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Marine Fishery Management Agent-Based Modeling

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Abstract

Fisheries in the United States not only provide seafood for us to enjoy and contribute significantly to the American economy, they also help us to sustain ecological balance and protect our ocean resources. Fishery management agencies in the United States conduct stock assessments to discover the changes in the abundance of fishery stocks in response to changes in the environment and effects of commercial and recreational fishing. Efficient stock assessment enables maintenance of healthy fisheries without permanently damaging the marine ecosystem. In order to forecast the future trend of fisheries, predicting fish migration patterns in response to the environmental factors is important. We present an agent-based model which through emergence, predicts migration patterns of Mackerel by exploiting their biological characteristics. We generalized the agent-based model proposed by SEASIM [4] by employing an optimal temperature of Mackerel for fish movement in response to environmental data. The experimental results suggested that integration of bio-energetics and an energy budget for each agent was necessary for improving the accuracy of the Mackerel spatial dynamics in the simulation.

Contents

1   Introduction

Fisheries in the United States contribute significantly not only to the American economy and generate over 1.5 million jobs, but they also help manage ecological balance and protection of ecosystems. Fishery stock assessment is used in order to provide an environmentally safe way to offer recreational and professional fishing. Stock assessment is a process of collecting, analyzing and reporting demographic information to discover the changes in the abundance of fishery stocks in response to fishing and possibly to predict the future trend of the fishery. Stock assessment contributes to maintaining the good health of fisheries for current and future use while maximizing the yield without doing permanent damage to the environment. Stock assessments enable sound fishery management which includes regulations such as establishing a benchmark for fishery annual harvesting levels to prevent over-harvest of resources.

Boyd et al.[3] highlight that stock assessment traditionally involves fitting the mathematical model to the available data to estimate biological reference points Biological reference points are benchmarks that are used to evaluate the current stock status. However, after the realizing dependence of those biological reference points depends on components of the ecosystem such as food-web interactions and environmental factors, many regulatory bodies are embracing ecosystem-based approaches to implement modeling tools for stock assessment. For example, SEAPODYM [7], and NEMURO [6] are numerical models which embrace environmental variability in different positions within the food chain hierarchy.

Focus on individual level interactions and inclusion of adaptive traits of the individual is necessary in order to observe the ecosystem-wide effects by the environmental drivers. Since representation of individual interactions and variation is difficult for traditional models, agent-based modeling approaches have been researched and explored. OSMOSE [11] and SEASIM[4] are instances of agent-based models for fishery management.

An agent-based model represents living organisms as autonomous and independent entities [10]. Agents, characterized by state variables such as size, age, or geographic location, are capable of locally interacting with each other and with the surrounding environment which enables them to simulate the local interaction of fish with the environmental drivers. Moreover, those agents are capable of adapting their behaviors to the changes in the surrounding environment. Because of this adaptive behavior of the agents, ABMs depict, through emergence how individuals in a system are influenced by the surrounding environmental driver and how the system is

influenced by the behavior of individuals. This exclusive focus on the relationship between system and individual, and the properties that emerge from it, differentiates agent-based models from traditional models. Because of the focus on the individuals in the system and the adaptive characteristic of agents, ABMs have also been drawing attention from ecologists for their application in ecological modeling.

We present a marine fishery ABM which is based on the basic behavioral characteristics and physiology of the species in question, Atlantic mackerel. Our model is spatially-explicit and implemented with a user-friendly interface. Users can select the starting and ending dates of the simulation. The simulation environment contains four variables to describe the landscape: bathymetry, sea surface temperature (SST), sea surface velocity (SSV) and chlorophyll concentration which serves as a proxy for representation of food availability. Agents interact with their local food availability, SST, and SSV and migrate according to the local data. We chose mackerel as the species to be experimented with because data such as stock biomass are available and also there has been research on ABMs with mackerel which we were able to reference as a proof of concept.

2   Literature Review

2.1   Scientific Modeling

Steven Railsback and Volker Grimm specified that a scientific model is a meaningful representation of a system or class of systems used to understand how a system works and to explain patterns we have observed [10]. As scientists, we are often interested in explaining changes, patterns and phenomena that we observe and are interested in being able to predict the future behaviors of in response to some changes. However, real systems are often too complex or their development is too slow to be observed and analyzed. Therefore we attempt to formulate a simplified representation of a system using equations or a computer program that we can easily manipulate and with which we can experiment [10]. When constructing a scientific model, we want to think of it as a system of filters that include what is most relevant to the objectives of our model.

2.2   Agent Based Modeling

An agent-based model (ABM) simulates a system which encapsulates unique, independent and autonomous entities, and their interactions with each other and with their surrounding environment locally. The model represents the system, individuals and their behaviors. The essential component of the agent-based model,

an agent, is a unique, independent, and autonomous entity which influences and is influenced by the system. Railsback and Grimm list the important aspects of properties of agents: local interaction, being autonomous, and adaptive behaviors [10].

- **Local interaction**: Agents do not interact with all other agents only with neighbors that are geographically close.
- **Being Autonomous**: Agents act independently of each other to pursue their objectives
- **Adaptive Behavior**: Agents are capable of adjusting their behavior to the current states of themselves, of other agents, and of their environment.

ABMs are different from traditional scientific models because they are concerned with two levels of abstraction and their interaction: ABMs depict what happens to the system because of what their individuals do and what happens to the individuals because of what the system does, while traditional models focus more on population level variables that describe the entire system. In addition to that, Railsback and Grimm mentioned that traditional mathematical models are limited by their tractability and their complexity, which tells us that the model must be simple enough that we can actually solve it [10].

2.3 Agent-Based Modeling and Ecology

Individual-Based Modeling and Ecology by Steven F. Railsback and Volker Grimm [9] begins by explaining why agent-based modeling is used in ecological modeling. They explain that the systems we deal with in the field of ecology are population, communities and ecosystem. The individuals are the building blocks of the system in ecology. More specifically, these individuals which would be represented in the model are living organisms that are adaptive; they can grow and change in many ways over a life cycle [9]. Contrary to atoms, living organisms are adaptive because they have an objective to seek fitness and this adaptation transpires at the lower, individual level in the system. This differentiates ecology from other fields such as physics in which individuals are not adaptive; things will be much simpler but the simulation will not persist for long [9]. Ecologists are interested in population-level properties that are persistent, resilient, and spatially, and temporally distributed. These are not individual level properties. However, we let the population level properties emerge from the local interaction of adaptive individuals with each other, and with the environment. We are concerned with creating a general method of formulating hypotheses about the adaptive behavior of individuals and testing them. Therefore,

Railsback and Grimm came up with the term individual-based ecology [9]. In individual-based ecology, systems are understood as collections of unique, adaptive individuals. System properties and dynamics emerge from the interactions of individuals with their environment and with each other while classical theoretical ecology is concerned with system properties and disregarding individuals and the effect of their adaptive behavior. The examples of individual based ecological modeling that are relevant to our research are the Stream Trout Model [9], and "SEASIM-NEAM: A Spatially-Explicit Agent-based SIMulator of North East Atlantic Mackerel population dynamics" [4]. We especially focused on examining the latter example to understand the approach to solve our problem for this research.

2.4   NetLogo

We developed our individual-based model using a programming language called NetLogo [14]. NetLogo is a programmable modeling environment for simulating natural and social phenomena which was developed by Uri Wilensky. Wilensky and Strout provide documentation which describes important features and components to help understanding how to code in NetLogo [15].

Railsback and Grimm [10] sufficiently describe what an agent is. Wilensky [15] explain that there are four types of agents in NetLogo: turtles, patches, links and observers. Turtles are agents that move around the world. The world is two-dimensional and is divided up into a grid of patches. A patch is a square that turtles can move around on. Links are the agents that connect two turtles. An observer is not physically involved and exists in the world. It is an agent that gives instructions to other agents, so it is supervising turtles, patches and links.

2.5   Mackerel and ABM for fishery management.

The objective of stock assessment is to enable management to maximise the long-term yield from a fishery without causing irreversible damage to the stock or wider environment [4]. Boyd et al. explain that regulatory organizations began to adopt ecosystem-based approaches to fisheries management because of the realization that a stocks' biological reference points depend on other physical environmental drivers such as food-web interaction [3]. They further explain that properties of agent based models are suited to capture the influence of ecosystem drivers at the population level. They emphasized that their model is spatially explicit, includes a realistic energy budget for agents and represents the full fish life cycle. This document provided us with a

realistic explanation of why we would like to use agent-based modeling in a marine ecological modeling context and served as an example for us as we started to develop our prototype.

After the previously mentioned research, [4] describe their methodology of developing an agent-based model using NetLogo for North Atlantic Mackerel. For agent based modeling, we employ a specific documentation called Overview, Design concepts and Details document (ODD) to provide a complete and comprehensible description of a model. This documentation helped us to grasp the facts that are relevant to the model easier and faster thus allowing easy replication of the model [10]. [4] goes further by describing the model in an ODD manner. [4] mention the resolution and scale of their grid of patches. Sea surface temperature, Sea surface velocity plankton concentration, and photoperiod are the most essential variables which should be included in our model.

 Boyd et al. [4] predetermined the Mackerel's spawning, overwintering area and migration dates instead of having them emerge like other properties as well as the migration dates. In the adult foraging section,[4] provide detailed information on profitability cues which are essential indicators for us to identify the location which fish would most likely go to when they are foraging for food.

"Essential Fish Habitat Source Document: Atlantic Mackerel, 'Scomber scombrus', Life History and Habitat Characteristic" [12] is a complete documentation on Atlantic Mackerel. Created by "NOAA Fisheries", this document provides vital information on the characteristics of species that we are interested in studying. According to this document, the Atlantic Mackerel is intolerant of temperatures below about $5°C$-$6°C$, and above approximately $15°C$-$16°C$. They also report that their preferred water temperature range is between $7°C$ to $15.8°C$. This information is reflected into the searching algorithm which determines where Mackerel could go. The adult mackerel with a body size greater than 26 cm, tend to stay around the depth of 40 m to 80 m. They do not like shallow water when they are most likely to feed.

2.6   Databases

Our model depends on a variety of datasets such as bathymetry dataset, sea surface temperature (SST) dataset, sea surface velocity (SSV) dataset and chlorophyll-a dataset to accurately represent the geographical location for the simulation. We import datasets that are in .asc format since NetLogo has a GIS extension which allows users to import GIS raster dataset into the model. We extract the SST datasets and chlorophyll-a data in a form of .asc file from Multi-scale Ultra-high Resolution (MUR) SST Analysis fv04.1 [1], Chlorophyll-a, Aqua

MODIS, NPP, L3SMI, Global, 4km, Science Quality, 2003-present (Monthly Composite) [8], and OSCAR Sea Surface Velocity, 1/3°, L4, Global, 1992-present, 5 Day Composite [5] managed by NOAA. Both datasets are weekly composited as we intend to update physical environmental factors weekly in our model. We initialized web scraping to extract data from the web using Python and carried out some data preprocessing in order to properly format the data into a .asc file that the gis extension can accept. Bathymetry data were downloaded from the GEBCO Gridded Bathymetry website.

2.7 Energy Budgets

One of the most important components in the agent-based model done by Boyd et al. [4] is the inclusion of an energy budget which allows them to represent the entire life cycle of mackerel. As Railsback and Grimm [9] argue, including the full lifecycle of species is an essential component that differentiates ABM from classical modeling in ecology. A research paper, "An introduction to Dynamic Energy Budget (DEB) models with special emphasis on parameter estimation," by Jaap van der Meer presents a dynamic energy budget model which elucidates the rates at which the organism acquires and utilizes energy for maintenance, growth, and reproduction as a function of state of the organism and of its environment [13]. We focused on this theory because it implies that the variables that are available for us: temperature and food density in our model to use, can express the state of the organism which is an essential building block to develop our ABM. Meer [13] mentions the dynamic energy budget theory developed by Bas Kooijman and the k-rule DEB model. The DEB theory supposes that the various energetic processes, such as ingestion rate, or maintenance are dependent either on the body surface area or on the body volume. The k-rule argues that a fixed fraction k is allocated to maintenance and growth and the remaining fraction is allocated to reproduction. This article provides us the general and accessible introduction to the DEB model and also the practical aspect of the energy budget model and parameters as we attempt to integrate the energy budget as part of our research model.

3 Methodology

As mentioned in the introduction, efficient and sound stock assessments enable building a sustainable and healthy fishery practice without permanently damaging the ecosystem . In order to exploit the correlation between fish abundance, spawning biomass and environmental drivers, many researchers started to develop

models which allow for explicitly capturing the interaction between fish and the surrounding environment.

Our agent based model was developed for observations of movement, migration, feeding and spawning patterns of species through emergence, by way of many iterations of simulations. [3] wrote an application that was similar to what we envisioned to develop using NetLogo. NetLogo enables local interaction between different types of agents that respond to environmental drivers: sea surface temperature, chlorophyll-a concentration, and sea surface velocity. [3] features an explicit spatial representation of fish distribution which is produced by their unique implementation of movement of fish and integration bioenergetics. We reviewed their research to learn how they made the movement of fish possible while integrating the influence of environmental data such as SST, SSV, and food availability.

3.1 Entities, state variables and scales

Our agent based model consists of two different entities: a number of fish as agents and square patches of ocean. As mentioned in 2.4, a patch is a type of agent that fish agents can interact with. The patches make a square grid landscape of 200 * 200 patches. Selected simulation location is George's Bank which is known as fishing location out in the east of Massachusetts. The geographical coverage spans from 36.8176° to 44.8601° in latitude, and −73.75369° to −65.57986° in longitude. Each patch consists of bathymetric data, chlorophyll-a, desirability, horizontal current velocity, and SST as its state variables. Fish are characterized by their location and their abundance. Fish have a state variable: super individual abundance. All state variables involved in the simulation are shown in table 1.

3.2 Movement

After implementing how fish and environmental data may be represented as agents and capable of inter-acting with each other, we were interested in the dynamic distribution of fish. Thus, movement of fish in this simulation is the most important part of this application. Boyd et al. [3, 4] classified movement of fish into a few different types of movement: migration movement, local movement, feeding movement and random movement.

Table 1. List of state variables and description

List of state variable in simulation			
State variable	Turtles/Patches	Unit	Description
A-SI	Turtles	N/A	Abundance number of actual individual represented by an agent. Derived from
Arrhenius	Turtles	N/A	Arrhenius constant
Bathymetry	Patches	m	Depth of water in the ocean
Chlorophyll	Patches	mg/m^3	Chlorophyll-A biomass
SST	Patches	$°C$	Sea Surface Temperature
U and V	Patches	m/sec	Sea Surface Velocity. They represents horizontal and vertical sea surface velocity respectively.

Boyd et al. [3, 4] associated specific geographical areas with specific activities such as spawning, feeding, and nursing based on empirical data which had been collected. In addition to that, some local movements included northward movement. We focused on implementation and approach of Boyd et al.[4] to the feeding movement instead of migration movement for the following reasons:

(1) The migration movement and northward movement is specific to the species. We were aiming to develop a simulation that was generalizable.

(2) We were concerned that predefined migration areas may interfere and prevent generating a result through emergence. Moreover, we were interested in observing how fish may respond to environmental drivers and change.

(3) We needed an algorithm which can take the surface velocity effects on fish movement into account.

Thus we focused on gradient area search algorithm (GAS) [4], defined as an algorithm which determined its migration orientation by calculating an increase or decrease in a magnitude of a property such as SST or desirability. In the model, fish agents were capable of detecting desirability of its four neighboring patches: north,

Table 2. List of constant used in simulation and their description

List of constants used in simulation				
Constants	Symbol	Value	Unit	Description
Maximum ingestion/consumption rate	C_{max}	0.69	$g/g^{-1}day^{-1}$	Amount of food or nutrients that can be digested by the species [3]
Strength of the predator density dependence	c	N/A	9.71×10^{-11}	[4]
Activation Energy	E_a	0.5	eV	minimum energy required for physiological chemical reaction [4]
Boltzmann's Constant	Boltz	$8.617333262145 \times 10^{-5}$	$eV\ K^{-1}$	
half saturation constant	h	1.26	$g\ m^{-2}$	
Kelvin	Kelvin	273.15	Kelvin	Temperature constant, equations uses kelvin for their unit, not celsius
Shape Constant	r	3	N/A	The constant that is used to determine the shape for Equation 3
Total biomass	Tbiomass	43519	metric tons	
Biomass Conversion Factor	BMass-conv	1.00×10^3	$kg\ /\ metricton$	Conversion constant for metric tons to kilograms

south, east and west patches of the super-individual's current location.

Each patch is characterized by a desirability value which represents how desirable the patch is given the effect of phytoplankton as a proxy for food availability, competition between fishes, an effect of photoperiod which represents length of daylight at the simulation location, and an effect of SST as Kelvin with a following equation:

$$desirability = A(SST) \times P_{photo} \times \frac{X}{X + h + cD} \tag{1}$$

where X is phytoplankton density (g/m^2), h is a half saturation constant, P_{photo}. D is a local mackerel density or local super individual abundance at a patch, c is a constant that determines the strength of predator density dependence. To capture the effect of temperature in a biochemical reaction, Boyd et al. [4] provided an Arrhenius function.

$$A(SST) = e^{\frac{-Ea}{Boltz} \times ((\frac{1}{SST}) - (\frac{1}{T_{opt}}))} \tag{2}$$

where E_a is an activation energy, K is a Boltzmann constant and T_{opt} is optimal temperature for the species. Arrhenius function is a function which allows us to model the effect of temperature on chemical reaction. As we reviewed this equation, we discovered that Equation 2 is an increasing function without absolute maximum. This indicated that higher the temperature, more active the species of our interest would be. This contradicted the empirical fact provided by Studholme [12] that mackerel is not tolerable of water temperature above 16°C. In order for us accurately model the chemical reaction within Mackerel by using Equation 2, we need to create thresholds or introduce weights to see the desired result. Additional logic or introduction of weights was not suitable as we aimed this project to be generalizable and simple for future expansion, we explored other researches and other types of Arrhenius equations.

Up on further investigation, we found generalized Arrhenius function in research done by Alexandrov and Yamagata [2]. Alexandrov and Yamagata [2] denoted Equation 2 as a normalized Arrhenius function and presented a generalized Arrhenius function G_A which allows for a modeling of an enzyme reaction to a temperature with a peak at the optimal temperature.

$$G_A = \frac{r * f_A}{(r - 1) + f_A} \tag{3}$$

f_A is the normalized Arrhenius function 2 and r is a parameter that balances between the activation energy above and below the optimal temperature in (2). r determines the slope of the curve and degree of symmetry of the Equation 3.

The generalized Arrhenius function was not a part of [4]. We introduced the equation to avoid implementing hard-coded conditional statement and to resolve the contradiction that we have realized. Implementation of normalized Arrhenius function prevented having conditional statements that filtered out certain temperature values, hence making application more generalizeble.

4 Experimental Result

4.1 Test and Validation

In order to test if the movement algorithm was accurately responding to the environmental drivers, we tested our application with test files for SST, chlorophyll and SSV. As the values for X, and SST in Equation 1 and 2 are the driving factor of the movement algorithm, We utilized test files with value zero and with gradient values to isolate each environmental driver to test whether the effect was accurately taking place.

For example, *desirability* of zero, and zero *current* indicate that there is no food and no ocean *current*; therefore, fish is driven by the Equation 3. Figure 1 (a), Figure 2 (a), and Figure 3 are the image taken prior to the test run. We distributed the agent randomly in the NetLogo world. Figure 1 (b) shows that the fish moved only according to the SSV data because it was the only non-zero .asc file loaded for the test case. Moreover, Figure 2 (b) and Figure 3 (b) depicts that our algorithm drives agents as they try to converge to the patch with the optimal temperature or the highest concentration of food. This test case consisted of SSV and chlorophyll dataset with zeros and non-zero SST data.

As shown in Figure 1 (a) and 1 (b) test demonstrated that the algorithm is in fact responding to the environmental drivers as we expected.

4.2 Experimental Result

We began from studying the biological characteristics of species and abstracting necessary information from previous empirical studies, and applied that information to an agent based modeling. We confirmed that the algorithm correctly responded to environmental driver data through testing by isolating each environmental driver. Finally we learned that the agents were responding to the real environmental data in accordance with the movement algorithm and that it is possible to simplify the movement algorithm; however, we were unable to find a consistent and apparent pattern in the fish movement through simulation. We expected to see more agents
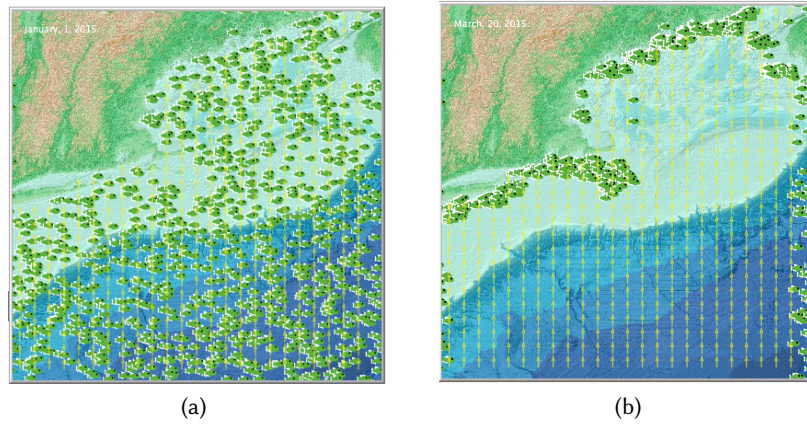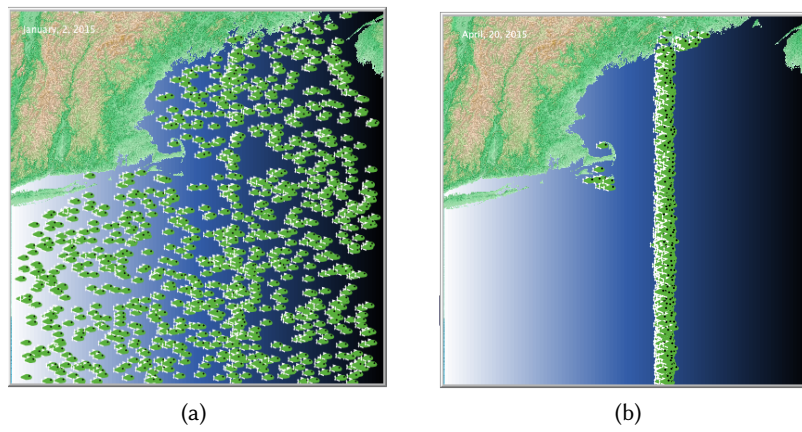
Fig. 1. Sea surface velocity testing
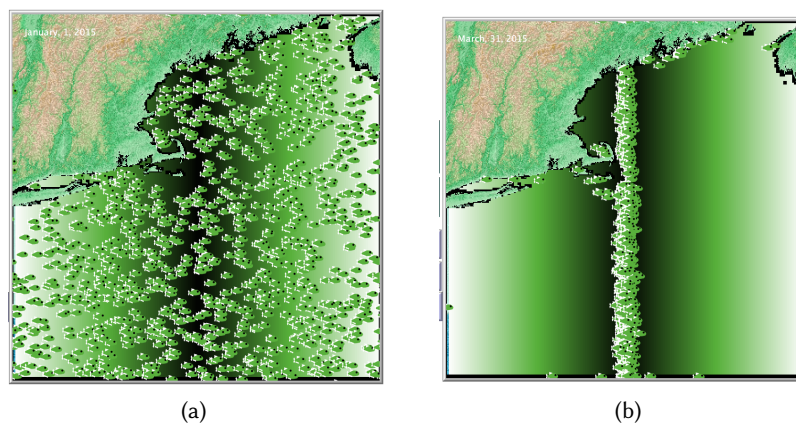

Fig. 2. Sea surface temperature testing

Fig. 3. Chlorophyll testing

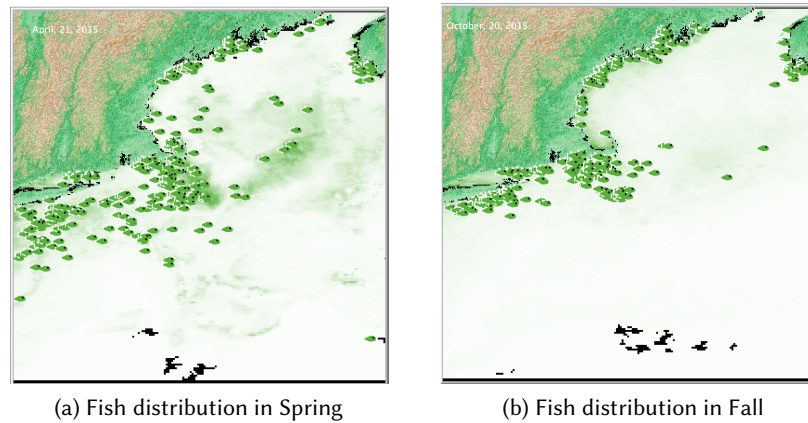(a) Fish distribution in Spring   (b) Fish distribution in Fall

Fig. 4. Experimental Results Images

move north during the summer and see the movement of fish going down to the south during the winter because fish want to migrate to areas with more comfortable temperatures.

Although, we were able to get some contrasting grouping of fish in Spring and Fall as shown in Figure 4 (a) and 4 (b), our expectation for the fish migration pattern was not met. We do not take into account the reproduction of fish on bioenergetics nor do we introduce new agents to the simulation, the number of agents decreases and never recovers at the beginning of run the simulation once agents move outside of the NetLogo world. This led us to losing a significant number of fish compared to the number as we began the simulation. In addition, many agents do not move out of coves or along the coast lines once inside them, with the result of losing a significant number of fish. Those two problems prevented agents from acting more dynamically and migrating to further areas.

5   Limitation and Future work

The simulation results were not conclusive due to following limitations:

- Lack of implementation of bio-energetics and reproduction led to losing significant number of fish during simulations.

- Coastal areas caused agents to remain in the same area and led to lack of dynamic movement throughout the simulation.
- Simulation was designed, developed and tested for only one geographical location, George's Bank and only one species of fish, mackerel.
- Data unavailability of chlorophyll-a data during winter months.

In spite of those limitations, this work represents a step forward in finding approach to simplify the implementation of movement algorithm and generalize the model for different species using fewer parameters such as an optimal temperature.

6 Conclusion

Based on the cited research the SEASIM research [4], a method for fish migration algorithm followed a deterministic approach which utilized different types of pre-defined migration area, and did not factor in the increasing exponential function related to the optimal temperature. Furthermore, [4] focuses primarily on mackerel.

We achieved the ability to generalize the algorithm with a generalized Arrhenius constant to figure out movement of fish in response to environmental data based on an optimal temperature instead of a range of preferred temperature. Our approach is unique compared to other researches on ABM marine ecological models such as SEAPODYM [7], and NEMURO [6] because we attempted to let the migration pattern emerge solely in response to the environmental drivers and simplified the types of movement to only one movement in respect to the food availability, sea surface temperature and sea surface velocity. In addition to the simplification of movement, we constructed a method to extract environmental data from online databases and pre-process them into the proper format for .asc files which allowed us to load necessary environmental data onto a simulation framework for George's Bank.

However, because of the time constraints of the project, we were unable to take into account the life-cycle of the fish and their reproduction which may have impacted the result to be inconclusive, especially the abundance data of each individual agent in the simulation. In future research, we plan to integrate bio-energetics and an energy budget for each agent into the representation of fish and continue to explore different parameters and characteristics of fish that we can utilize to improve the generalization of application to different species of fish.

7   Discussion

In order to maintain a healthy fishery, efficient stock assessment is required. Fishery managers are interested in knowing the location of the fish and stock biomass, and abundance of fish. Through this research we aimed to develop an agent-based model capable of simulating the migration pattern of species in question through emergence based on an algorithm which utilized bio-characteristics and environmental drivers.

While we simplified the movement algorithms and types of movement in order to achieve generalizing the model for other species, we believe that bioenergetics plays a significant role in order to improve the accuracy of the simulation and to answer the question of population dynamics for fishery managers. Changes in the environmental drivers directly influences the productivity and concentration of chlorophyll and sea surface temperature. Bio-enegertics and energy budget allows the dynamic representation of abundance of fish. Therefore, incorporation of bio-energetics will enable observations of how climate change influences not only the migration pattern of fish but the population dynamics and reproduction of species.

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