM there is an implicit assumption that the model operates with a time step of one hour.

Validation and sensitivities of the module coupled to the NORWECOM.E2E model is to be published in Hjøllø et al. (2011). In that paper a one year long simulation (year 1997) are analyzed and compared to observations of chlorophyll-a and *C. finmarchicus* distribution and production estimates for the Norwegian Sea. In addition experiments are done to study the effect of early/late diapause termination, food availability and initial stock size on the sensitivity testing of selected parameters. For more details, information, updates and access to code please contact: [morten@imr.no](mailto:morten@imr.no).

#### D.1.1 The life history of *Calanus finmarchicus*

The copepod *Calanus finmarchicus* is the dominant species of the mesozooplankton in the Norwegian Sea (Melle et al., 2004). The species is largely herbivorous and constitutes an important link between the phytoplankton to the higher trophic levels in the Norwegian Sea food chain (Aksnes and Blindheim, 1996; Melle et al., 2004). The *C. finmarchicus* is vital to many of the planktivorous fish species including Norwegian spring spawning (NSS) herring (*Clupea harengus* L.), blue whiting (*Micromesistius poutassou*, Risso), and mackerel (*Scomber scombrus* L.), which feed in the Norwegian Sea during summer to utilize the abundant zooplankton resources (Dalpadado et al., 2000; Dommasnes et al., 2004; Broms and Melle, 2007). In addition to these migrating predators, there are large standing stocks of invertebrates and mesopelagic fish that feed on different stages of *C. finmarchicus* (Dalpadado et al., 1998; Skjoldal, 2004). *C. finmarchicus* overwinter at depth mainly as

copepodite stages 4 (C4) and 5 (C5), ascend towards the surface during early spring, mature, and produce eggs prior to and during the spring phytoplankton bloom (Marshall and Orr, 1955; Niehoff et al., 1999; Broms and Melle, 2007; Broms et al., 2009; Stenevik et al., 2009). The new generation stays in the upper waters and grows to stage C5. At this point, individuals may continue to mature and produce a new generation, or build up fat reserves and descend to overwintering (Hirche, 1996a; Broms and Melle, 2007; Broms et al., 2009).

Population dynamics of plankton results from net reproductive and advective rates (Aksnes and Blindheim, 1996). The export losses from the Norwegian Sea population of *C. finmarchicus* into the Barents and North Seas provide very important input to these areas (Heath et al., 1999). Fish recruitment success in the Barents Sea is consequently positively correlated with inflow of warm *C. finmarchicus* rich water from the Norwegian Sea and coast (Sætersdal and Loeng, 1987). In the North Sea, there has been substantial reduction in the abundance of *C. finmarchicus* during the recent decades (Planque and Fromentin, 1996; Reid et al., 2003) that is partly attributed to a reduction in inflow from the Norwegian Sea (Heath et al., 1999) and partly due to change in species composition due to climate change. The low abundance of *C. finmarchicus* is a prime candidate for poor fish recruitment in the North Sea in recent years (Beaugrand et al., 2003; Nash and Dickey-Collas, 2005; Payne et al., 2009) and *C. finmarchicus* is therefore a key species in many respects.

To organisms inhabiting the sea there are inherent problems in upholding life cycle closure due to the advective and diffusive forces that continuously act to disperse populations. While many marine fishes have solved this problem by counter current homing to distinct spawning areas, planktonic organisms face greater difficulties in maintaining life cycle closure. Instead planktonic species need to utilize the vertical and horizontal differentiation in the current pattern to close their life cycle. This is a particular problem in areas of strong advective regimes such as those bordering the Nordic Seas. Bryant et al. (1998) studied the drift pattern resulting from different vertical positioning that mimicked the vertical distribution of *C. finmarchicus*. They found that some areas of the Norwegian Sea such as the Norwegian Basin were able to retain particles over several years. Such retention is maintained by the seasonal vertical migration pattern with a northward flow during summer in the upper waters and compensatory southward flow in deep waters (>600 m) during winter. The model applied by Bryant et al. (1998) did not include growth, mortality, reproduction, and inter annual variability in drift pattern. In order to fully understand the mechanisms governing retention of *C. finmarchicus* in the core area in the Norwegian Sea it is important to include these factors.

#### ***D.1.2 Modeling spatial dynamics of plankton***

There are two distinct methods for simulating the spatial dynamics of plankton, namely the Lagrangian (IBMs) and Eulerian approaches (e.g. Carlotti et al. (2000)). Several models have been developed to simulate the spatial and population dynamics of *C. finmarchicus* both using 1D IBMs (Carlotti and Nival, 1992; Carlotti et al., 1993; Carlotti and Radach, 1996; Carlotti and Wolf, 1998), 3D IBMs (Pedersen et al., 2001; Tittensor et al., 2003), and 3D Eulerian (Speirs et al., 2005, 2006) models. The different approaches have their pros and cons and in particular the Eulerian models are numerically more efficient than IBMs, which on the other hand allow a more detailed biological description of individuals. Another key element in IBM is the emphasis on mechanistic process formulation and emergent features in vital rates and traits (Huston et al., 1988; Huse et al., 2002; Grimm and Railsback, 2005).

Huse (2005) presented a 1D IBM for *C. finmarchicus* based on evolving traits using a genetic algorithm under different predation levels. The results showed that the emergent life history traits were sensitive to the predation regime. This model was the core of the study by Samuelsen et al. (2009) which addressed the advection of *Calanus* from the Norwegian Sea onto the Norwegian shelf. This version of the model was 3D and coupled to the biogeochemical NORWECOM model. However the coupling was only one way so that the grazing by the *Calanus* was not taken into account in the model. Huse et al. (2011) developed the 1D *Calanus* IBM into a full 3D model and addressed the links between the adaptation of life history strategies and retention of *Calanus* in the Norwegian Sea basin. Skogen et al. (2007) ported the North Sea NORWECOM model to the Norwegian Sea and showed that the model reproduced the dynamics in the phytoplankton of the Norwegian Sea reasonable well. What has been lacking is a two-way coupling of *C. finmarchicus* and phytoplankton, taking into account the close interactions between plankton that is important for understanding the dynamics of the Norwegian Sea ecosystem (Skjoldal et al., 2004).

## D.2 Model description

The 3D *C. finmarchicus* individual based model takes into account growth, mortality, movement and reproduction of *C. finmarchicus* as well as adaptive traits (Huse, 2005), which control the interaction with the environment. The model addresses the entire life cycle of *C. finmarchicus*, and the main life history features and vertical movement are emergent properties resulting from many generations of evolution using a genetic algorithm. The purpose of the model is to evolve behavioral and life history strategies of *C. finmarchicus* using a genetic algorithm, a physiological model, and a detailed description of the environment in order to understand the *C. finmarchicus* behavioral and life history strategies and their effect on population dynamics and retention. The *C. finmarchicus* IBM has been described in previous studies (Huse, 2005; Samuelsen et al., 2009) and for more details on the exact representation of the details see Huse et al. (2011).

### D.2.1 State variables

The model comprises individuals and their environment. The attribute vector (Chambers, 1993) of individuals consists of 17 different states including their stage, internal number, weight, fat level, age, depth (Table 2.1). The strategy vector (Huse et al., 1999), which is evolved, contains all the life history and behavioral strategies of individuals and comprises four behavioral and life history traits. The life history traits include the date for ascent from overwintering to the surface (WUD), the day for initiating fat allocation (AFD) in copepodite stage 5 (C5), fat/soma ratio needed before descending to overwintering (FSR), overwintering depth (OWD). The three former traits were introduced by Fiksen (2000). Even though the individual-based structure is appealing, it is impossible to simulate copepod population dynamics on a truly individual basis due to the great abundances involved, and *C. finmarchicus* is therefore simulated using the super-individual approach (Scheffer et al., 1995). A super-individual represents many ( $\sim 10^{12}$ ) identical individuals and the number of such identical siblings is an attribute of the super individual.

Type	Name	Description
integer	mynumb	Unique identifier
real	xpos	Position (x)
real	ypos	Position (y)
real	zpos	Position (z)
logical	alive	true if alive, false if dead
integer	stage	0 is egg, 1-6 nauplia, 7-11 copepodits, 12 adult, 13 mature female
real	inumb	Internal number in individuals
real	sweight	Structural weight in micrograms
integer	lstage	Stage longevity
real	fat	Fat energy level in KJ
real	moult	Moult cycle fraction (Egg,N2,N3) OR cum. egg number (adult)
real	maxegg	Total number of eggs in each individual
integer	diapause	0 diapause, 1 active, 2 move down, 3 move up
real	ingestion	Ingestion rate
real	egestion	Engestion rate
real	grate	Growth rate
integer	death	Cause of death
real	wud	Wake Up Day (from diapause)
real	fsr	Fat to Soma Ratio (if larger than FSR, then go down after AFD)
real	afd	Allocation to Fat Day (before this day feeding goes to maturing after to fat)
real	owd	Over Wintering Depth

**Table 2.1:** Attribute and strategy vectors for the *calanus finmarchicus* IBM

### **D.2.2 Processes overview and scheduling**

The processes governing the individuals are growth, mortality, movement and reproduction. *C. finmarchicus* has 14 different stages including an egg stage, six nauplia stages, five copepodite stages and an adult stage. *C. finmarchicus* does not commence feeding until the third nauplia stage (N3), and for stages below this, stage longevity was calculated as a function of temperature (Carlotti and Wolf, 1998). For stages N3 and above, growth is calculated as a function of phytoplankton density, temperature and size using a bioenergetics model (Carlotti and Wolf, 1998). The *C. finmarchicus* is assumed to change stage when a stage specific critical weight is achieved. For the egg and nauplia stages, mortality consists of unspecified causes (taken from Ohman et al. (2004)) and tactile predation. For the copepodite and adult stages mortality is attributed to predation from herring, mackerel, mesopelagic fish and tactile predators, starvation when the weight goes below the critical weight and exhaustion if more than 800 eggs have been spawned. For individuals in diapauses, no vertical movement is calculated, but for other individuals, movement is calculated either as a function of turbulence and sinking (stages < N3) or by adapted rules. A sex ratio of 50% is assumed, and males are removed from the population after one spawning event, as male *C. finmarchicus* have only a brief functioning after which they are expendable (Hirche, 1996b). Fat is allocated to structural growth for immature individuals, but mature individuals and C5s preparing for overwintering allocate their surplus energy into fat storage. During times of negative growth, the stored fat is depleted before the structural weight is reduced.

### **D.2.3 Reproduction**

Adults can reproduce when their structural weight is above 90 µg, they have attained enough fat reserves to spawn a batch of eggs, and they are positioned within the upper mixed layer (< 40 m). If these criteria are fulfilled new super-individuals are produced. An offspring inherits the strategy vector from its parent, but random changes take place with a probability of 0.06 per trait or weight on the strategy vector. Such mutations take place by changing the values randomly by ±20% of the value. The internal number of the new super-individual is a function of the batch size and the internal number of the parent individual. New super-individuals are initiated as eggs at the same depth as the parent. Following reproduction the weight reserve of the parent super-individual is reduced by an amount corresponding to the clutch size multiplied by the egg weight.

### **D.2.4 Flows between sub models**

The models are linked so that the IBM receives input on phytoplankton density. In the present implementation type definitions and names (TBIO, IDIA, IFLA) are assumed from the NORWECOM model, but this can be easily changed. The *Calanus* individuals then feed on the phytoplankton in sequence and the local phytoplankton abundance is updated continuously, and at the end the new phytoplankton biomass is calculated and updated in the NORWECOM model. The *Calanus* feed simultaneously in order to avoid any consistent differences in food provisioning among individuals. This is done by first adding up the total demand for food, and then adjust the available resources so that all IBMs get the same fraction of food compared to their request. Based on initial test simulations with one way coupling of NORWECOM and *Calanus* models, a threshold on grazing on phytoplankton is set so that the phytoplankton biomass in a square can not be removed at a rate larger than 20% day<sup>-1</sup>.

### **D.2.5 Initialization**

At start of a simulation the overwintering population can either be generated on random (READPOP=0) or from an existing distribution of super individuals generated by data or another model (READPOP=1,2). This part of the code should be checked and revised by the user according to the way of use.

#### **1. Module: calanus.F90**

This is the main module containing the following subroutines:

- **CALIBM:** This is the main routine that controls the calling sequence within the IBM during one time step

- **CALSTA:** This routine calculates growth from a regular bioenergetics model with ingestion, egestion and respiration processes. The routine also calculates stage dynamics and the phytoplankton predation field.
- **INITIALISE:** This routine reads (or calculate) the initial distribution together with attribute and strategy vectors for each super individual. It also sets a number of species dependent parameters to be used within the IBM.
- **PREDDENS:** Included in INITIALISE. Calculate the vertical distribution of tactile predator density
- **CALCPRISK:** Set predation risks from different predators of the calanus finmarchicus.

The routines that are included here are (except for CALIBM) those who are assumed being species dependent. This means that if another species than calanus finmarchicus is to be modeled, these routines are likely to be completely rewritten or re-parameterized.

## 2. Module: zoo generic.F90

This module contains the following subroutines:

- **KILL SUPER:** Set the status of a super individual to dead.
- **WRITE SUPER:** Write the attribute and strategy vector of a super individual to screen
- **INIT SUPER:** Initialize a super individual given attribute and strategy as input
- **SPAWN SUPER:** Spawn a new super individual given the parent as input. Calling INIT SUPER.
- **COUNT SUPER:** Count the number of alive super individuals
- **POPZIP:** Compress data structure by removing dead super individuals
- **INIT BINORMAL:** Initialize bi-normal density function being used to distribute a super individual horizontally
- **PHYTOMORT:** Calculate the 2D phytoplankton mortality field.
- **CALMORT:** Compute mortality (and kill super individuals) for a number of reasons (outside area, exceed max number of eggs spawned, stage longevity). Internal number is also reduced due to starvation and predation.
- **CALREP:** Calanus reproduction. Find super individuals that are ready to spawn. New super individuals are generated by calling SPAWN SUPER.
- **VERTMOV:** Vertical movement of super individuals. Update of diapause status.
- **COMBIND:** Routine to combine super individuals within a short distance and with similar attributes

The module also contains all type definitions. The module rely on the Fortran 2003 type extensions and polymorphic variables, with a hierarchical extension of data types from *particle* to *superind*, *ibm* and *calanus*. If another species and IBM is to be included, this can simply be done by including an additional extended data type from the *ibm* type. An example (*krill*) is given. The routines included are those that are assumed being general, in an object oriented sense. This means that if the IBM is rewritten for another species (or another species are added to the model), only minor revisions should be done to make these routines general so that they can be used by *all* species included (possibly using the *select type* construct

## 3. Module: tools.F90

This module contains the following subroutines:

- **GETR:** Obtain visual range by solving a non-linear equation by means of Newton-Raphson iteration and derivation in subroutine DERIV.
- **EASYR:** Obtain a first estimate of visual range by using a linear expression in GETR
- **DERIV:** Derivation of equation for visual range of a predator
- **SURLIG:** Calculate surface light
- **VAL3D:** Finds the value in a 3D field in position (x,y,z)
- 

Neither of these subroutines is specific for the IBM, but is included for completeness as they are used by CALANUS or ZOO GENERIC.

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