

# Sea-Scale Agent-Based Simulator of *Solea solea* in the Adriatic Sea

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**Abstract.** DISPAS is an agent-based simulator for fish stock assessment developed as a decision making support for the sustainable management of fishery. In this work we enlarge the underlying model of DISPAS allowing it to model and simulate a multi-scale scenario. We retain the currently available spatial scale, able to represent a limited average region of the sea, and we introduce a new spatial macro-scale, able to represent the whole sea. At the macro-scale a single agent represents an area of five square nautical miles and manages groups of fish in different age classes. The interactions among the macro agents permit the exchange of individuals of each class among neighbor areas. A case study regarding the *Solea solea* (Linnaeus, 1758; Soleidae) stock of the northern Adriatic Sea is used to show the intended approach, taking into account the available data, coming from fishery independent scientific surveys.

**Keywords:** Modeling and simulation · Agent-based modeling · Ecosystem modeling · Common sole · Adriatic Sea · Multi-scale modeling

## 1 Introduction

Marine ecosystems are undoubtedly an important environmental resource for the life they support and, from a more ordinary point of view, as a source of food through fishing activities, which are a relevant sector of the economy of mostly all of the coastal Countries. Because of its importance, in the last twenty years, a global concern about the sustainable management of marine resources has risen [10]. In particular, as a partial consequence of weak or ineffective fishery management policies, a rising overfishing in the Mediterranean Sea have been put forward by scientists [5]. Within this scenario, national and regional management bodies, with the support of research institutes, are currently cooperating to

study, address and try to minimize the impact of fishery both on target species and on their environment.

The northern part of the Adriatic Sea, as part of the Mediterranean Sea, is one area of interest for these studies. Here, flatfish resources are highly vulnerable to certain fishing activities (e.g. rapido trawling [25]) and to anthropogenic impacts, such as the presence of contaminants and the disruption of sea-floor integrity (e.g. dredging for beach nourishment). Within the group of flatfish, the common sole, *Solea solea* (Linnaeus, 1758), is one of the most commercially important species in the Adriatic Sea, which contributes for around 23 % to the overall sole catch of the FAO-GFCM (Food and Agriculture Organization-General Fisheries Council for the Mediterranean) area (Mediterranean and Black Sea; FAO-FISHSTAT source). The majority of this contribution is provided by the northern and central parts of the Adriatic basin, where around 64 % of the common sole catches come from the Italian rapido trawl fleets, 33 % from the Italian, Slovenian and Croatian set netters operating mostly within 3 nautical miles from the coast, and the remaining 3 % from the Italian otter trawlers [9]. In particular, approximately 80 % of sole rapido trawl landings in the area occur during the fall season [7].

In this scenario, marine biologists are required by management bodies to monitor the sole fish stock in order to estimate its current size, determine the impact of the fishing effort and give support for establishing fishing policies to contrast overfishing. Among other initiatives, the SoleMon project [9] was started in order to get fishery independent data, from scientific surveys, about soles in the northern Adriatic Sea. These data are being applied to assess the stock, implementing methodologies typical of the marine ecology sector. As a new promising way of using the available data and supporting the stock assessment, DISPAS (Demersal fish Stock Probabilistic Agent-based Simulator) [2,22,23] was introduced. DISPAS is an agent-based simulator that was designed, implemented and validated with the aim of having a tool to simulate how a (demersal) fish stock would react to different scenarios of fishing efforts, considering also seasonal and environmental conditions. The current version of the simulator is able to reproduce an average square kilometer of sea in which each individual fish is represented by an agent. The behavior of each agent is timed and probabilistic. At every time step, simulating one month, any individual grows according to a parametrized growth function. In the same step it is also subject to a natural mortality probability - modeling interaction with other species (not explicitly represented in the simulator) and with the environment - and to a probability of being fished, which can vary at different months and can be set in different ways to express a range of fishing efforts. In [2,22,23] it is shown that DISPAS simulations are able to reproduce with a good degree of accuracy the biomass (total weight of the stock), the abundance (total number of individuals in the stock, divided by age class) and other indices of the considered stock in the target period 2005–2011, as they are established by marine biologists [9].

Studies to evaluate existing *spatial* management regimes and potential new spatial and temporal closures in the northern and central Adriatic Sea have

been carried out employing a simple modeling tool [30]. However, a *quantitative analysis* of spatial management options is quite complicated to perform. This is mainly due to the fact that information on the spatial dynamics of fleets and stocks is often unavailable and effective spatial models are difficult to construct [14]. In response to this need, in this work we present the main ideas and machineries that will enable DISPAS to model and simulate a bigger portion of a sea. The main motivation of doing this is to develop a spatial simulator enabling marine biologists to experiment with their hypotheses and data on the spatial distribution of the common sole stock in the northern Adriatic Sea. Our solution is mainly guided by the paradigm of Complex Automata [11–13] that permits the specification of multi-scale simulations in a flexible and general way. In particular, we define a macro model of simulation at the sea scale that is essentially a Cellular Automaton [3, 32], with specific features, in which each cell represents an hexagonal area of the sea of approximatively five square nautical miles. The evolution of the individual soles in each area is simulated through a “micro” model that corresponds, ideally, to the current DISPAS implementation. Migration vectors in every possible direction are applied at each time step, which is kept as one month, in order to accomplish the movement of individuals from an area to neighbor areas. To obtain a more efficient multi-scale simulation, in terms of time and space, a strategy for uncoupling of the ideal schema suggested by the Complex Automata paradigm is proposed. This involves a preliminary set of simulations, performed with the currently available version of DISPAS, in order to obtain a “decoupling operator”. This operator is used to perform the macro simulation as a standalone process.

The paper is organized as follows. Section 2 introduces some biological and ecological information about the target species (common sole), while Sect. 3 recalls the main features of the current version of DISPAS. In Sect. 4, the paradigm of Complex Automata is introduced to be then adapted, in Sect. 5, to our needs and to the context of our case study. Finally, Sect. 6 concludes.

## 2 Biological and Ecological Background

The common sole belongs to a family of Soleidae and is a demersal fish. Among other areas, e.g. in the North Sea, it lives in the whole Mediterranean Sea. However, due to particular environmental conditions, the main concentration of soles are in the seabeds of the northern and central part of the Adriatic Sea (FAO GFCM Geographical Sub-Area 17).

Over time, a rising fishing effort has been applied to the sole fish stock; this situation, together with a weak management of the fishery policies, has led to an overfishing situation [29]. An example of the fishery policies that have been applied by the Italian government is the closure of the trawl fishery along the Italian shore (3 nautical miles from the coast) [1]. Another example of fishery management policy is the fishing ban in the summer period (June, July and August), or the legal minimum landing size for sole in the Mediterranean (20 cm; EC reg. n. 1967/2006). Notwithstanding these policies, the fish stock of

the common sole in the Adriatic Sea is still overfished and its sustainability is considered at risk [29].

It is well known that the spatial distribution of individuals in a species are in general not random, but depends on biological and environmental factors, e.g. availability of food, climate, temperature and so on. In [9] the data of the SoleMon project were reported. Data in the period 2005–2011 were used to study the distribution patterns of the demersal fish species that inhabit the Adriatic Sea. The results of this work were the determination of the spatial distribution of the common sole in the Adriatic Sea, differentiated by age classes.

In [30], a spatial management of fishing effort patterns was presented, precisely for *rapido trawling* techniques, which is the most important activity targeting the common sole in GSA 17. Two spatial fishing scenarios were proposed: ban the rapido trawling (i) within 6 and (ii) within 9 nautical miles of the Italian coast, from October to December. The aim was to study the impact of this fishing technique on the stock, especially on the sole juveniles, and also the collateral impact on the environment, e.g. habitat degradation by the seabed trawling.

Data from SoleMon (period 2006–2011) and data from Vessel Monitor System (VMS) [26–28], which are about the fishery activity of 100 rapido trawl vessels in the northern and central part of the Adriatic Sea, were used to estimate the spatial pattern of the fleet. It was shown that the bigger fishery effort is applied on the juveniles of the sole (classes from 0 to 2). A significant contribution of the work was the idea of a management policy driven by a spatio-temporal restriction on the fishery zones, especially where the juvenile age classes are concentrated. The works presented above are the main biological references on which we base on, in this paper, for introducing the multi-scale model for DISPAS.

### 3 DISPAS at Work

In this section we briefly summarize the main features of the current version of DISPAS (Demersal fish Stock Probabilistic Agent-based Simulator), underlying some results already obtained [2, 23]. For more details we mainly refer to [22].

DISPAS was developed since the beginning with the aim of studying and supporting fish stock sustainability. The common sole stock of the northern Adriatic Sea was selected as target case study, given the importance of the stock from an ecological point of view and the availability of data (see Sects. 1 and 2). Agent-based modeling [8, 15] was selected as the main paradigm of design, given the vision of introducing in the marine ecology sector a tool using a different approach from the classical ODE- or PDE-based modeling techniques. For modeling the behavior of a single agent, which should emulate an individual fish (a sole), we defined a class of automata called EPDTA (Extended Probabilistic Discrete Timed Automata) [2]. Applying this automaton-based model we can formally specify the behavior of an individual fish, depending on time. We represent the interaction with other species and with the marine environment as probabilities of natural mortality. The fishing effort is also expressed as a probabilities of being fished. All these probabilities depend on time and on the age of the fish.

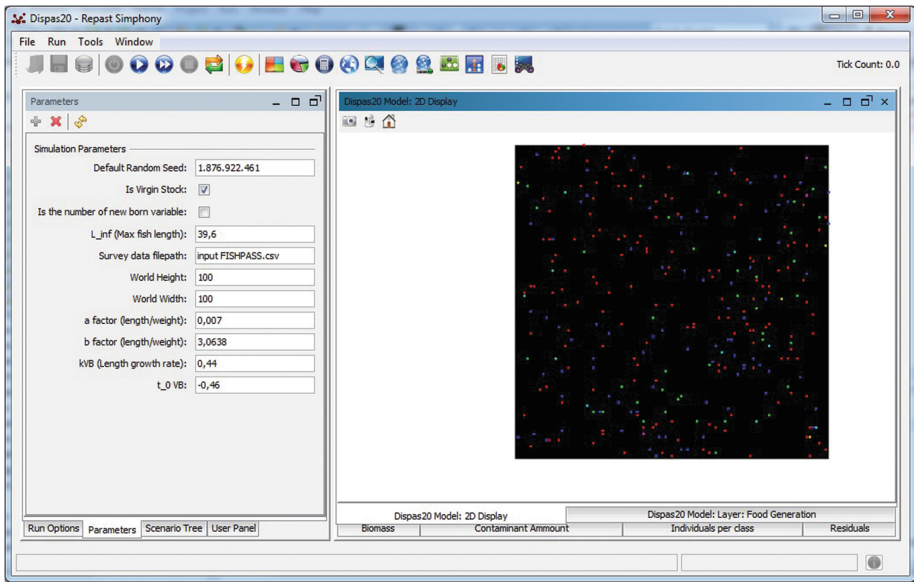


Fig. 1. DISPAS screen shoot.

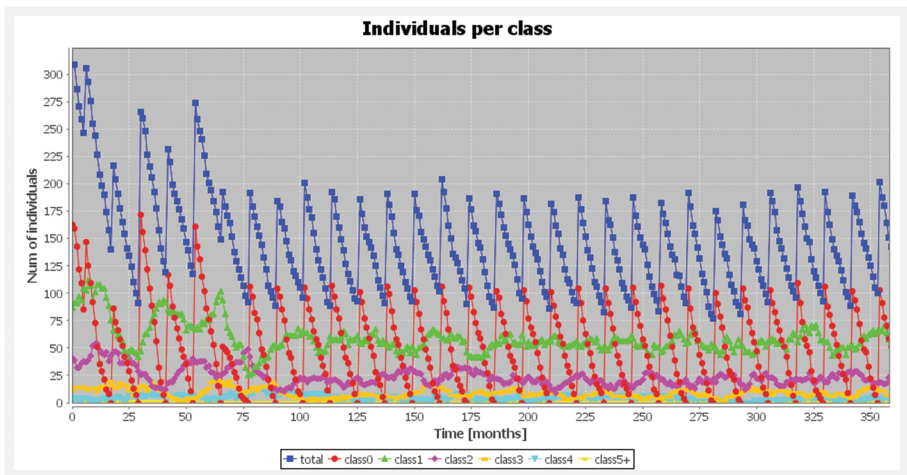


Fig. 2. Number of Individuals chart, divided by age classes, derived from a DISPAS execution.

The simulator has been developed, following the agent-based methodology, on the Repast Symphony suite [19]. DISPAS (see Fig. 1 for a screen shot) is currently able to manage a virtual space of a square kilometer of sea where the

sole agents live<sup>1</sup>. The discrete time step of the simulation is equal to one month. Each sole agent has its own attributes, among which an important one is the length. Assuming a constant growth rate for the period of the simulations, this attribute determines to which *age class* the specimens belongs. It is noteworthy that differences in body size within the same age class and functional groups may also occur and could reflect changes in climatic conditions (e.g., global warming and its impacts on phytoplankton [24]) or human pressure (e.g., overfishing; [20]). Natural and fishing mortality probabilities change on the base of time and of the sole age class. The longevity of common sole in the Adriatic Sea has been estimated as 8–10 years [9]. Due to the exploitation pressure, the ages from 5 to 8/10 are not well represented both in the commercial catches and in the survey. For these reasons, a plus group 5+ has been used, an approach that has also been used in [30].

The von Bertalanffy growth equation [31] is employed to estimate the sole length from its age. This is the most widely used growth equation in fisheries studies. Its growth rate parameter,  $K$ , can be considered as an abstraction, among others, of the interactions of each individual agent with the environment. For instance, a food abundance can be connected to a larger growth rate. In the current version of DISPAS the parameter  $K$  is constant, but in the following versions it will become dependent on time, on space and on environmental conditions, e.g. temperature.

Data coming from the SoleMon Project [9] are used to estimate other parameters, e.g. the ones relating the weight of a sole from its length. Moreover, they are used as abundance index in analytical models (XSA, SCAA, and so on) to estimate fishing mortality in the years 2005–2011.

The user of the simulator can easily create different simulation scenarios or tune the parameters of a simulation in order to first reproduce observed results, as a validation, and, then, to make predictions varying environmental conditions and/or fishing effort. The simulation outcomes are the predicted quantities of agents in a month divided by age classes. They are saved for off-line data analysis and also displayed in charts, with different views on the state of each agent, during the execution of the simulation. As an example, Fig. 2 shows the number of individuals divided per age class in the simulated square kilometer, obtained in one simulation.

The natural mortality probabilities and the fishing probabilities can be specified in an external text file. It is possible to specify a different value for each month along the whole simulation time. It is also possible to instruct DISPAS to create a random value (in a given range) of newborn individuals, which are introduced along the months of the year in which the species is observed to offspring. As an alternative, the simulator can take the information about newborns from an external file. In this case the values are estimated by the user analyzing available data. Finally, a list of other parameters can be set on the GUI of the simulator.

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<sup>1</sup> The latest version of the simulator can be downloaded from <http://giano.cs.unicam.it>.

In [22, 23] DISPAS was validated using two different methodologies. The first one was entirely based on SoleMon data. The simulator was instructed to perform 50 different runs and the outputted data about abundance and biomass for each age class were processed offline to determine mean and variance. The resulting curves were compared with real observed data at survey moments, i.e. November of each year from 2005 to 2011. The approximation of real data by the simulated ones was fairly accurate, apart from an overestimation of the stock made by DISPAS in years 2008 and 2009. For a detailed discussion we refer to [22]. The second validation methodology was based on SURBA (SURvey-Based Assessments) [18], a well-established software tool in the context of stock assessment. In particular, SURBA was fed with the simulation outputs of DISPAS and the results were compared with the ones obtained feeding SURBA with the SoleMon data. Also in this case the approximation was fairly good with an overestimation in years 2008 and 2009. The discrepancies are currently under study for further tuning the model by introducing more environmental information (we refer to [22] and to future works for a complete discussion).

## 4 Cellular and Complex Automata

Different approaches have been introduced in the literature for scaling from a micro-scale simulation to a macro-scale one. Some references can be found in [21], in particular for what concerns agent-based models. In this paper we mainly refer to the strategy suggested by Complex Automata.

Complex Automata (CxA) [11–13] are a computational model in which it is natural to define multi-scale simulations at different time and space scales. CxA are based on Cellular Automata (CA) [3], a well known discrete model that has been applied in several fields: physic, chemistry, theoretical biology, complexity theory and so on [32]. A CA can be informally thought as a *two-dimensional* grid of cells containing variables, which represent the *state* of each cell. The values of such variables change over time in discrete steps using a set of rules that depends on the current state of each cell and on those of its neighbor cells, which can be identified using different topological patterns. For instance, in a two-dimensional grid, a typical neighbor topology is defined as the eight surrounding cells of each cell. In the following we introduce a definition of CAs that is useful for our objectives. We refer to [3] and to the references therein for a full introduction to cellular automata.

**Definition 1.** *A Cellular Automaton  $A$  is a tuple*

$$\langle D(\Delta x, \Delta t, L, T), \mathbb{F}, \Phi, f_{init}, u, O \rangle$$

where:

- $D$  is the domain, made of spatial cells of size  $\Delta x$  and spanning a region of size  $L$ ;



- $\Delta t$  is the time step and  $T$  is the (approximatively) maximal time reached through the evolution of  $A$ ; i.e.  $T/\Delta t$  is the maximal number of iteration steps of execution;
- $\mathbb{F}$  denotes the set of possible states; typically an array of states of dimension  $L/\Delta x$ , one position of the array representing one cell;
- $f_{init} \in \mathbb{F}$  is the initial state;
- $\Phi$  is the update rule according to which every state evolves along time steps;
- $u$  is a function that puts  $A$  in communication with external data, i.e. its environment; it is called at each iteration on the domain  $D$ ;
- $O$ , the observable, is a function that specifies a quantity, calculated from the current state, that is given as an output.

According to the discussion in [4], the update rule  $\Phi$  is constrained to be in the form of  $\Phi = P \circ C \circ B$ . This is different from the classical way of describing the updating of a CA at each step and is mainly inspired from Lattice Boltzmann models. As a general description, the *Boundary condition*  $B$  is needed for the updating of the cells on the border of the domain  $D$ , using some strategy, e.g., in a closed world, the cells on one border are connected to the cells of another border. *Collision*  $C$  acts locally on every cell changing the state, according to information gathered in the neighbor cells. *Propagation*  $P$  propagates the information calculated during the collision to the neighbor cells. We refer to [4] for a more detailed description. The behavior of a CA  $A$  can be described by a generic *main loop* structure, shown in Algorithm 1. Note that *EC*, meaning *Equilibrium Condition*, is a generic predicate on the state indicating that the CA has reached an intended configuration and can stop.

```

// Initialization of domain, state and time
D = Dinit; f = finit; t = 0;
while not EC do
    t = t + Δt; // time step advances
    D = u(D); // domain communicates with external environment
    // updating: composition of Boundary, Collision and Propagation:
    f = B(f); f = C(f); f = P(f);
    Oi(f); // outputs the intermediate state observable
end
Of(f); // outputs the final state observable

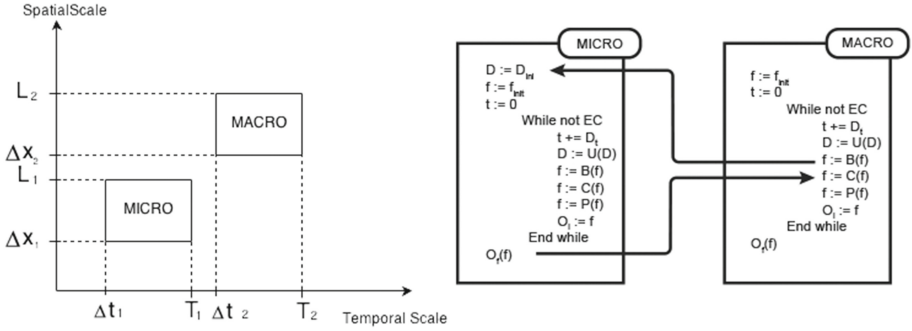
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**Algorithm 1:** Main loop of a Cellular Automaton.

The key observation that leads to the definition of CxAs is that it is always possible to connect any two CAs by a flow of data between a pair of the operations of the main loop using well-defined *coupling templates*. Such templates only depend on the spatio-temporal “positions” of the connected CAs in a *Scale Separation Map* (SSM) [13]. An SSM is a two-dimensional map in which temporal and spatial scales can be represented. Consider the SSM shown in the left part of Fig. 3. On the horizontal axis two temporal scales are represented



by the pairs  $(\Delta t_1, T_1)$  and  $(\Delta t_2, T_2)$ , corresponding to two CAs,  $A_1$  and  $A_2$ . On the vertical axis, two spatial scales are represented by  $(\Delta x_1, L_1)$  and  $(\Delta x_2, L_2)$ . The corresponding regions on the plane are separated. In this case, CAs  $A_1$  and  $A_2$  can be coupled with the so-called “micro-macro” coupling template, that is to say,  $A_1$  operates on a micro spatial-temporal scale, while  $A_2$  operates on a macro spatial-temporal scale. Their executions are coupled connecting the two main loops as shown in the right part of Fig. 3.



**Fig. 3.** A Scale Separation Map (left) showing that the two CAs can be coupled by a micro-macro Coupling Template (right) [12].

**Definition 2.** A Complex Automaton  $\mathcal{S}$  is a graph  $(V, E)$ , where  $V$  is the vertex set and  $E$  is the edge set, such that:

- $V = \{A_k \mid A_k \text{ is a CA}\},$
- $E = \{E_{h,k} \mid E_{h,k} \text{ is a coupling template between } A_h \text{ and } A_k\}.$

Informally, the execution of the particular micro-macro coupling template works in the following way. The macro CA,  $A_2$ , starts its execution normally. At each iteration, during the execution of the updating function  $\Phi_2$ , precisely before the collision step,  $A_2$  calculates for each of its  $L_2/\Delta x_2$  cells the initial conditions for starting the execution of the corresponding micro CAs of type  $A_1$ . Such data are calculated only from the state of the  $A_2$  cells. Each micro CA of type  $A_1$  is executed in parallel with  $A_2$ , but it immediately stops due to a blocking receive at the first instruction. This corresponds to the upper arrow of the right part of Fig. 3, which represents the flow of data among the CAs. In these flows the receive is always blocking and the send is always non-blocking. After receiving the initial conditions from  $A_2$ , each CA of type  $A_1$  enters its main loop and continues the evolution until the equilibrium condition (at most after time  $T_1$ ) is reached. After that, it sends the results of its whole evolution back to  $A_2$  (lower arrow in Fig. 3). In the meantime,  $A_2$  was suspended after its collision phase due to the blocking receive. Upon receiving the data from all the micro CAs and adapting the state of each cell accordingly, it restarts performing its current propagation phase. Then, the cycle is restarted.

Note that the whole evolution of all micro cells is performed at every cycle until the end of the macro execution. Thus, the execution time of the described coupling template can be estimated as proportional to the total number of micro steps required for reaching the end of the whole evolution ( $N_{ex}$ ):

$$N_{ex} \sim \left( \frac{T_1}{\Delta t_1} \left( \frac{L_2}{\Delta x_2} \right) \right) \frac{T_2}{\Delta t_2}$$

This means that the execution of a micro-macro multi-scale simulation can require a very high computational cost, in terms of time, but also of space.

## 5 Multi-scale DISPAS

In this section we put the basis for the multi-scale version of DISPAS. We mainly get inspiration from the CxA paradigm presented in Sect. 4. However, the multi-scale DISPAS cannot be directly an instance of a CxA model. The first fundamental observation is that the running model of the current DISPAS, which is the natural candidate for the “micro” part of the multi-scale simulation, is a Multi-Agent System (MAS), not a CA. Nevertheless, the Repast Symphony suite, on which DISPAS is developed, gives the possibility of defining a CA in a very simple way. Indeed, the sole agents in DISPAS can be easily placed in a grid of cells, but, as summarized in Sect. 3, their behavior is based on a timed and probabilistic automaton-based model and the fundamental interaction of the agents is with the environment. All in all, the current DISPAS version could be certainly rephrased as a CA, instead of a MAS, but this appears to be an effort with a low pay off and also does not naturally fit the behavioral assumptions that we made on the fish individuals.

As far as the macro part of the simulation - the one at the sea level - is concerned, instead, the paradigm of CA fits particularly well. Indeed, it is possible to divide the area of interest, northern Adriatic Sea, into adjacent cells, each of which contains a certain number of individual per age class. Such individuals evolve using a properly parametrized version of the current DISPAS model and, as a further action, at each step they exchange individuals with neighbor cells using space-dependent migration vectors (see Sect. 5.2 below).

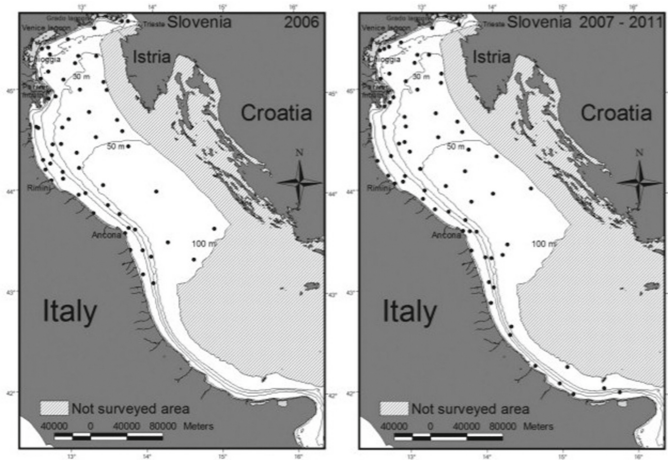
Before proceeding with the specification of the multi-scale schema, it is important to analyze which kind of data are available in the considered scenario, in order to have design directions towards an effective model that can also be validated.

### 5.1 Available SoleMon Data

The SoleMon project [9] has been surveying, from November 2005 each year in November, sixty seven stations placed in different parts of the Adriatic Sea (see Fig. 4). In each station, fishing samples are performed with the typical catch techniques used for the common sole. The caught soles are then analyzed for determining the total length (which in turn determines the age class), the individual

weight, the sex, the maturity stage and several other biological and toxicological indicators.

The important data that are needed in our project are the number of individuals, for each age class (from 0 to 5+), estimated to live in each area. Since some areas of the sea can not be surveyed, in these cases the number of individuals are estimated by interpolation techniques, in particular the Kriging method [16,17] will be used.

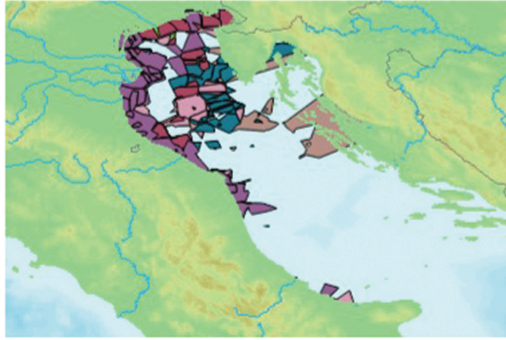


**Fig. 4.** SoleMon project stations (dots) and not surveyed areas [30].

SoleMon data have also been integrated within a Geographic Information System (GIS). As a result, several shapefiles [6] have been created, each of which maps on the sea the number of individuals (using appropriate ranges), for each age class (see Fig. 5). The spatial distribution of individuals for each age class is studied in [30]. This distribution can be considered an emergent behavior, at the sea level, of the behavior of the common sole in the northern Adriatic Sea, depending also on environmental, geographical, climatical factors as well as on the fishing patterns that are applied at each geographical area. This kind of aggregated data are what we intend to reproduce, as a validation, with the multi-scale version of DISPAS that we are proposing.

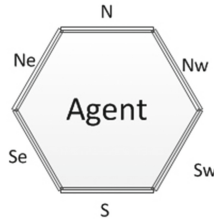
## 5.2 Macro CA Specification

Let us now specify the CA  $A_s$  representing the macro model, at the sea level, of the multi-scale DISPAS. Concerning the spatial scale, we consider as  $\Delta x_s$  an hexagonal cell whose area is approximatively 5 square nautical miles (see Fig. 6), that is we take hexagons with side equal to 1.38726 nautical miles. This dimension has been chosen on the basis of the haul length of *rapido trawlers*,



**Fig. 5.** Adriatic Sea with areas showing the distribution of the common sole age classes.

the main fleet exploiting soles in the northern Adriatic Sea, in order to better standardize their fishing effort in terms of number of hauls and space exploited per day [30]. Moreover, the area is compatible with the average movement that a sole has been observed to perform in the chosen temporal time step  $\Delta t_s$ , which we take as one month (equal to the one-scale DISPAS time step). In this way, the neighbor topology for the Propagation phase can be limited to the surrounding cells of each cell. Finally, the hexagon shape is suitable for representing the migration among adjacent areas. For each cell there are six possible directions of migration (outgoing and ingoing): North, North-East, North-West, South-East, South-West and South.



**Fig. 6.** Cell representation, with migration directions.

We keep Repast Symphony as the implementation platform, the same on which the current version of DISPAS is implemented. Using the facilities of the platform, the macro CA is represented as a MAS in which each agent is a cell, positioned at certain coordinates, that does not move, and such that all the positioned cells do not overlap. They cover an area corresponding to the northern Adriatic Sea, which is the value of the spatial scale parameter  $L_s$  in squared nautical miles. The time scale value of parameter  $T_s$  depends on the particular simulation that is performed; typically a number of years between 5 and 10. The state of each macro agent/cell contains the number of sole individuals in each

age class currently present in the hexagon area. Notice that, at the sea scale, we loose the resolution of individual fish, keeping only the number of individual per class. These are also the observables  $O_s$  output by the CA. The function  $u_s$  is the identity function.

Regarding the update function  $\Phi_s$ , let us analyze the three phases one by one. For the Boundary phase, the cells at the borders, i.e. those in contact with the coast, do not require any particular management. Simply the migration vectors are null towards the land. The Collision phase must consist in a growth, during a month, of the individuals of each age class, which possibly can change class if their new length, through the von Bertalanffy function, make them to get over the threshold of their current class. Furthermore, each individual should be subject to the natural mortality and fish mortality probabilities, correctly parameterized for the considered geographical area. Indeed, there are areas in which the fishing effort is greater than the average and others (called sole sanctuaries in [30]), in which the fishing effort is null.

The Propagation phase acts on the six surrounding cells of each cell. For each cell  $h_i$ , it is defined a *migration vector*  $M_i$  representing the outgoing probabilistic migration rates, i.e. the probability that a given number of individuals migrates in a certain direction in a considered month. The possible directions are six:

$$M_i(t, ac) = [N, Nw, Sw, S, Se, Ne]$$

The migration vector depends, in general, on the time  $t$  (a month along the simulation), and on the age class  $ac$ . In this way, several scenarios can be represented. The estimation of the values of the migration vectors will be crucial for the reproduction of the distribution of the various age classes observed in [30]. This task will be based on the available data and performed in strict collaboration with marine biologists, to exploit biological and environmental information.

At each step, for cell  $M_i$ , the number of individuals that are going to migrate, for each age class, in any direction, is probabilistically calculated. Then, one by one the values are propagated to the neighbor cells.

### 5.3 “Uncoupled” Coupling Template

Ideally, every cell  $h_i$  of  $A_s$  must be associated with a current DISPAS model, say  $A_d$ , adapted to represent five square nautical miles instead of a square kilometer. This would imply only the changing of the initial number of the individuals for each class, then the evolution would follow accordingly. Since the temporal scale of the macro CA  $A_s$  and the MAS  $A_d$  is the same ( $\Delta t =$  one month,  $T = N$  years), technically the coupling template is not a micro-macro one. However, it is very similar, the only difference being the fact that the “micro” execution, for each macro cell, consists of only one “micro” step. This mitigates the high computational cost that would be needed to perform the multi-scale simulation. Nevertheless, the computational cost of representing  $L_s/\Delta x_s$  MASs of type  $A_d$  and let all of them to advance of one month would be still very high in our target scenario.

To further simplify, we perform an abstraction by introducing an operator  $\mathcal{C}(t, h, ac)$  that should tell, with an appropriate degree of randomness, for each particular area  $h$ , for each month  $t$ , how many individuals of age class  $ac$  will be present at time  $t + 1$  in the same class. The operator should take into account the  $K$  growth rate, the natural mortality probability and the fishing probability typical in the particular area  $h$ . In this way, the Collision phase of the macro CA  $A_s$  corresponds to call, at time step  $t$ , the operator  $\mathcal{C}(t, h_i, ac)$  for each cell  $h_i$  and for each age class  $ac$  and to update accordingly the number of individuals for each age class in the cell.

The operator  $\mathcal{C}$  can be obtained by using the current version of DISPAS to perform a *preliminary* set of “micro” simulations on each specific 5 square nautical miles area, with specific values for  $K$ , for the natural mortality and for the fishing mortality probabilities, as well as for other parameters. The means and variances calculated with these simulations can then be used to define the operator  $\mathcal{C}$  in order to perform the macro simulation of  $A_s$ . This configures a sort of “*uncoupled semi-micro-macro*” multi-scale simulation, which appears to be suitable for reaching our objective of reproducing the spatial distribution of the common sole age classes in the northern Adriatic Sea area.

#### 5.4 Plausible Scenarios of Simulation

We plan to implement the macro CA simulation on the Repast Symphony suite, developing a new version of DISPAS that retains the current features and adds the possibility to perform the uncoupled multi-scale simulation suggested above. Besides the reproduction of the spatial distribution of the soles, this would also enable the users to set different scenarios of simulation in order to validate the model and/or to perform predictions varying the settable parameters. A non-exhaustive list of such possible scenarios follows.

- An interesting scenario would be, as shown in [30], the reproduction of one or more particular “sanctuary” areas in the Adriatic Sea, i.e. areas in which the fishing effort is null due to technical difficulties of the rapido trawl on irregular sea bottom. In this way the impact of this and other possible sanctuary areas could be evaluated on the stock evolution and on the age class distribution.
- Another possible scenario would be the simulation of fishing bans on particular areas, e.g. those in which a high number of juveniles has been observed, in particular periods of the year. This should have an impact on the abundance of the lower age classes and maybe on the spatial distribution of the higher age classes.
- Finally, it would be interesting to simulate a permanent or periodical fishing ban close to the coast line. This is due to the hypothesis that juveniles mainly stay in this area, at least on the Italian shore below the Po river mouth.

## 6 Conclusions

We have introduced the basic model for building a new multi-scale version of the DISPAS simulator. The main motivation for the new features comes from

the need of studying the spatial distribution of the common sole species in the northern Adriatic Sea. In particular, the new simulator would allow marine biologists to test hypotheses on the movements of the individual fish and would enable the simulation of new sea-scale scenarios to predict the spatial impact of fishing efforts and/or particular temporal measures (e.g. summer fishing bans) on the considered fish stock.

As future work, we plan to implement the defined model on the Repast Symphony agent-based programming suite, retaining the features of DISPAS already implemented. In particular, the current MAS simulation capabilities will be used for the execution of a preliminary phase of the defined multi-scale “uncoupled” coupling template.

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