

## 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 can create serious environmental risks, such as changing the attributes of ecosystem, displacing the native species, clogging the natural waterways and channels. Careful examination of the possible consequences before implementation can prevent the adverse consequences of invasive species. However, policy analysis for such an action is often difficult, due to the complexity of the marine environment, and the interactions among the species therein.

This paper presents a spatial-explicit agent-based simulation model for analyzing the environmental risks of introducing non-native species, Suminoe oyster (*Crassostrea ariakensis*). It is considered to be introduced into the Chesapeake Bay, USA., where there is a native Oyster species (Eastern oyster, *Crassostrea virginica*) with declining population. The simulation result indicates that the non-native species will likely displace the native species, but this can be controlled by setting up a different harvest plan, and the location and the number of initial spat introduced.

Keywords: Marine environmental risks, biological competition, ABM simulation, non-native species

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### 1. INTRODUCTION

Invasive species is a rapidly growing economic and environmental problem worldwide. It has been identified as one of the leading factors causing tremendous, irreversible environmental changes at an ecosystem level (GISP, 2003; USDA, 1999). Many countries have suffered from huge damage caused by invasive species. For example, in China, one third of the endangered species problems are caused by 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 the invasive species amounted to \$120 billion per annum (Pimentel et al, 2005). The economic damage of just one species, Pink Hibiscus Mealybug, is estimated to be \$4,674 million per annum in U.S.A. (Ranjan, 2006).

The term “invasive” is applied to non-native species that caused 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). Major efforts have been put in controlling invasive species from international transportation activity (Batabyal, 2007; Batabyal and Nijkamp, 2005). However, managing the intentional introduction of non-native species for the commercial reason is equally important in preventing the non-native species, or the “hitch hikers”, from becoming invasive in the new environment.

Despite all the problems associated with invasive species, great social benefits originate from with some non-native species. Many non-native species are non-invasive and support highly valued commercial activities and improve our quality of life. They include many introduced agricultural crops, livestock species, ornamental plants and household pets. Thus, it is not desirable to base invasive species control policies on a wholesale prohibition on the introduction of all non-native 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 non-native 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.’*

Furthermore, policies based on absolute prohibition of introducing non-native species are likely to be unsuccessful in eliminating risks, and may even increase risks associated with introduced species. Overly conservative policies regarding introduction of potentially profitable commercial species might encourage some to illegally introduce the species with the intention of subsequently harvesting it. This pathway of introduction may increase risks of invasive species, since it circumvents existing measures to control spread of both the intentionally introduced species and the “hitchhikers” that might be harbored.

Estimating the risks in introducing non-native species presents a challenge due to the complex, yet most of the time unknown biological and ecological adaptation of the

introduced species in the environment. It is one of the important factors in 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 satisfaction to the human being.

This paper describes a case involved in the introduction of non-native Suminoe oyster species into the Chesapeake Bay area where the oyster industry is under threat because of the declining population of the native eastern oyster. We will first briefly introduce the oyster industry in Chesapeake Bay and issues in the introduction of the Suminoe oyster. Then we will describe the simulation model, and data used in the simulation process. The simulation result will be presented at the end.

## **2. Background**

### **2.1. Oyster Industry in Chesapeake Bay**

Chesapeake Bay is located in the middle lower part of US East Coast, across the State of Maryland and Virginia. Eastern oyster has been an important commercial industry in the Chesapeake Bay, with a harvest exceeding 142 million pounds in the 1880s. Today, the oyster population is estimated to be less than 1% of its original abundance due to the effects of over-fishing, channel dredging, pollutants, sediments runoff, and diseases (Gottlieb and Schweighofer, 1996). However, in recent decades, the diseases MSX and Dermo have been identified as the core reasons for further decline of native oyster population. MSX, first identified in the Chesapeake Bay in 1959, is caused by the invasive protozoan parasite, *Haplosporidium nelsoni*, which was introduced to the East Coast from Asia (Burreson, Stokes and Friedman, 2000). Fisheries management efforts, use of disease-resistant strains and various oyster reef restoration programs have not been successful in restoring the oyster stock to date. The cost of restoring the native oyster population is higher than its benefit (Tarnowski, 2007). The loss of the oysters has been devastating to the oyster industry and its dependent communities.

Recently, it was considered to introduce non-productive non-native Suminoe oyster into the Chesapeake Bay area, to restore the oyster industry in the region. There is considerable controversy surrounding this proposal. Although the population of native oysters is currently at very low levels, there are ongoing attempts to restore native oyster populations and to develop disease resistant native strains. The introduction of non-native oysters could be a stop-gap measure, to be used until efforts to restore native oysters prove successful. However, the introduction represents a risk of undermining the recovery of native oysters or of displacing the other species of shellfish. Furthermore, there is a risk that the introduction of the non-native oyster into the environment may result in invasive organisms, such as the other molluscan species, worms, protozoa and seaweeds that are associated with the non-native oysters. Of particular concern are those that may cause disease in the native oyster or the other species. Indeed, it is believed that the diseases that have so devastated native oysters in the Chesapeake were introduced with non-native oysters.

One approach that has been suggested for introduction of non-native oysters is to release hatchery raised triploid Suminoe oysters into the environment to be “grown out” on designated open-water aquaculture sites. The introduction of the hatchery

farmed, triploid non-native Suminoe oyster from Asia may be a solution to this difficult problem, but it is not without risk. Triploid oysters are strains that are unable to reproduce, although there is a probability that some triploid oysters will revert to diploids (referred to as mosaics), which are capable of reproducing. Additionally, in the process of releasing triploid oysters, some number of diploids will also accidentally be introduced. Hence, introducing triploid oysters reduces the probability that the species will become invasive, but does not completely eliminate the risk.

## **2.2. Literature review**

Many existing papers have studied the biological property of Suminoe oyster and how it interacts 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 efforts 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 on 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 an agent based modeling approach is not frequently seen in the literature. One of the papers is addressing the ecological system problem in the Coastal lagoons ecosystem where the human being (like oyster farmer) is involved in the complex decision-making process (Pereira *et al*, 2004). One of the examples 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 directions.

Our focus in this research is to simulate the spatial growth of the introduced oyster in the Chesapeake Bay. Factors considered in the model include spatial distribution of oyster habitat, competition between native and non-native species, as well as the population dynamics and life history parameters of the native and non-native oysters. This enables the analysis for possible results with different management policies, including the location and size of initial stocking, Total Allowable Catch (TAC) and initial non-harvesting period.

We use Agent Based Model (ABM) to simulate 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, localized behavior of each individual agent. Because of this, ABM has been applied in the study of collective economic behavior (Tesfatsion, 2006), biology (Politopoulos, 2007), and complex social, economic, and biological system (Bobashev *et al*, 2007). For the same reason, we use ABM to analyze the result of spatial growth, diffusion and species competition by designing a virtual oyster population agent to manage the population dynamics and spatial diffusion of oyster, which will be explained next.

### **3. Specification of the Model**

This section describes the specification of the model, including the population dynamics of and the spatial movement of Oysters. The population dynamics explains the survival, growth and reproduction of oyster populations. It includes all life history parameters of oysters 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 “cell” of oyster habitat. Secondly, we examine interactions between two species of oysters, native oysters and the introduced oysters. In locations where the two stocks co-exist, they compete for food and habitat space. Also, we model stock interactions though reproduction, as discussed below.

#### **3.1. Population dynamics of Oysters**

In this section, we present the detailed population model for oysters at various life stages from spawning through survival of young-of-the-year. Our model focuses more extensively on modeling the details of the early life stages of oysters than is typical for bioeconomic models, as the mobility after these stages is low.

At present, we use identical life history parameters for the two species, 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.

*Oyster fecundity with the environmental condition*

The actual fecundity of Oyster is determined by the potential fecundity ( $F_{ij}$ ), adjusted by salinity ( $F_s$ ), fertilization success ( $F_{ij,i}$ ), and sex ratio ( $F_{qi}$ ). First, we model fecundity or the production of gametes. The number of gametes produced at time  $t$  and age class  $j$  increases with the number of adult oysters ( $N_{ij}$ ) and the size of oysters ( $L_{ij}$ ). For non-reproductive triploid oysters introduced, the reproductive potential is determined by the fraction of introduced oysters that revert from triploid to diploid ( $R_{ij}$ ) and the fraction of diploids that are accidentally introduced ( $T_{ij}$ ). The equation for fecundity is:

$$F_{ij} = 39.06 \left[ 0.000423 L_{ij}^{1.17475} \right]^{2.36} N_{ij} (R_{ij} + T_{ij}) \quad (1)$$

For native oysters and non-native oysters are stocked as reproductive diploids,  $R_{ij}=0$  and  $T_{ij}=1$ .

Salinity affects potential fecundity, although not affecting adult oysters. This suggests a spatially explicit policy to reduce risk of invasions by planting non-native oysters in areas where reproduction is limited by salinity, or in areas where non-native oysters are confined by salinity. For example, the risk of spread of the non-native species can be controlled by limiting planting to inlets that are isolated from the rest of Chesapeake Bay. If the salinity of area is unfavorable to survival of larvae, it can reduce the likelihood of geographic dispersal of non-native oysters.

The fecundity adjustment factor accounting for salinity ( $S$ ),  $F_s$ , is zero for salinity less than 8 ppt, reaches a maximum at salinity of 13.5 ppt, then declines 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

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 non-native 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 the decision within a multi-species framework, with both native and non-native 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 a hard surface to attach to, including other oysters, i.e., oysters provide their own habitat. Second, since oysters

are broadcasting spawners, fertilization success increases with concentration of oysters. We specify an equation for fertilization success as:

$$F_{ft,i} = 0.0049D_{t,i}^{0.72} \quad (2)$$

Where  $D_{t,j} = \frac{N_{t,j}(R_{t,j} + T_{t,j})}{A}$  is the density of reproductive oysters, and  $A$  is the area in square meters. Total zygote production ( $F_{total,t}$ ) is the sum over all age classes of potential production, corrected for salinity, the sex ratio ( $F_{qi}$ ), the fraction not lost to disease ( $F_d$ ) and the fertilization rate:

$$F_{total,t} = \sum_i (F_{revert_{t,i}} * F_s * F_{qi} * F_d * F_{ft,i}) \quad (3)$$

#### *Dynamic population of spat*

Spat are zygotes that have successfully metamorphosed, settled and attached to hard substrate. The total number of zygotes is the sum of the number of reproduced from the population net of the emigrated zygotes ( $E$  percent), plus the number of zygotes 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:

$$N_1 = \left( F_{total}(1 - E) + \sum_{n=1}^N \alpha_n F_{total}^n \right) P_{met} (1 - L_{mort})^{21} (1 - m_0) \quad (4)$$

where  $N_1$  is the number of individuals at age class one in one cell,  $F_{total}^n$  is the total larvae from the  $n^{th}$  cell,  $\alpha_n$  is the percentage of the larvae 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 non-native species. More discussion of this issue is contained below.

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

$$N_{t+1,j+1} = N_{tj} (1 - M_{tj})(1 - H_{tj}) \quad (5)$$

where  $H_{tj}$  is the harvest rate, 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 the sum over all age classes:

$$N_t = \sum_{j=1}^M N_{ij} \quad (6)$$

### *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 reside 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:

$$C_{it}^o = \delta \cdot C \text{ and } C_{it}^n = (1 - \delta)C \quad (7)$$

where  $\delta = \frac{W_{it}^o}{W_{it}^o + W_{it}^n}$  is the percentage of the non-native oysters in total weight of the oyster in the cell.  $C_{it}^o$  and  $C_{it}^n$  are the capacity limited of the non-native oysters and native oysters, respectively. Thus the species with higher growth rate will eventually dominate in the cell, if all other factors remain constant.

### *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 broadcasting 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 result in a hybrid that is not viable, which can adversely affect reproduction of both species. Therefore, whenever non-native species resides 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.  $p_A = \frac{N_A}{N_A + N_B}$  is the ratio of the gametes of native species in the total number of gametes 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



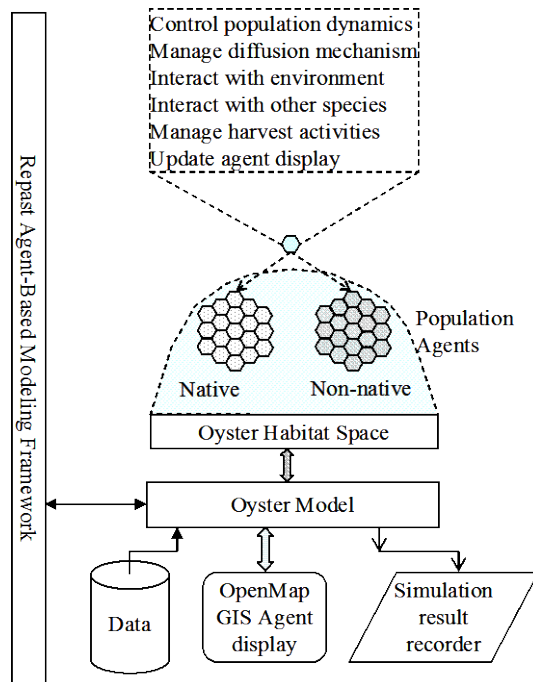
from the less numerous species, and become hybrid. Since these hybrids are not viable, they die. However,  $\frac{3}{4}$  of the gametes from the less numerous species will join with gametes from the more numerous species, producing hybrids which subsequently perish. Therefore, less numerous species is 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 invasions 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 non-native 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 reproduction 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. Furthermore, 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.

### **3.2. Simulation the Spatial Movement of Oysters**

We developed a spatial-explicit agent-based model to simulate the growth, transport and harvest of the native and non-native oyster species in Chesapeake Bay. The agent-based framework extends Recursive Porous Agent Simulation Toolkit (RePast@), which supports general simulation activities, such as graphical user interface for starting and stopping simulation, controlling time steps, changing simulation parameters, and coordinating with basic simulation functions. Research specific simulation procedures start with the oyster model, which reads in necessary data, creates oyster habitat space, displays oyster habitat and the population agents, and records 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 virtual habitat space during simulation. 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 in Figure 2. More detailed simulation results, such as the levels of oyster populations over time and space, harvest, etc. are stored for later analysis. Next we will explain the detail configuration of the habitat space and the simulation environment.

#### *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 and 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 cells if all the areas were oyster habitat. This grid configuration is changeable before each simulation to fit the needs of different research purposes. In addition, we only included cells with a hard bottom type (oyster rock, shell mud, and shell sand), as oyster can only fix and grow on a hard surface.

With this arrangement of cells, each cell is identified by its coordinates  $x$  and  $y$ , starting from the upper left corner of the simulation area (Figure 3). This specification facilitates the conversion between coordinate system and the longitude and latitude, and calculation of the distance between any two cells. Further, it facilitates the diffusion mechanism by simplify the algorithm in searching the neighboring cells at specific range measured by the number of rings.

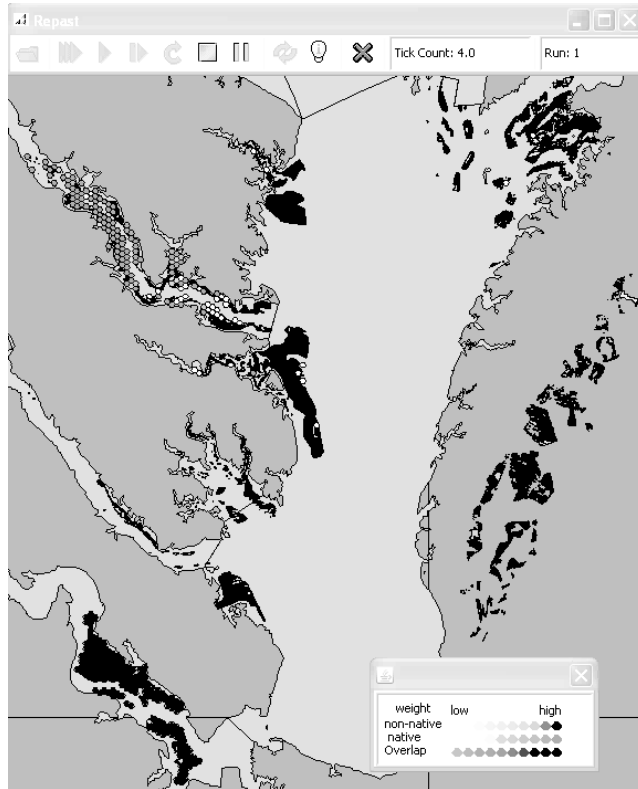


Figure 2: Illustrative output from the simulation model

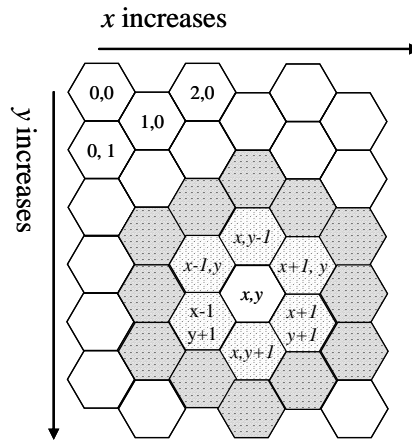


Figure 3: Illustration of the coordinate system of Oyster habitat space

Residing in each cell is one population agent that manages the population dynamics for each species in that cell. It is identified by its species name and its coordinates, has information about the life-history parameters of the species (such as age, length, growth mechanism, mortality rate, reproductive capability.). In addition, it can access the environmental information such as location, bottom type, the tributary information, and whether there is another species in the same cell.

### Spatial diffusion of oyster

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

Many 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. 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 ( $\rho_{ij}^s$ ) (Table 2) to model the zygotes movement within the same tributary ( $i=j$ ), and the movements to other tributaries ( $i \neq j$ ).

**Table 1: Oyster larval transport distance and estimated standard error and max. distance (Km)**

Tributaries	<i>C. Virginica</i>			<i>C. Ariakensis</i>		
	<i>distance</i>	<i>Std</i>	<i>Max.Dist*</i>	<i>distance</i>	<i>Std</i>	<i>Max. Dist*</i>
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 2: Oyster diffusion rate within and across tributaries**

		Destinations (V.: <i>C. Virginica</i> ; A: <i>C. Ariakensis</i> )						
		Rappa-hannock	Plana-tank	York	Virginia Mainstem	Mobjack Bay	James	
Source	Rappahan-nock	V	92.10%	2.00%	0.40%	5.30%	0.30%	
		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 Mainstem	V	8.80%	4.00%	6.10%	72.70%	6.20%	1.60%
		A	11.30%	2.10%	1.70%	62.30%	1.10%	19.30%
	Mobjack Bay	V			5.90%	1.80%	92.30%	0.03%
		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 that the transportation distance of zygotes follows a positive portion of normal distribution. Since distances cannot be negative, using  $d_i^s$  for the mean zygotes transport distance, we can find the standard deviations ( $\sigma_i^s$ ) that make the cumulative probability from origin to the mean distance ( $d_i^s$ ) equal to 25%:

$$\frac{1}{\sigma_i^s \sqrt{2\pi}} \int_0^{d_i^s} e^{-\frac{t^2}{2\sigma_i^s}} dt = 25\% \quad (8)$$

The standard deviations that satisfy above condition are shown in Table 1 (*Std* column). They are used to calculate the percentage of larvae being transported into cells at different distance. Figure 4 illustrates an example of half-normal distribution when standard deviation equal to 2. It also includes the percentage 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  $\Phi_{ik}^s$  for the cumulative probability at the  $k^{\text{th}}$  ring, if all of the cells at that ring are oyster habitat, then the percentage of larvae ( $\lambda_{ik}^s$ ) moved to any one cell at that ring is:

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

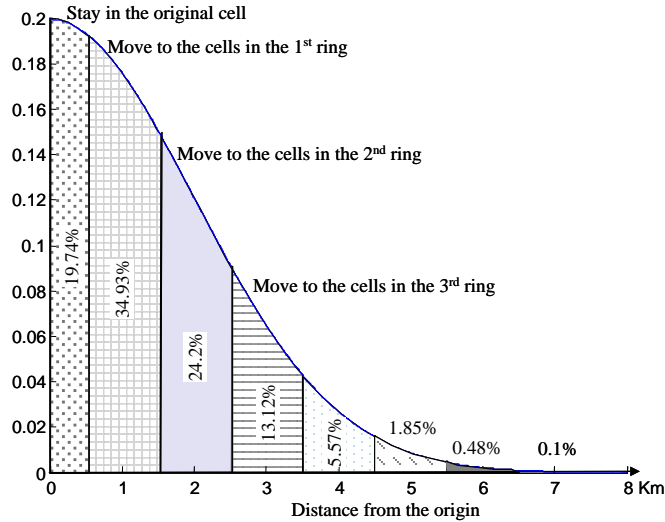


Figure 4: Percentage of zygotes transported to different rings for standard deviation=2

The diffusion to the cells not in the same tributary is simulated 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 they moved into a cell that is an oyster habitat, they can survive; otherwise, they will be parish.

In either case, the new population agent will be created if there is not a population agent in the receiving cell. Then the agent will manage the oyster population dynamics, interact with the other agents and the environment. If the oyster population in a cell becomes zero, the population agent will be removed from the system.

#### *Data used in the Agent-Based Simulation Model*

Data used in this simulation model includes the actual larvae movement statistics 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 prices for the native and non-native species (Table 3).

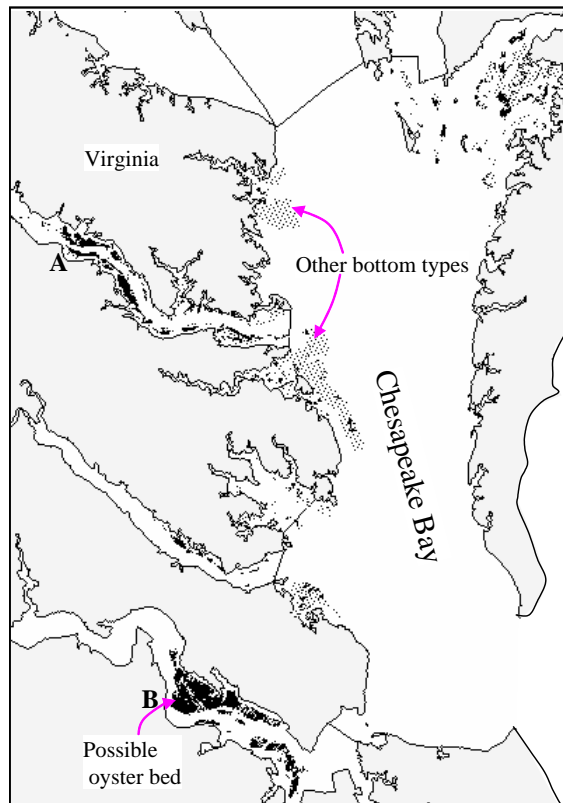


Figure 5: Oyster bed and other bottom types in Virginia part of the Chesapeake Bay (Dark spots in the figure (A, B) indicates oyster bed. Other bottom types are currently not suitable for oyster to grow, but possible oyster beds.)

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

**Table 3: 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. Source: Oyster landing price in Chesapeake Bay, 2004

Owing to lack of data for non-native Suminoe oyster, we assume that non-native oyster, *C. arkansis*, has very similar life history parameters as the native one. The only difference is their susceptibility to disease. Native species' mortality is 80% higher than the non-native one. Besides, due to the preference of the local people, the market price of native oyster is higher than the non-native one. The native oyster prices are collected *ex quay* at Chesapeake Bay area, and non-native price are assumed to be around 40% of the native ones.

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. When it is less than one, this parameter actually reduces the harvest rate for both native and non-native species. For native species, this will increase the probability of restoring native oysters. For non-native species, it increases the risk of forming a self-sustaining population.

#### 4. SIMULATION RESULT

The benefit/cost analysis without introducing non-native species can be inferred from the recent report by Tarnowski (2007), which compared the cost of restoring native oysters with its benefits. This paper focuses on the possible problems for introducing non-native species. The concern for introducing non-native species includes whether it will become a self-sustaining species, drive out, and replace the native oysters in the Chesapeake Bay. The risk for it to form a self-sustaining population depends on many factors. Our model will analyze how it changes with the initial stocking place and size, and the impact of the species competition with native species. The simulation model will provide a dynamic, visual display of the simulation result about spatial oyster population, as illustrated in Figure 2. Due to data availability in the bottom types, we only simulate the area in the Virginia part of the Chesapeake Bay.

##### 4.1. Simulation scenarios

We devise several scenarios to demonstrate the simulation results for different locations and initial quantities of the native and non-native species, with or without harvest activities. To show the difference with 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.

#### **4.2. Scenarios with single species**

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

##### *Scenario 1: Non-native Triploids at James River*

In this scenario, the initial stocking population is 150 million spats at the one oyster cell in James River, which equals to 230/m<sup>2</sup> in spat density. In the initial 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 habitats within the same tributary in the first 5 years. From the 10<sup>th</sup> year, it spreads over other tributaries. However, due to limited density, oyster population starts to decrease at the 20<sup>th</sup> year. At the 45<sup>th</sup> year, only the oyster bed in James River still has some oyster left. At the year 48, all oysters 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 non-native oyster will not be sustainable in the Chesapeake Bay. It will disappear even without harvest activity.

##### *Scenario 2: Non-native Triploids in Rappahannock River*

With the same amount of initial spat, the simulation result indicates that the non-native species will 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 can spread easily; hence have high probability to sustain.

The difference between these two scenarios can be attributed 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. James River is at the downstream of the water flow, its larvae diffusion is not as efficient as that in Rappahannock River. The diffusion rates among the tributaries in the bay area are in Table 2.

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

With the same initial spat population and the place of stocking for non-native oyster as in Scenario 2, the simulation result shows that the species will not be self-sustaining if harvests are allowed after 10 years. The TAC is 20% of the oysters in the total simulation area, and the certainty of catch is 95%, as the oyster is fixed at the oyster bed. Thus 5% of the legal size oysters will be available for reproduction in each cell.

The population dynamics in the initial cell of oyster stocking are presented in figure 6. From the graph, we can see that the initial growth period in scenario 1 is just not long enough to sustain future growth. The difference between scenario 2 and 3 is the harvest after year 10. Comparing these two scenarios, we can conclude that it is possible to



introduce a non-native species into the Bay area for economic benefits without the risk of having an invasive species.

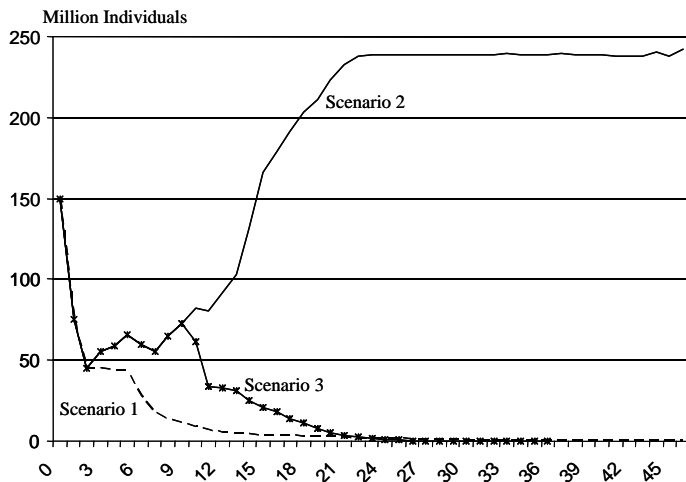


Figure 6: Simulated Population Dynamics at the initial cell for scenarios 1 to 3

### 4.3. Scenarios with competing species

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

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

Although the number of initial spat increased to 200 million, the oyster population still cannot support itself if we allow 20% TAC from the 10<sup>th</sup> year of the simulation. Although native specie has better location, it still cannot compete with the non-native species, because its high market price, and high mortality rate. Therefore, the non-native species will begin to spread over in the Rappahannock River at 20<sup>th</sup> 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 native species in the whole simulation area is shown in figure 7. At the very beginning, the number of native oysters is larger than the non-native one, because only a very small percent of the introduced species is reproductive. However, once introduced oysters are generated from the reverted triploids, they all become reproductive, so it will have higher growth rate. It also shows that the harvest activity after the 10<sup>th</sup> 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.

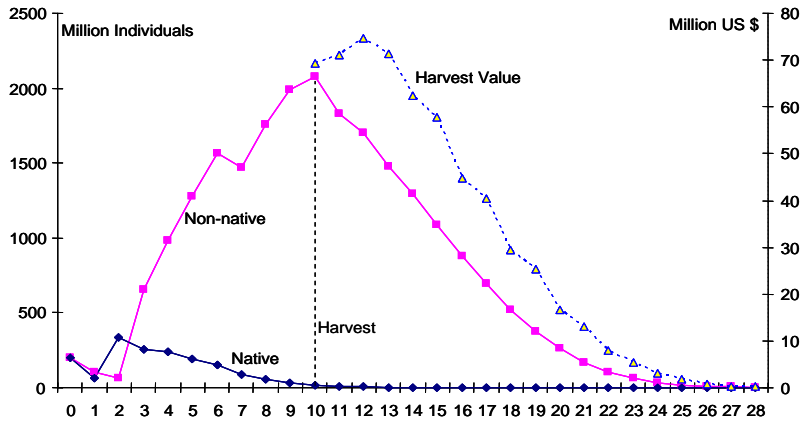


Figure 7: Simulated Population Dynamics for Scenario 4 for the Whole Simulation Area

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 20% TAC, 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 include: clogging the waterway, eradicating the native oyster species, competing with other living organisms for space and food, and changing 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.

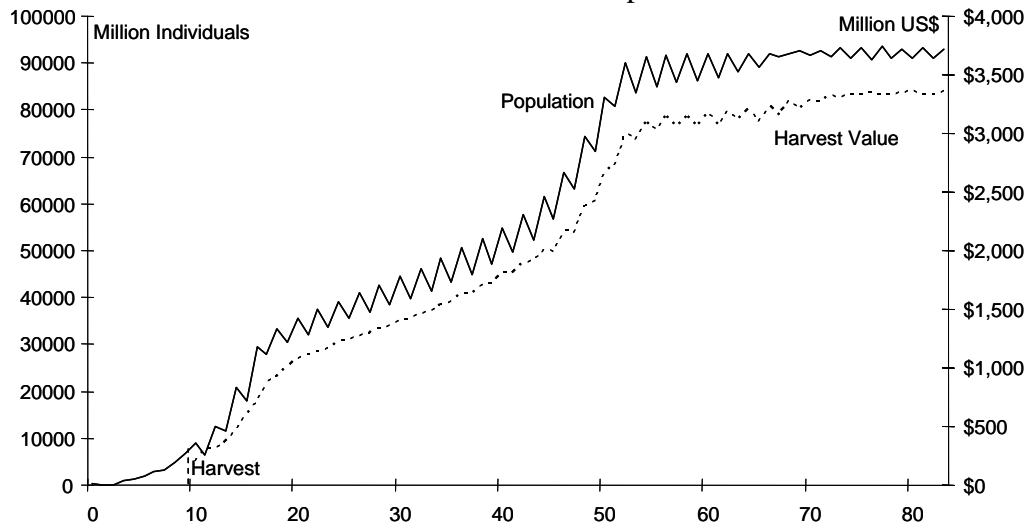


Figure 8: Simulated population growth and harvest for scenario 5

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 species and two species), it reveals that non-native species will be more easily spread and fill in all the oyster beds when it is stocked in the Rappahannock River. In scenario 2, the non-native oyster will spread all over the oyster bed in the simulation 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 shows that the

oyster population will not last forever with harvests. 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 becomes perpetual even with 20% TAC, which illustrate higher catching rate or lower initial stocking level should be adopted, to minimize 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 a 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 is 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.

## **5. Conclusion**

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 careful when 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 implies that the simulation without consider the distribution of the oyster bed and spatial interaction may underestimate the risks for the non-native species to become invasive.

There are a couple of limitations 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, and then to select a location and level of non-native species to minimize its impact on the native species. Second, the simulation model only included the Virginia part of the Chesapeake Bay, since the bottom type data are not available in upper part of the bay.

Nonetheless, this simulation model revealed one important issue 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, and at the same time the local ecological environment can be preserved.

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