

**Analyze the Risks of Biological Invasion:
An agent based simulation model for introducing non-native oysters
in Chesapeake Bay, USA**

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Abstract

Introducing non-native species into the coastal and marine environment, both intentionally and accidentally, could have significant ecological and environmental consequences. Analyzing the possible consequences of nonnative species is vitally important in preventing invasive species, as well as challenging due to the complexity of the marine ecosystem and the interactions among the existing species. This paper presents a Spatial-Explicit Agent Based Simulation (SEABS) model and its application on risk analysis of a non-native oyster in Chesapeake Bay, USA. The result shows that the risks for the introduced species to become dominant species depend on its initial stocking location and level.

Keywords: Marine environmental risks; Biological competition; ABM simulation; Non-native species

1. Introduction

Invasive species are a rapidly growing economic and environmental problem worldwide. It has been identified as one of the leading factors causing tremendous, irreversible environmental changes at ecosystem level (GISP, 2003; UDSA, 1999). Many countries have suffered from huge damage caused by invasive species. For example, in China, one third of the endangered species are the result of invasion of foreign species. United States, for example, has been invaded by approximately 50,000 alien species. One study estimated that the environmental and economic cost of invasive species amount to \$120 billion per year (Pimentel *et al*, 2005).

The term “invasive” is applied to nonnative species that cause or are likely to cause economic losses, harm to the environment and/or adverse impacts on human health which are disproportionate to any associated social benefit (e.g., National Invasive Species Council, 2002). Majority of nonnative species are introduced through human activities, either intentionally or unintentionally (National Research Council, 2002), especially with the increase of international trade. Since human actions are largely responsible for introduction, and it is also the pathway that can be managed effectively, many of the management efforts are focusing on this issue.

One example in preventing unintentional introduction of invasive species in international trade is the effort in controlling the discharge of ballast water in maritime transportation. Ballast water is necessary during the ship loading/unloading process for stabilization. With the increase intensity and extensiveness of international trade, this pathway has been identified as the main vector for the introduction of nonnative species. It is estimated that some 3000 species are transported in ships’ body or on ships hulls each day (Firestone and Corbett, 2005).

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To control the risk of spreading invasive species from shipping activity, International Maritime Organization (IMO) adopted International Convention for the Control and Management of Ships' Ballast Water and Sediments (Ballast Water Convention) on 13 February, 2004, which requires ships to develop ballast water management plans, maintain a ballast water record book, undertake certain ballast water management measures, and eventually comply with concentration-based discharge limits.

Intentional introduction of nonnative species for commercial reasons may also result in invasive species either because the introduced species could become invasive in the new environment, or there may be "hitch hikers" that become invasive. Not all nonnative species are invasive. Many nonnative species support highly valued commercial activities and improve our quality of life, such as many introduced agricultural crops, livestock species, ornamental plants and household pets. Thus, it is not desirable to base invasive species control policies based on a wholesale prohibition on the introduction of all nonnative species. This is recognized in extant policy guidance such as Executive Order 13112 and the associated National Invasive Species Management Plan (National Invasive Species Council, 2001), which forbid actions to introduce or enhance nonnative species unless "... the benefits of such actions clearly outweigh the potential harm caused by invasive species; and that all feasible and prudent measures to minimize risk of harm will be taken in conjunction with the actions."

Estimating the risks accompanied with the accidental and intentional introduce of invasive species present a challenge due to the complex, yet most of the time unknown biological and ecological adaptation of the introduced species in the environment. However, it is also one of important elements in the decision-making process of controlling the incidents of invasive species from non-intentional introduction, and the permission to intentionally introduce some non-native species into the environment, to provide the satisfaction of our human being.

This paper presents an Agent-based Simulation model for assessing the risks of non-native species to become invasive species, using a case study on the introduction of non-native Suminoe oyster species (*Crassostrea ariakensis*) in the Chesapeake Bay area where the oyster industry is under threat because of the declining population of the native eastern oyster (*Crassostrea virginica*). We will first briefly introduce the oyster industry in Chesapeake Bay and issues in the introduction of the Suminoe oyster. It will be followed by the description of the simulation model, and data used in the simulation process. The simulation result will be presented at the end as a conclusion.

2. Background

Chesapeake Bay is located in the middle lower part of US East Coast, across the State of Maryland and Virginia. Oyster industry there has been decreased dramatically in the past century from a billion-dollar industry in the 1880s to less than 1% of that value today, due to the effects of over-fishing, channel dredging, pollutants, sediments runoff, and diseases (Gottlieb and Schweighofer, 1996), and especially, the diseases called MSX and Dermo, caused by an invasive protozoan parasite, *Haplosporidium nelsoni*, which was introduced to the East Coast from Asia (Burreson, Stokes and Friedman, 2000).

A recent initiation on introducing non-productive nonnative Suminoe oyster into the Chesapeake Bay area is under debate because it presents risks in both undermining the ongoing recovery effort of native species, and the risks that the introduced species may become invasive. The hatchery raised triploid Suminoe oyster is supposed to be non-productive, but some of the triploid oysters will revert to diploids, which is capable of reproduction. In addition, some diploid oysters may also be mixed with the triploid oysters and get into the environment accidentally. Hence, introducing triploid oysters reduces the probability that the species will become invasive, but does not completely eliminate the risk.

Therefore, one main task of this research is to find out if the introduced species can generate a sustainable population mass in the bay area under different condition, whether it is diverted diploid oyster, or the oysters accidentally mixed with the diploids. If there is no hope that the introduced species can form a sustainable population, then it can be considered as "low risk" for the introduction of

non-native species. However, if the introduced species can form a sustainable population, then we have to be more cautious in deciding to introduce the species into the environment.

Many existing papers have studied the biological property of Suminoe oyster and how it is interacting with the environment. Langdon and Robinson (1996), for example, discussed the aquaculture potential of non-reproductive Suminoe oyster in the West Coast of USA. It presented many life history parameters of Suminoe oysters, spawning environment and period, and its environmental tolerances. Similar research including Nell (2002) who discussed the possibility to use triploids for oyster farming activity in France, and Calvo *et al* (2000) which studied the environmental requirement for oyster growth.

Dew *et al* (2003) built a simulation model for assessing the Likelihood of self-sustaining populations resulting from commercial production of triploid Suminoe Oysters in Chesapeake Bay. The life-history parameters of this simulation draw heavily from a previous research by Mann and Evans (1998), which estimated the standing stock for the native eastern oyster in the James River. The variables in the simulation include salinity, stocking density, reversion rate from triploids to diploids, reproduction potential, natural and harvest mortality. The spatial interaction and the competition are not considered in the model. Similar modeling effort using oyster population dynamics could also be found for Pacific oyster (*Crassostrea gigas*) in Mediterranean coastal lagoon at Thau, France (Gangnery *et al*, 2004), at Port Stephens, Australia (Honkoop and Bayne, 2002).

A recent report on the background economic analysis for the environmental impact statement regarding the introduction of non-native Suminoe oyster in Chesapeake Bay (Lipton *et al*, 2006) presents an extensive economic analysis for the benefits and costs with the introduction of Suminoe oyster. However, in estimating the future benefits from the introduced oyster growth, the limitation and spatial distribution of the oyster habitat on the population growth of the introduced species were not included.

Large scale simulation analysis for modeling the spatial biological interaction between species and with environment using agent based modeling approach is not frequently seen in the publications. One of such paper is addressing the ecological system in the Coastal lagoons ecosystem where human being (like oyster farmer) is involved in the complex decision-making process (Pereira *et al*, 2004). One of the example provided in the paper simulates the anthropogenic environmental pressure resulted from the tourism and shellfish/fish farming in Sungo Bay, People's Republic of China. It was modeled as a 2D model including the hydrodynamic process and biochemical process in the region, based on a finite difference bathymetric staggered grid with 1120 cells and a spatial resolution of 500m (side length of rectangular cell). This grid configuration is not optimal in modeling the homogeneous diffusion in all direction.

Our focus in this research is to simulate the spatial growth of the introduced oyster in the Chesapeake Bay, taking into consideration many realistic factors such as the spatial distribution of oyster habitat, species competition between native and non-native species, in addition to the population dynamics and life history parameter of the native and non-native oysters. It also allows the analysis of different management policies, such as selecting the level and site of initial stocking, setting policies on Total Allowable Catch and initial non-harvesting period, etc.

We use Agent Based Model [ABM] in simulating the oyster population dynamics and spatial diffusion over the oyster habitats in the Chesapeake Bay. ABM is a relatively new computational modeling paradigm, originally derived from the Computer Science and refers to the modeling of various phenomena as dynamical systems of interacting software agents. The outstanding feature of ABM is its ability to derive the intricate behavior of the whole system based on the simple, local behavior of each individual agent. Because of this, it has been applied in the study of collective economic behavior (Tsfatsion, 2006), biology (Politopoulos, 2007), and complex social, economic, and biological system (Bobashev *et al*, 2007). As it is rather complex to model the result from the interaction of oysters in different area of the bay, we design a virtual oyster population agent to manage the population dynamics and spatial diffusion of oyster within each cell.

3. Population Dynamics for Oysters

This research simulates the behavior of oysters using a detailed model of survival, growth, reproduction and transport of oyster populations. The model described in this section, including all life history parameters of oysters closely follows Mann and Evans (1998) and Dew *et al* (2003), with two significant departures. First, we include detailed modeling of larval transport. The population dynamics specified in this section are for each specific oyster habitat “cell”. The specification of the cell will be explained in next section. Secondly, we examine interactions between the native species and the introduced species. In locations where the two stocks co-exist, they compete for food and habitat space. Also, we model stock interactions through reproduction, as discussed below.

Once oysters set, they are secured to hard surface (including other oysters), so that transportation of adult oysters is minimal. Rather, transport of oysters occurs almost exclusively during reproduction and the larval life stages. Various means of controlling the spread of nonnative oyster involve management actions that effectively reduce the production of gametes (sperm and eggs), such as introducing non-reproductive triploid oysters, and actions that reduce the viability of larvae, thereby reducing the production of juvenile nonnative oysters. For example, planting of non-native oysters could be restricted to isolated habitat locations, where larvae are unlikely to spread. Or since larvae are far more sensitive to salinity levels than adults, the risk of uncontrolled spread of non-native oysters could be reduced by introducing non-native oysters in locations where salinity is unfavorable for survival of larvae.

In order to model policies that control potential spread of nonnative oysters, we need to carry out detailed modeling of various stages of the process from spawning through survival of young-of-the-year. For these reasons, our model focuses more extensively on modeling the details of the early life stages of oysters than is typical for bioeconomic models. Our model includes separate equations for production of gametes, fertilization into zygotes, and setting of spat on hard substrate.

At present, we utilize identical life history parameters for the two species of oysters, with the important exception of susceptibility to disease. The primary rationale for introducing *C. ariakensis* is its resistance to disease. Therefore, we adopt available estimates for susceptibility of the native species, *C. virginica*, but assume that the introduced species is not affected by disease.

3.1 Modeling the oyster fecundity with the environmental condition

First we model fecundity or the production of gametes. The number of gametes produced depends upon the number of oysters and the size of oysters, where gamete production increases at an increasing rate with size. Also, in the case of introducing non-reproductive triploid oysters, the reproductive potential is determined by the fraction of introduced oysters that revert from triploid to diploid and the fraction of diploids that are accidentally introduced. The equation for fecundity is:

$$F_{ij} = 39.06 \left[0.000423 L_{ij}^{1.17475} \right]^{2.36} N_{ij} (R_{ij} + T_{ij})$$

where F_{ij} is total potential fecundity (in millions of eggs) at time t for age class j , L_{ij} is the length at time t for age class j , N_{ij} is the number of adults at time t for age class j , R_{ij} is the percentage rate of revision from triploid to diploid, and T_{ij} is the percentage of diploids accidentally released into the environment. Note that for native oysters and nonnative oysters are stocked as reproductive diploids, $R_{ij}=0$ and $T_{ij}=1$. Salinity is used to relate potential fecundity to actual fecundity. Although adult oysters are relatively unaffected by salinity, reproductive effects can be important. This suggests a spatially explicit policy to reduce risk of invasion by planting nonnative oysters in areas where reproduction is limited by salinity, or in areas where nonnative oysters are confined by salinity. For example, the risk of spread of the nonnative species can be controlled by limiting planting to inlets that are isolated from the rest of Chesapeake Bay by an area with salinity that is unfavorable to survival of larvae, thereby reducing the likelihood of geographic dispersal of nonnative oysters.

The fecundity adjustment factor accounting for salinity, F_S , is zero for salinity less than 8 ppt, reaches a maximum at salinity of 13.5 ppt, then declines back to zero when salinity reaches 35 ppt. We specify the relationship between fecundity and salinity as a piecewise linear function of the level of salinity.

Salinity (S)	$S < 8$	$8 \leq S < 13.5$	$13.5 \leq S < 35$	for $S \geq 35$
F_S	0	$(S-8)/5.5$	$(35-S)/21.5$	0

where F_S is the salinity factor that relates potential to actual fecundity, and S is salinity measured in parts per thousand.

We introduce a disease factor to account for the effect that various diseases can have on reproductive success. The disease factor goes from 0 to 1, where zero indicates no reproductive success, and 1 indicates no disease-related mortality. Although nonnative oysters have proven to be resistant to diseases that are prevalent on the east coast, they may be affected by other diseases. Also, the disease factor will be important when the model is used to analyze decision within a multi-species framework, with both native and nonnative oysters.

Oysters tend to congregate in highly concentrated communities, called oyster bars. Indeed, oyster bars were significant hazards to shipping in Chesapeake Bay when oyster populations were at historic high levels. Oysters benefit from high concentrations in at least two ways. First, oysters require hard surface to attach to, including other oysters. Therefore, oysters provide their own habitat. Also since oysters are broadcast spawners, fertilization success increases with concentration of oysters. We specify an equation for fertilization success as:

$$F_{ft,i} = 0.0049 D_{t,i}^{0.72}$$

$$\text{where } D_{t,j} = \frac{N_{t,j}(R_{t,j} + T_{t,j})}{A}$$

and $F_{ft,j}$ is fertilization efficiency, $D_{t,i}$ is the density of reproductive oysters, and A is the area in square meters. For hexagon with side length 500 meters, A is equal to 649519.05 square meters.

Total zygote production is the sum over all age classes of potential production, corrected for salinity (F_S), the sex ratio (F_{qi}), the fraction not lost to disease (F_d) and the fertilization rate ($F_{ft,i}$)

$$F_{total,t} = \sum_i (F_{revert,t,i} * F_S * F_{qi} * F_d * F_{ft,i})$$

3.2 Dynamic population of oyster population

Spat are zygotes that have successfully metamorphosed, settled and attached to hard substrate. The total number of zygotes is sum of the number of reproduced from the population net of the emigrated zygotes (E percent), plus the number of population from all other cells. Spat are then produced by metamorphosis of the zygotes and setting onto hard structure. The number of spat is determined by multiplying the number of zygotes by the probability of successful completion of metamorphosis (P_{met}), corrected for larval mortality through the time of settlement. The daily larval mortality rate is L_{mort} , and it takes approximately 21 days from metamorphosis to finish. Finally, the number of one-year-old oysters is the number of spat times the total mortality rate for oysters less than one year old (m_0). The equation relating the number of zygotes to the number of one-year-old oysters is:

$$N_1 = \left(F_{total}(1-E) + \sum_{n=1}^N \alpha_n F_{total}^n \right) P_{met} (1-L_{mort})^{21} (1-m_0) \text{ for } l \neq n$$

where N_1 is the number of individuals at age class one in one cell, F_{total}^k is the total larvae from the k^{th} cell, α_n is the percentage of the larvae moved from n^{th} cell to this cell, N is total number of cells that have larvae being transported to this cell. When working in the multi-species framework, this will be extended to include a fraction of non-viable zygotes that result from hybridization between the native and nonnative species. More discussion of this issue is contained below.

Numbers of individuals at various age classes then progress through the equation:

$$N_{t+1,j+1} = N_{tj}(1 - M_j)(1 - H_{tj})$$

where H_{tj} is the harvest rate for age class j at time t , and M_{tj} is the natural mortality rate at time t for age class j . Harvest also varies by time to account for changes in the different management policies over time. The total number of individuals in the population is simply the sum over all age classes:

$$N_t = \sum_{j=1}^M N_{tj}$$

3.3 Competition of habitat space through biomass Capacity

In real environment, the oyster population cannot grow over certain limit. In the simulation model, we specify the upper limit for the total weight of oyster per square meters (C). If the total weight of the oysters in one cell is larger than its capacity, the population of the oysters in all the age class will be reduced proportionally, so that the total weight will below the capacity limit.

When two species resides in the same cell, they will compete for available limited space. For example, if the total weight of native oysters in cell i at time t (W_{it}^n) and non-native oysters (W_{it}^o), $W_{it}^n + W_{it}^o$ is larger than C , then it is necessary to limit the number of oysters for each species. The upper limits for each species will be:

$$C_{it}^o = \delta C \quad \text{and} \quad C_{it}^n = (1 - \delta)C$$

where $\delta = \frac{W_{it}^o}{W_{it}^o + W_{it}^n}$ is the percentage of the non-native oyster weight in total weight of the oyster in the cell. C_{it}^o and C_{it}^n are the capacity limited of the non-native oyster and native oyster, respectively. Thus the species with higher growth rate will eventually become dominate in the cell, if all other factors not changed.

3.4 The effect of gamete sink on oyster population

Another potentially important issue associated with co-existence of two oyster species in the same area is the gamete sink (e.g., Meritt *et al*, 2005, Bushek *et al*, 2007). Oysters of all species are broadcast spawners, and fertilization occurs when sperm and egg join in the environment. This raises the potentially important issue of the extent to which gametes of the two species interact. If the two species of oysters synchronize spawning, then a fraction of eggs from one species will join with a sperm from the other. This results in a hybrid that is not viable, which adversely affects reproduction of both species. Therefore, whenever non-native species happen at the same cell as the native species, we compute the result of gamete sink on both species. Assume the number of gametes for native species is N_A and that for non-native N_B , then $N'_A = p_A N_A$, and $N'_B = (1 - p_A) N_B$ are the number of gametes for native and non-native species, respectively, after the gamete sink effect, where

$$p_A = \frac{N_A}{N_A + N_B}$$

is the ratio of the gametes of native species in the total gametes number in this cell.

This specification shows that the effect on the less numerous species may be far more devastating from a reproductive viewpoint. For example, suppose that the gametes (eggs and sperm) of one species outnumber those of the other by a ratio of 3 to 1. In this case, $\frac{1}{4}$ of the gametes from the more numerous species will join with gametes from the less numerous species, and become hybrid. Since these hybrids are not viable, they die. However, $\frac{3}{4}$ of the gametes from the less numerous species will join with gametes from the more numerous species, producing hybrids which subsequently perish. This means that less numerous species in an even worse competitive position in each future generation, and their gametes will become outnumbered by an even larger ratio in the future. Hence, even in cases where the population of less numerous species is viable in the absence of the more numerous species, the potential for the gamete sink could make the species reproductively non-viable. This notion of the gamete sink is incorporated in calculating the viability of zygotes in the multi-species version of our simulation model, as discussed above.

The effect of the gamete sink could be advantageous or disadvantageous when considering potential risks of invasion by intentionally introduced species. If the gametes from the introduced species significantly outnumber those of the native species, the native species could be driven out (assuming synchronized spawning), and attempts to restore the native species could be futile if a large population of reproductive nonnative species is established. However, if the number of gametes from the introduced species is kept sufficiently below those of the native species, then the gamete sink effect could reduce the risk of invasion by the introduced species, and the number of gametes of the introduced species could be kept low by introducing non-reproductive triploids. Thus, even if the population of the introduced species is significantly larger than that of the native species, the number of gametes from the introduced species could be kept low by introducing non-reproductive triploids. The gamete sink effect could reduce the probability of successful reproductive by mosaics and accidentally introduced diploids.

However, it would be advised not to become too reliant upon the gamete sink notion to control the risks of invasion by the introduced oysters. If spawning is not well synchronized across the two species, then the gamete sink notion is not relevant. And even if the populations start out synchronized, one might expect evolutionary pressures to disrupt the synchronization of spawning: oysters whose reproduction is not synchronized with the competing species might become relatively more successful, and the two populations might naturally move out of synchronization.

4. Simulation the Spatial Movement of Oysters

We developed a spatially explicit agent-based model that simulates the growth, transport and harvest of the native and nonnative oyster species in Chesapeake Bay. The agent-based framework extends Recursive Porous Agent Simulation Toolkit (RePast), which supports general simulation activities, such as GUI for starting and stopping simulation, controlling time steps, change simulation parameters, and coordinating with basic simulation functions. Simulation procedures specific to this project are started with oyster model, which read in the data necessary and simulation parameters, create oyster habitat space for oyster population agent, a display for oyster habitat and the population agents, and a data recorder to take down the numerical simulation results. A general structure of the simulation model is in Figure 1.

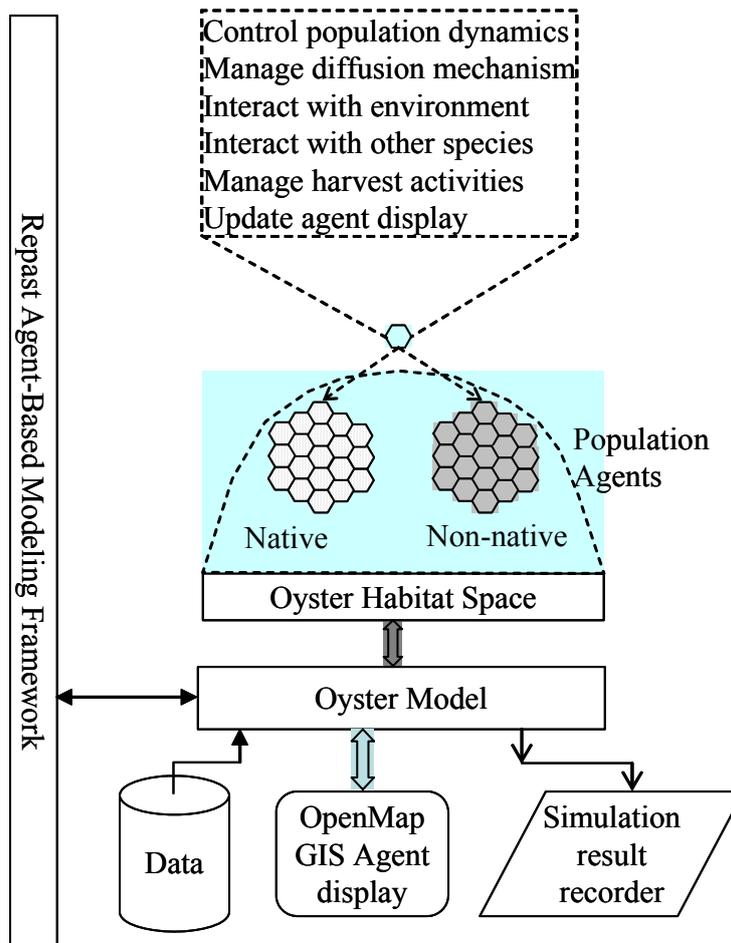


Figure 1: Depiction of the modeling system architecture

The oyster model also creates the initial oyster population agent at the initial stocking cell for each species, and let them grow and spread in the simulation process in the virtual habitat space. Model results are passed back to OpenMap to create a dynamic visual representation of oyster population on electronic maps. The OpenMap depiction of simulation area in Chesapeake Bay and an illustrative view of a spatial distribution of oyster population are presented in Figure 2, as they would be seen by the model user. More detailed simulation results, such as the quantitative levels of oyster populations over time and space, harvest, etc. are stored for later analysis. Next we will explain more on the configuration of the habitat space and the simulation environment.

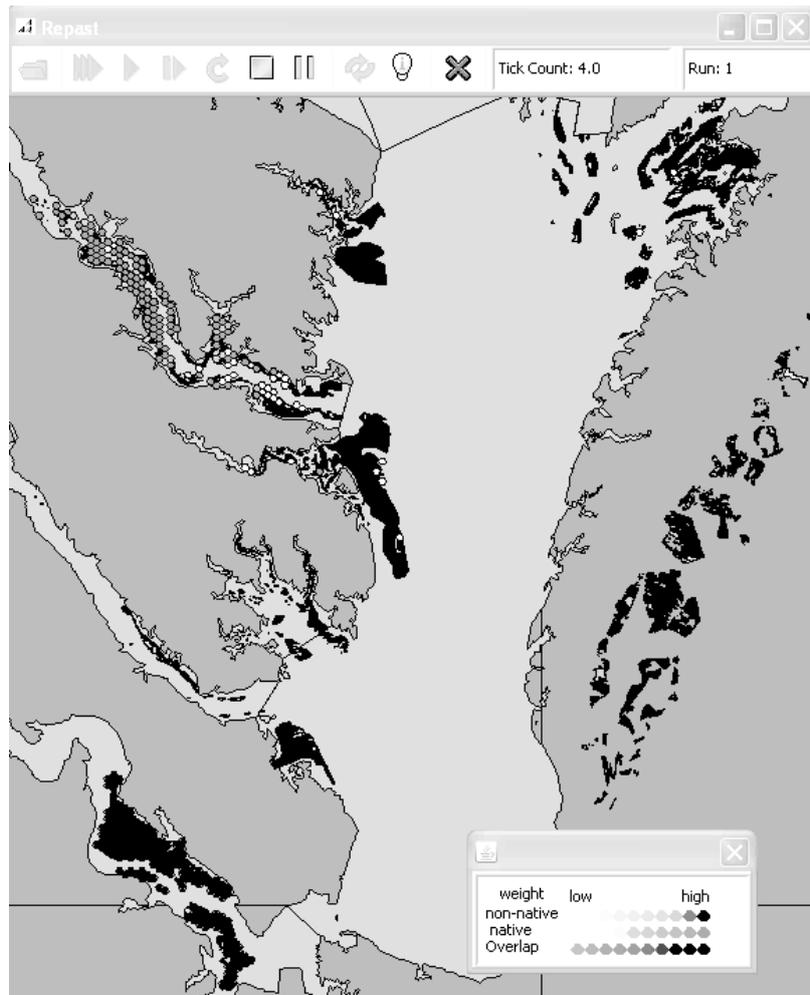


Figure 2: Illustrative output from the simulation model

4.1 Spatial configuration of oyster habitats

The oyster habitats in Chesapeake Bay are scattered in different tributaries, and cover only a small part of the bay area. To enable the simulation of the spatial diffusion of oyster larva as well as the harvest activities for adult oysters, we divided the habitat space into many small hexagonal cells, 500 meters on each side. The whole simulation area, as shown in Figure 3, could be divided into 200 by 200 such cells if all the area were oyster habitat. This grid configuration could be changed before each simulation to accommodate the need of different research purpose. In addition, we only included cells with hard bottom type (oyster rock, shell mud, and shell sand), as oyster can only fix and grow on hard surface.

With this arrangement of cells, each cell is identified by its coordinates x and y , with the origin being the upper left corner of the simulation area (Figure 3). This specification will greatly facilitate the conversion of coordinates system with the longitude and latitude, and calculate the distance between the any two cells. Further, it facilitates the diffusion mechanism by simplify the algorithm in finding out the neighboring cells at specific range measured by the number of rings.

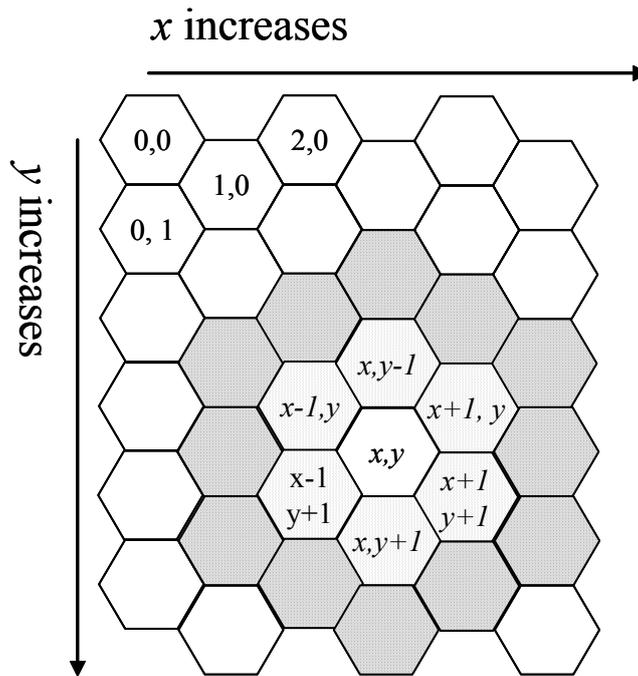


Figure 3: Illustration of the coordinate system of oyster habitat space

Residing in each cell is one population agent that manages the population dynamics from each species. It is identified by its specie name and its coordinates, has information about the life-history parameter of the specie (such as age, length, growth mechanism, mortality rate, reproductive capability, etc), and can access to the environmental information such as location, bottom type, the tributary information, and information about whether there is other specie resides in the same cell.

4.2 Spatial diffusion of oyster

Agent in one cell interacts with the agents in the neighboring cells through spreading oyster larvae into other cells within certain range, and accepting larvae drifted from other cells. This is the main mechanism for oyster to diffuse over the bay area.

Many of the environmental factors participated in the movement of the oyster larvae in the water column, such as the geographical condition, hydrodynamic characteristics of the bay, tidal and water current, etc. To simplify the simulation process, for each species (s), we used the actual observations on the transportation distance d_i^s at each tributary (i)(Table 1), and the connectivity among tributaries (ρ_{ij}^s) (Table 2) to model the zygotes movement within the same tributary ($i=j$), and the movements to other tributaries ($i \neq j$).

Table 12: Oyster larval transport distance and estimated standard error and max. distance (Km)

Tributaries	C. Virginica			C. Ariakensis		
	distance	Std	Max.Dist*	distance	Std	Max. Dist*
Rappahannock R.	10.9	16.16	26.58	7.2	10.67	17.56
Piankatank River	6.2	9.19	15.12	3.9	5.78	9.51
York River	9.2	13.64	22.44	7.1	10.53	17.31
VA Mainstem	20.7	30.69	50.48	16.7	24.76	40.73
Mobjack Bay	6.4	9.49	15.61	5.9	8.75	14.39
James River	9.3	13.79	22.68	7	10.38	17.07

* Max. Distance: the distance where the cumulative distribution is equal to 95%.
Source: North *et al* (2006)

Table 13: Oyster diffusion rate within and across tributaries

		Destinations (V.: C. Virginica; A: C. Ariakensis)					
		Rappa-h annock	Plana-ta nk	York	Virginia Mainstem	Mobjac k Bay	James
Source	Rappahan V	92.10%	2.00%	0.40%	5.30%	0.30%	
	-nock A	99.60%	0.20%		0.30%		
	Planatank V	3.40%	69.40%	0.50%	26.30%	0.40%	
	A	7.70%	86.50%		5.70%		
	York V			93.70%	0.70%	5.50%	0.05%
	A			97.90%	0.30%	1.30%	0.50%
	Virginia V	8.80%	4.00%	6.10%	72.70%	6.20%	1.60%
	Mainstem A	11.30%	2.10%	1.70%	62.30%	1.10%	19.30%
	Mobjack V			5.90%	1.80%	92.30%	0.03%
	Bay A			8.80%	0.60%	90.60%	0.01%
	James V				1.60%		98.40%
	A			0.001%	0.020%	0.001%	100.0%

Source: North *et al* (2006).

To model the zygotes movements within same tributary, we first assume the transportation distance of zygotes follows positive portion of normal distribution. Since we don't have the negative part, and d_i^s is the mean value of zygotes transport distance, we can find the standard deviations (σ_i^s) that make the cumulative probability from origin to the mean distance (d_i^s) equal to 25%:

$$\frac{1}{\sigma_i^s \sqrt{2\pi}} \int_0^{d_i^s} e^{\frac{-t^2}{2\sigma_i^s}} dt = 25\%$$

The standard deviations that satisfy above condition are shown in Table 1 (std.). They are used to calculate the percentage of larvae that will be transported into cells at different distance. Figure 4 illustrates an example of half-normal distribution when standard deviation equaling to 2, and percentages of larvae remain in the initial cell and that transported to each ring. As the cell length is 500 meters, and its center is the starting point of the half-normal distribution, the first ring starts at 500 meters, then each of next ring will start 1 km away from the previous one, until the cumulative probability is larger than 95%. Table 1 also includes the computed maximum distance ($d_{i,max}^s$). As the cell diameter is 1 km, $d_{i,max}^s - 0.5$ is actually the number of rings for species s in tributary i . Using Φ_{ik}^s for the cumulative probability at the k^{th} ring, if all of the cells at that ring are oyster habitat, then the percentage of larvae (λ_{ik}^s) moved to any one cell at that ring is:

$$\lambda_{ik}^s = \frac{\rho_{ii}^s \Phi_{ik}^s}{6k}$$

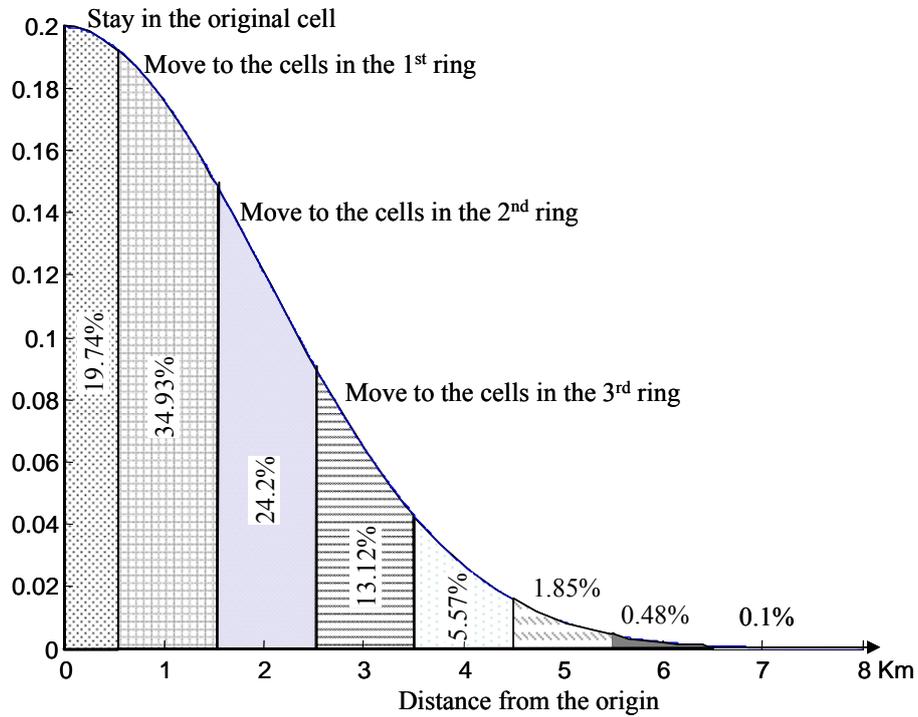


Figure 4: Percentage of zygotes transported to different rings for standard deviation=2

The diffusion to the cells not in the same tributary is done by randomly pick up one cell from the tributary where $\rho_{ij}^s \neq 0$ in table 2, and assume all that friction of the zygotes are transported to the chosen cell. If the cell is an oyster habitat, it can survive; otherwise, they will just disappear.

In either case, the new population agent will be created if the cell that accept new larva does not have a population agent in it. Then the agent will manage the oyster population dynamics, and interaction with the other agents and with the environment. If the oyster population in a cell becomes zero, the population agent will be deleted.

4.3 Data used in the Agent-Based Simulation Model

Data used in this simulation model include the actual larvae movement data for native and non-native species in the Chesapeake Bay (Table 1 and Table 2), the GIS database for different bottom types in the Virginia part of the Chesapeake Bay (Figure 5), and the life-history parameters and economic price of the native and non-native species (Table 3).

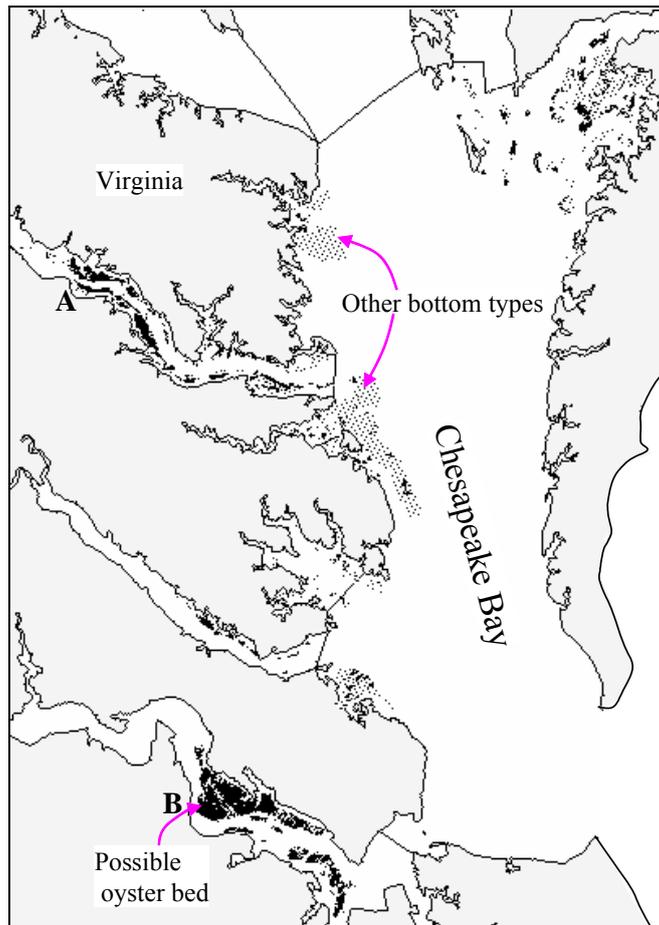


Figure 5: Oyster bed and other bottom types in Virginia part of the Chesapeake Bay (Dark spots in the figure (A, B) indicates oyster bed. Other bottom types are currently not suitable for oyster to grow, but possible oyster beds.)

Table 14: Life-history parameters and economic price for native and non-native oysters

Year		0	1	2	3	4	5	6
Length (mm)		0	54.5	96.9	124.2	151.5	178.7	196.9
R		0	0	0	0.049	0.009	0.014	0.019
T		0	0.001	0.001	0.001	0.001	0.001	0.001
Fq		0	0.28	0.66	0.8	0.9	0.95	0.95
M	Native	0.98	0.7	0.6	0.5	0.4	0.3	0.2
	Non-native	0.98	0.5	0.4	0.3	0.3	0.2	0.2
H		0	1	1	1	1	1	1
Price (P*)	Native	0	0.2	0.65	0.55	0.55	0.55	0.1
	Non-native	0	0.2	0.25	0.3	0.25	0.2	0.1

* US Dollar per piece.

Figure 5 shows that there are not so many areas in the Virginia part of the Chesapeake Bay suitable oyster to settle down and grow. The black areas in the map are either oyster rocks, shell mud and shell sand area, which are scattered in different tributaries, separated by place not suitable for oyster to grow. The other bottom types, such as buried shell, sand, sand mud, clay, etc, cannot be used as oyster habitat.

Owing to lack of data for non-native Suminoe oyster, most of the parameters used in this simulation are actually from native Eastern species. We assume that nonnative oyster, *C. arikansis*, has very similar life history parameters as the native one. The only differences are their susceptibility to disease. Nonnative species' mortality is 80% higher than the nonnative one. Besides, due to the preference of the local people, the market price of native oyster is higher than the non-native one.

For each simulation trail, we specify initial settings for the oyster model to build the habitat space and start the simulation. They include the simulation area, grid specification (side length of hexagon), initial stocking level and position, biomass capacity, TAC, and certainty of catch. Certainty of catch is the probability of harvest for legal-size oyster in a cell. It actually reduces the catchability, for both native and non-native species. For native species, it will increase the probability for restoring native oyster population. For non-native species, it increases the risk of forming a self-sustaining population.

5. Simulation Result

The concern for the introduction of the non-native species including whether the introduced species can become a self-sustaining species in the Chesapeake Bay, and whether it will out-compete with the native species, become the only species in the Bay. The risk for the non-native species to become self-sustaining population depends on many factors. We will address the quantity and place of stocking, the whether there are native species competing with them. The major part of the simulation result is a dynamic, visual display of the spatial oyster population agents in the simulation process. A snapshot of such dynamic visual display is shown in Figure 2. Because of the data availability in the bottom types, we only simulate the area in the Virginia part of the Chesapeake Bay.

5.1 Simulation scenarios

We use several scenarios to demonstrate the simulation results with respect to different locations and initial quantities of the native and non-native species, with or without harvest activities. To illustrate the different outcomes with or without specie competition, we will first present the result for the introduced species only. Then we will specify the scenario for two species. Two places considered for stocking oyster spats in the simulation are A, in Rappahannock River, and B, in James River, as shown in figure 2.

5.2 Scenarios with single species

We start with the simulation with only non-native species in the Chesapeake Bay, to show the survivability of introduce non-native triploids with respect to the place of stocking.

5.2.1 Scenario 1: non-native Triploids at James River

In this scenario, we specify initial stocking population 150 million spats at the one oyster cell in James River, which equals to 230/m² in spat density. In the first some years, the oyster will just stay at its original place, as spats are fixed to the oyster bed. New larvae will only appear when the undetected/reverted diploids become mature. These larvae will quickly spread over the oyster beds within the same tributary in the first 5 years. From the 10th year, it begins to spread over the oyster habitats in other tributaries. However, due to limited density, oyster population starts to decrease at the 20th year. At the 45th year, only the oyster bed in James River still has some oyster left. At the year 48, all oyster disappeared from Chesapeake Bay.

This scenario indicates that the risk for the introduced species to be dominating species in the Chesapeake Bay is low if the initial stocking site is in James River. The nonnative oyster will not be sustainable in the Chesapeake Bay. It will disappear even without harvest activity.

5.2.2 Scenario 2: non-native Triploids in Rappahannock River

With the same amount of initial spat, the simulation result shows that the non-native species will be able to exist perpetually in the Chesapeake Bay, if the initial stocking place is in Rappahannock River. Because of the position of Rappahannock River, the oyster species stocked in this river is easy to spread, and hence have high possibility to sustain itself.

The difference between these two scenarios may be partly attributable to the water current movement in the Chesapeake Bay area. In Rappahannock River, the water flow enables the spreading of the oyster larvae into other parts of the bay area, while in James river, as it is at the downstream of the water flow, it larvae diffusion is not as efficient as that in Rappahannock river area. This can be represented by the diffusion rate among the tributaries in the bay area (Table 2).

5.2.3 Scenario 3: Non-native triploids in Rappahannock River with harvest

With the same initial spat number and the place of stocking for non-native oyster as in Scenario 2, the simulation result shows that the species will also become not sustainable if we allow harvest 10 years after stocking. The harvest is so arranged that only 20% of the oysters in the total simulation area can be harvested, i.e., the Total Allowable Catch (TAC) is 20%. Also, as the oyster is fixed at the oyster bed and easy to catch, it is assumed that the certainty of catch is 95%. Thus 5% of the legal size oysters will be available for reproduction in each cell.

The simulation result of introducing non-native species when there is no competition species in the bay area can be illustrated by the population dynamics in the initial cell (Figure 6). It shows that the initial growth period in scenario 1 is just not enough to sustain future growth. The difference between scenario 2 and 3 is the starting of harvest after year 10. This shows the possibility to introduce non-native triploids, get the economic benefit from such introduction, and at the same time prevent the risk having an invasive species.

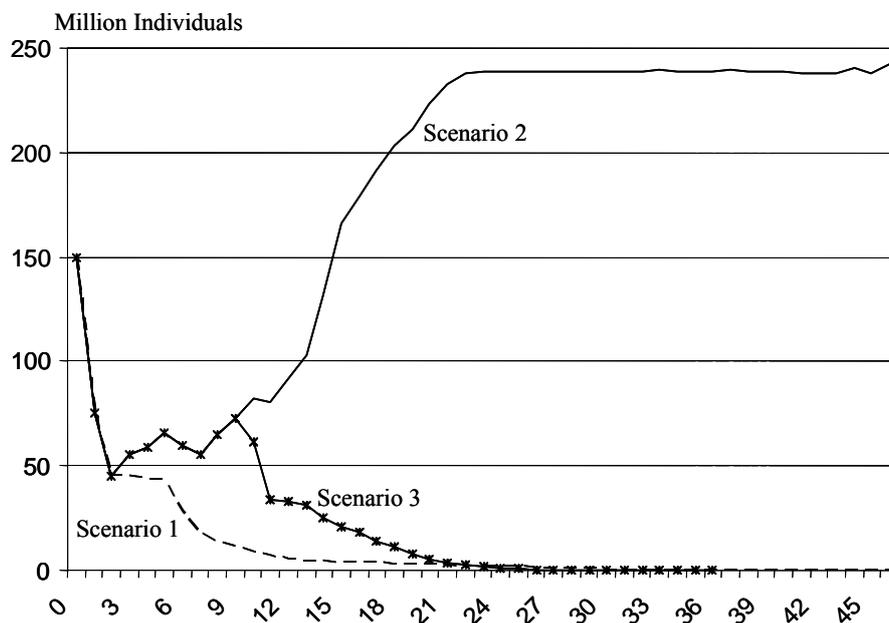


Figure 6: Simulated population dynamics at the initial cell for scenarios 1 to 3

5.3 Scenarios with competing species

With two species in the same bay area, they will interaction with each other through competing for limited spaces and possible gamete behavior during the spawning time. Next several scenarios will demonstrate the simulation result for such interaction. In both scenarios, the initial stocking number is set to 200 million spats ($307/m^2$), to allow for this mutual impact.

5.3.1 Scenario 4: native oyster in Rappahannock River, and non-native specie in James River

Although the number of initial spat number increased to 200 million, the oyster population still cannot support itself if we allow harvesting 20% of the total oysters in the Bay area from the 10th year of the simulation. Although native species has better location, it still can not compete with the non-native species, because of its high market price, and high mortality rate. Therefore, the non-native species will begin to spread over in the Rappahannock River at 20th year, and will become dominant after that. However, as the population size is not sufficient to support reproduction, the non-native will start to diminish and disappear in the bay area.

The simulation result for the total population of native and non-native species in the whole simulation area is shown in Figure 7. At the very beginning, the number of native oysters is higher than the non-native one, because only a very small percent of the introduced species is reproductive. However, once the introduced oyster is generated from the reverted triploids, they all become reproductive, so it will have a higher growth rate. It also shows that the harvest activity after the 10th year is the main factor for the diminishing of non-native oyster population. The value of the harvest could be around 75 million dollars at the peak time of the harvest.

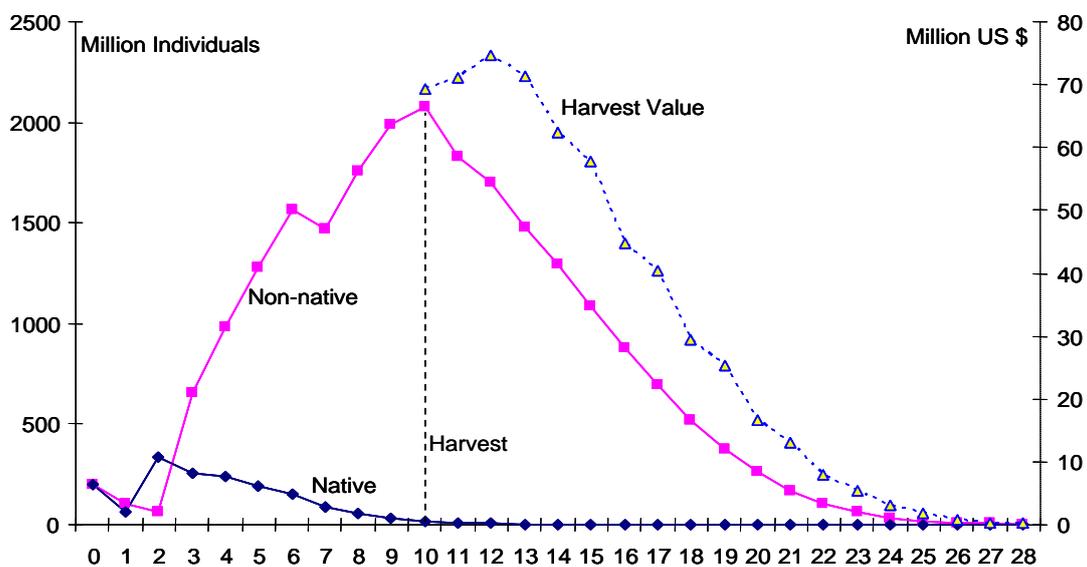


Figure 7: Simulated population dynamics for scenario 4 for the whole simulation area

5.3.2 Scenario 5: native in James River and Non-native in Rappahannock River

With native oyster in James River, non-native oyster will dominate the simulation area, able to sustain harvesting 20% of the total oyster, and still exist perpetually in the bay area. Because of that, the value of the harvest could also last forever (Figure 8). However, this scenario does not consider any possible negative impacts from the over-dominating population of non-native oyster species in the Bay area. The main concerns for the negative impact includes: clogs the waterway, eradicate the native oyster species, compete with other living organisms for space and food, change the bio-diversity of the local environment, and the biological structure of the ecosystem. These are actually the main concerns for the introduction of the non-native species.

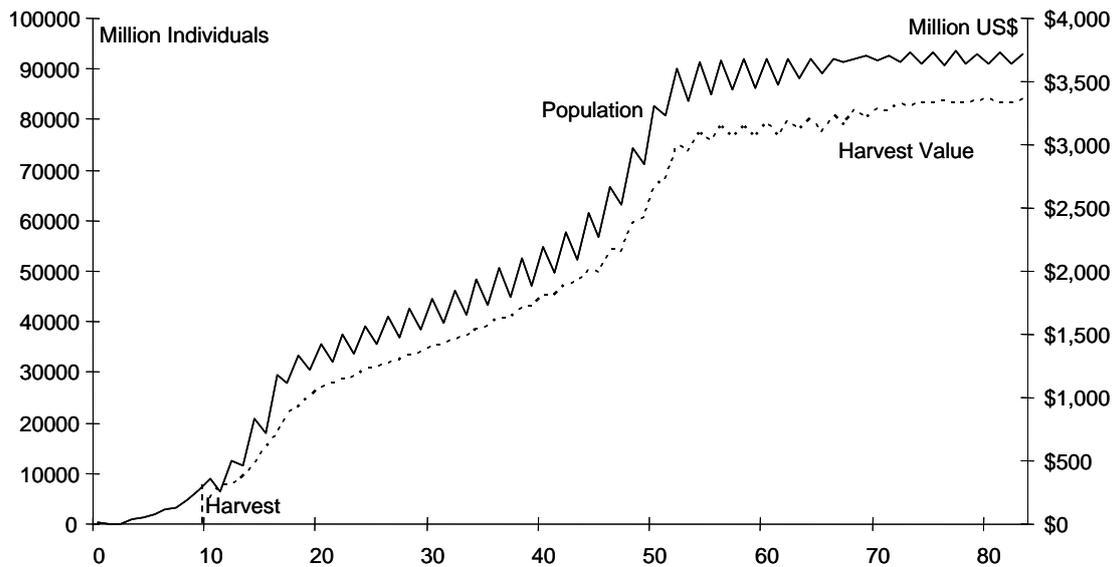


Figure 8: Simulated population growth and harvest for scenario 5

These five scenarios demonstrate the different outcomes with different initial stocking levels at different tributaries of the bay area, with or without the interactions of the native species. For both cases (single specie and two species), it reveals that non-native species will be more easily spread and fill in all the oyster beds when they are stocked in the Rappahannock River. In scenario 2, the non-native oyster will spread all over the oyster bed in the simulated area and grow to the capacity level without harvest. The risk exists for the non-native species to become invasive. As the purpose of introducing non-native species is for its economic value, scenario 3 show that the oyster population will not last forever with harvest after 10 years. This minimizes the risk for the introduced species to become invasive, and at the same time, meet the market demand for oysters. It is not an issue for the disappearing of the non-native species, as it can be re-stocked again if it is diminishing. Scenario 5 illustrates a case where the oyster population become perpetual even with 20% TAC, which illustrate higher catching rate or lower initial stocking level should be adopted, to eliminate the risks for the introduced species to become invasive.

Scenario 4 and 5 also demonstrate the concerns on how to protect the native species that is under threat due to both over harvest and the impact of diseases. With the introduction of non-native species with lower mortality rate, the native species are under unfavorable position in the specie competition. In both scenarios, the native species will be replaced by the non-native species. If the management decision is to protect the native species, then it is necessary to adopt a more conservative policy in introducing the non-native species.

6. Summary

This paper introduced the Agent Based Simulation Model for spatial population growth and species competition, and applied it to the risk analysis for the intentional introduction of the non-native oyster species into the Virginia part of the Chesapeake Bay. It integrates the bio-economic model of Oyster population dynamics with the spatial spreading and movement of the oyster larvae over the actual distribution of the existing oyster habitats in the real environment.

Compare with Dew's results, the simulation results from this research indicate that it should be more cautious when considering introducing non-native triploids into the bay area. With the similar stocking density, the non-native oyster would become self-sustaining with 30 years' stocking period in Dew's simulation, while in our simulation only one year is necessary. This means that the simulation without consider the distribution of the oyster bed and spatial interaction may under-estimate the risks for the non-native species to become invasive.

There a couple of limitation to this research, which may require further studies. First, the position and level of existing stock of the native oyster is not known. To enable the restoration of the native species, it is necessary to survey the existing status of the native species, so as to decide the location and level of non-native species, to make it not replace the native species. Second, the simulation model only included the Virginia part of the Chesapeake Bay, due to the fact that the bottom type data is not available in upper part of the bay.

Nonetheless, this simulation model reveals some important issues regarding the policy of introducing non-native species in the marine environment. Effective measures for reducing the risks of invasive species could be employed, so that economic benefits could be obtained at the same time preserve the local ecological environment. This could also be employed to analyze the invasive species problems in the maritime transportation sector, so as to allow the economic benefits from shipping and port activity, and protect the local environment from the negative impact of invasive species.

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