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[Christophe Lett](#), [Philippe Verley](#), [Christian Mullon](#), [Carolina Parada](#) ...+3 more authors

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A Lagrangian tool for modelling ichthyoplankton dynamics

Lett Christophe^{a*}, Verley Philippe^{b,c}, Mullon Christian^d, Parada Carolina^e,
Brochier Timothée^d, Penven Pierrick^b, Blanke Bruno^c

^a IRD, UR GEODES, IXXI, ENS, 46 allée d'Italie, 69364 Lyon Cedex 07, France

^b IRD, UR ECO-UP, Centre de Bretagne, BP 70, 29280 Plouzané, France

^c LPO, UMR 6523 CNRS IFREMER UBO, 6 avenue Le Gorgeu, C.S. 93837, 29238 Brest
Cedex 3, France

^d IRD, UR ECO-UP, CRHMT, rue Jean Monnet, BP 171, 34203 Sète, France

^e SAFS, University of Washington, 1122 NE Boat St, Seattle, WA 98105, USA

* Corresponding author. Fax: +33 4 26 23 38 20. E-mail: christophe.lett@ird.fr

Abstract

Ichthyop is a free Java tool designed to study the effects of physical and biological factors on ichthyoplankton dynamics. It incorporates the most important processes involved in fish early life: spawning, movement, growth, mortality and recruitment. The tool uses as input time series of velocity, temperature and salinity fields archived from ROMS or MARS oceanic models. It runs with a user-friendly graphic interface and generates output files that can be post-processed easily using graphic and statistical software.

1 **Keywords**

2

3 Ichthyop; Biophysical model; Lagrangian model; Individual-based model; Particle tracking;

4 Fish early life; Fish eggs and larvae; Transport.

5

6 **Software availability**

7

8 **Name of software** Ichthyop

9 **Developer** Verley Philippe

10 **Contact details** info@previmer.org

11 **Hardware required** Pentium IV and 512 Mb of RAM memory advised

12 **Software required** Java Runtime Environment (JRE) 1.6v or above

13 **Program language** Java

14 **Program size** ~ 12 Mb

15 **Availability and cost** free software declared under GPL license, download from

16 <http://www.ur097.ird.fr/projects/ichthyop/>

17

18 **Introduction**

19

20 The dynamics of ichthyoplankton (fish eggs and larvae) is heavily influenced by advective

21 processes. These processes largely determine the transport of ichthyoplankton within the

22 system, and therefore the environmental conditions that it experiences. Many models coupling

23 physics with ichthyoplankton dynamics have been developed (reviewed in Miller 2007). To

24 our knowledge, the computer implementations of these models are however not easily

1 available, and certainly not as user-friendly tools. There is an ongoing effort to structure the
2 community who uses such models. A recent example is the “Workshop on advancements in
3 modeling physical-biological interactions in fish early-life history: recommended practices
4 and future directions” (Gallego et al. 2007). Sharing tools also helps to structure a
5 community. We developed the Ichthyop tool with this idea in mind.

6

7 **The tool**

8

9 Ichthyop has been developed to study how physical (e.g., ocean currents, temperature) and
10 biological (e.g., growth, mortality) factors affect the dynamics of ichthyoplankton. The tool
11 uses time series of velocity, temperature and salinity fields archived from oceanic simulations
12 of the “Regional Oceanic Modelling System” (ROMS, Shchepetkin and McWilliams 2005) or
13 the “Model for Applications at Regional Scale” (MARS, Lazure and Dumas 2008). It also
14 enables to track virtual drifters and the ocean properties (temperature, salinity) that they
15 experience.

16

17 Ichthyop is a free Java tool that can be downloaded from
18 <http://www.ur097.ird.fr/projects/ichthyop/>. A Java Runtime Environment (JRE) is needed to
19 run it. The distributed package consists of a compressed archive (~ 12 Mb) that contains the
20 program source code, byte code, libraries, and an example of ROMS simulation allowing
21 first-time users to run the program. A user guide (pdf format, ~ 0.7 Mb) is also provided.

22

23 Ichthyop offers two functioning modes. The first one allows a visualization of the transport of
24 virtual eggs and larvae in a user-friendly graphic interface (Figure 1). The second mode

1 enables to run series of simulations based on pre-defined sets of parameters, with a minimalist
2 interface.

3

4 Figure 1

5

6 The tool is a generic version of previous modelling experiments investigating the effects of
7 physical and biological factors on the dynamics of anchovy and sardine ichthyoplankton in
8 the Benguela (Mullon et al. 2002, Huggett et al. 2003, Mullon et al. 2003, Parada et al. 2003,
9 Lett et al. 2006, Miller et al. 2006, Lett et al. 2007b) and in the Humboldt (Lett et al. 2007a,
10 Brochier et al. submitted) upwelling systems.

11

12 **The model**

13

14 The model description follows the Overview-Design-Details (ODD) protocol for describing
15 individual- and agent-based models (Grimm et al. 2006) and consists of seven elements. The
16 first three elements provide an overview, the fourth element explains general concepts
17 underlying the model's design, and the remaining three elements provide details.

18

19 **Purpose**

20

21 Ichthyop is an individual-based model (IBM) designed to study the effects of physical and
22 biological factors on the dynamics of fish eggs and larvae.

23

24 **State variables and scales**

25

1 The IBM comprises individuals and their physical environment. Individuals are characterized
2 by the state variables: age [day], length [mm], stage (egg, yolk-sac larva or feeding larva),
3 location (longitude [$^{\circ}$ E], latitude [$^{\circ}$ N] and depth [m]) and status (alive or dead). The physical
4 environment is characterized by ocean state variables: current velocities [$\text{m}\cdot\text{s}^{-1}$], temperature
5 [$^{\circ}$ C] and salinity.

6

7 The environment state variables are provided on a discrete three-dimensional grid by archived
8 simulations of the ROMS or MARS oceanic models. As an example of typical spatial scales
9 used to characterize the environment, we describe the ROMS southern Benguela
10 configuration grid (Penven et al. 2001) It extends from 28 to 40 $^{\circ}$ S and from 10 to 24 $^{\circ}$ E. The
11 horizontal resolution ranges from 9 km at the coast to 16 km offshore. The vertical resolution
12 ranges from 1 to 4.7 m at the surface and from 3.1 to 1030 m at the bottom of the ocean.

13

14 The IBM sees the Eulerian velocity field at the same spatial scale as the Eulerian primitive
15 equation models (ROMS/MARS). Subgridscale parameterizations can be added in the IBM to
16 address scales unresolved by the primitive equation models (see the dispersion terms in the
17 IBM movement submodel below).

18

19 In ROMS, the current velocities, temperature and salinity fields are typically averaged over
20 time and stored every day or so. In the IBM, these fields are interpolated in space to provide
21 values at any individual location. They are also interpolated in time to feed the IBM time step
22 (typically one hour). Simulations consist in tracking the locations and properties of the
23 individuals (typically during a few weeks or months).

24

25 **Process overview and scheduling**

26

1 After initialization (spawning), the IBM proceeds in discrete time steps. Within each time step
2 each individual moves, grows and tests for mortality and recruitment. The spawning,
3 movement, growth, mortality and recruitment submodels are described below. The
4 environment state variables are updated during the simulation at a frequency equal to that of
5 the ROMS/MARS stored outputs.

6

7 **Design concepts**

8

9 *Stochasticity.* The release location of each individual is chosen randomly within the specified
10 spawning areas. This is used to simulate patchy or uniform distributions depending on a
11 patchiness parameter (see the spawning submodel below). The horizontal and vertical
12 dispersion components of the movement (see the movement submodel below) are also
13 stochastic.

14

15 *Observation.* The advection part of the movement submodel has been tested by recording
16 trajectories of individuals and comparing them to trajectories obtained using two other
17 Lagrangian tools (“Roff”, Capet et al. 2004, Carr et al. 2008,
18 http://www.atmos.ucla.edu/~capet/Myresearch/my_research_floats.html]; “Ariane”, Blanke
19 and Raynaud 1997, Blanke et al. 1999, <http://www.univ-brest.fr/lpo/ariane>). The present tool
20 offers two functioning modes (a graphic interface and a serial mode, see “The tool” section
21 above) and associated observation modes (output files, see “The simulations” section below).

22

23 **Initialization**

24

1 The IBM first loads a configuration file (see “The simulations” section below). Then
2 individuals are released according to a spawning strategy set by the user (see the spawning
3 submodel below), at the egg stage, with an initial length of 0.025 mm.

4

5 **Input**

6

7 The fields of environment state variables are the input of the IBM. They are provided by
8 archived simulations of ROMS or MARS.

9

10 **Submodels**

11

12 *Spawning.* The spawning strategy is defined by the user. The tool offers two modes for
13 releasing eggs. The first one, zone release, implies setting the number of eggs and the
14 spawning areas, depth, frequency and patchiness. Each spawning area is defined by the
15 coordinates (longitude [°E], latitude [°N]) of four points and by two bathymetric lines [m].
16 The four points delimit a polygon and the spawning area is set as the portion of the polygon
17 contained between the bathymetric lines. Depth of spawning is defined by upper and lower
18 depth levels [m]. Spawning begins at the beginning of the simulation. There may be several
19 spawning events: the number of spawning events and the time between two events are set by
20 the user. Eggs may be released by patches inside the spawning areas: the user defines the
21 number of patches, their radius (horizontal dimension [m]) and thickness (vertical dimension
22 [m]). The alternative release mode allows reading the initial location of the released
23 individuals from input files (see the Ichthyop user guide).

24

1 *Movement.* The movement submodel simulates the following processes: horizontal advection,
2 vertical advection, horizontal dispersion, vertical dispersion, egg buoyancy and larval vertical
3 migration. Horizontal advection is always used in the movement equation. Vertical advection
4 is always used too, except at the larval stage if the user chooses to apply the vertical migration
5 scheme instead. The vertical migration scheme implemented is diel vertical migration where
6 larvae spend daytime and night-time at user-specified depths. Daytime begins at 7 a.m. and
7 night-time at 7 p.m. A user who wants to change these values or to consider another vertical
8 migration scheme will have to make changes in this submodel (see the Ichthyop user guide).
9 The user can choose to apply a buoyancy scheme at the egg stage. When buoyancy is taken
10 into account a term is added to the vertical velocity. This term depends on the difference
11 between egg density and water density. Egg density [$\text{g}\cdot\text{cm}^{-3}$] is a parameter chosen by the user
12 and water density is a function of temperature and salinity. For a complete description of the
13 buoyancy scheme we refer to Parada et al. (2003). The user can also choose to apply
14 horizontal dispersion and vertical dispersion. Horizontal dispersion has been implemented
15 following Peliz et al. (2007). A random displacement model has been implemented for
16 vertical dispersion (Visser 1997), using a cubic spline interpolation of the vertical diffusivity
17 fields read in the environment state variables. For time-stepping a forward-Euler or a 4th order
18 Runge-Kutta integration schemes can be used.

19 *Growth.* Length l [mm] increases linearly with time t [day] (eq. 1a), at a rate r taken as a
20 linear function of temperature T [°C] (eq. 1b).

21

$$l(t + \Delta t) = l(t) + r\Delta t \quad (1a)$$

$$r = 0.02 + 0.03T \quad (1b)$$

22

1 Individuals change stages according to their length, going from egg to yolk-sac larva at 2.8
2 mm, and from yolk-sac larva to feeding larva at 4.5 mm. These values and equations (1) are
3 used to simulate the growth of anchovy in the southern Benguela upwelling system. A user
4 who wants to consider another species or location may have to make changes in this
5 submodel (see the Ichthyop user guide).

6

7 If plankton concentrations are provided in the environment state variables used in Ichthyop
8 (e.g., they result from simulations of a NPZD biogeochemical model coupled to ROMS, Koné
9 et al. 2005), the user may choose to apply, at the feeding larvae stage, a growth function
10 limited by food (eq. 2):

11

$$r = \frac{Food}{K_s + Food} (0.02 + 0.03T) \quad (2)$$

12

13 where K_s is a half saturation constant and $Food$ a function of phytoplankton and zooplankton
14 concentrations (Koné 2006) that can be specified in the source code.

15

16 *Mortality.* Individuals die when they are in waters at a temperature below a certain value. This
17 value of lethal temperature [°C] may be different for eggs and for larvae, and is user-
18 specified.

19

20 *Recruitment.* Individuals are considered as recruited when they have reached a minimum
21 length (or age) and spent a minimum amount of time within a “recruitment area”. Recruitment
22 areas are defined in the same way as spawning areas (see the spawning submodel above). The

1 minimum length (or age) at recruitment and the minimum duration of stay within recruitment
2 areas are determined by the user.

3

4 **The Simulations**

5

6 Simulations are performed using either the graphic interface (SINGLE) mode of the tool or its
7 series of simulations (SERIAL) mode. Which of these two modes is used depends on the
8 value of the “*run*” field in the configuration file.

9

10 *Configuration files.* Configuration files enable the user to specify the conditions under which
11 simulations are performed. As part of the Ichthyop tool a configuration editor helps designing
12 configuration files for the SINGLE mode. Configuration files for the SERIAL mode have to
13 be designed using a text editor. Basic examples of SINGLE and SERIAL configuration files
14 are provided in the tool. We refer to the Ichthyop user guide for details about configuration
15 files.

16

17 *Output files.* Output files are screen snapshots (Figure 1) in the SINGLE mode, and NetCDF
18 files in both SINGLE and SERIAL modes. In the NetCDF output files are recorded the state
19 variables of all individuals and of the environment they experience. We refer to the Ichthyop
20 user guide for details about these output files. They can be post-processed easily using
21 graphic and statistical software. Routines in R (Hornik 2007) for plotting trajectories of
22 individuals or for computing the number of individuals transported from spawning areas to
23 recruitment areas can be sent upon request.

24

1 **Conclusion**

2

3 Ichthyop is a tool designed to be shared within the community using models coupling physics
4 with ichthyoplankton dynamics. Though it has been historically developed to study the
5 dynamics of small pelagic fish ichthyoplankton in upwelling systems, Ichthyop is a generic
6 tool in the sense that it incorporates the most important processes involved in ichthyoplankton
7 dynamics. Using Ichthyop for other species in other systems may imply a few changes in the
8 source code (e.g., changing the growth function, implementing a specific larval vertical
9 migration scheme, etc.). This code is organized simply, commented and documented, which
10 should make it easy to modify by a user with basic programming skills.

11

12 **Acknowledgements**

13

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16 their helpful comments.

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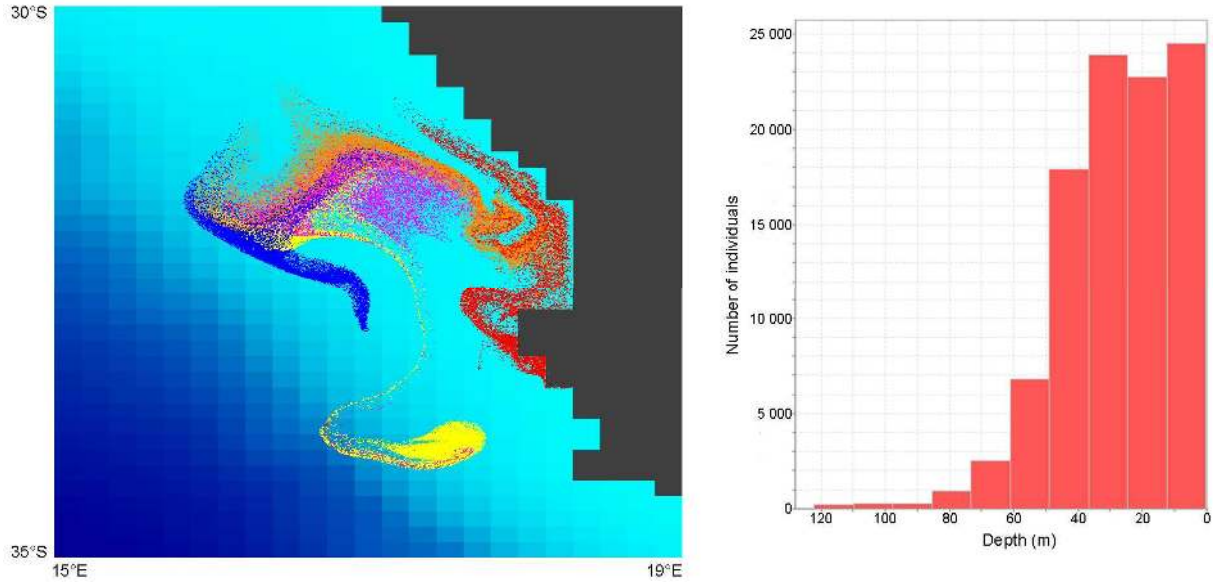
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1 Figures

2



3

4 Figure 1: The simulated eggs and larvae dispersal pattern is displayed on a longitude-latitude
5 plot in the main frame of the graphic user interface (GUI). A snapshot (with individuals
6 coloured according to the area where they were released) is shown in the left panel. Control
7 graphs, like the one in the right panel (showing the depth distribution of individuals), can be
8 added in the GUI.