

OysterFutures Model Description

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Introduction

The purpose of OysterFutures model is simulate potential outcomes of potential management and restoration options for oysters in the Choptank River complex in Maryland, U.S.A. (Figure 1). The model was collaboratively developed with the OysterFutures stakeholder workgroup. The model is written in AD Model Builder (<https://www.admb-project.org/>), and the model files are oyster_sim_model2.tpl (the model code), and two data files, oyster_sim_model.dat and options.dat.

The operating model describes the population and fishery dynamics. The model tracks age classes 0-14+ (plus group is an aggregate age class for age 5 and older), and has length classes 10 mm-180 mm+ (the plus group is individuals that size and larger) with a 5 mm bin width. The model operates for 26 years, with two 6-month time steps annual, with the initial values set in year 0 at the most recent estimates of abundance from Damiano and Wilberg (2019). The oyster abundance on each reef was downscaled from Damiano and Wilberg (2019) so that polygons with higher habitat quality and larger area got more oysters.

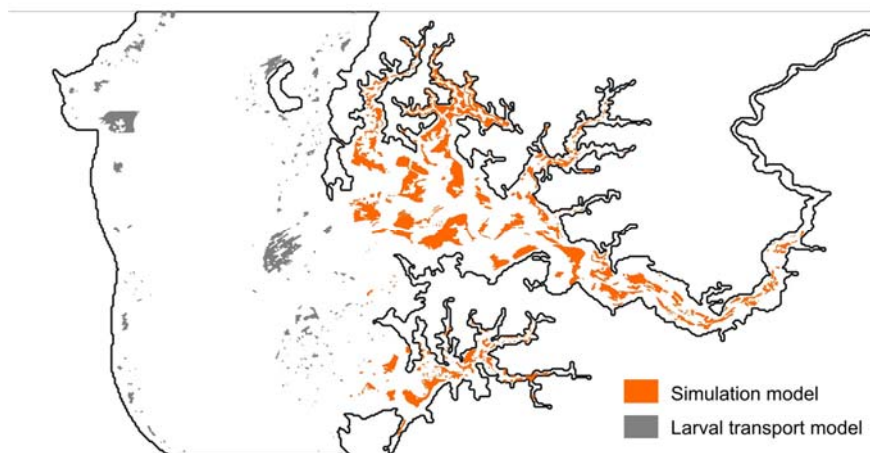


Figure 1. Map of polygons included in the OysterFutures model (orange). Polygons were based on the NOAA sonar mapping ArcGIS base layers. We included additional polygons in the Little Choptank River in areas that were not part of the sonar survey based on input from our workgroup about the size and location of oyster bottom. Each polygon was assigned a starting habitat value based on the SONAR map. Because initial models created too many oyster in the lower Choptank River, the amount of habitat in this region was downgraded. The hypothesized mechanism is that habitat quality is lower in that region due to sedimentation and hypoxia.

Biological model

Egg production

Egg production on a bar was the sum of the product abundance, fecundity-at-length, sex ratio-at-length, and, density dependent fertilization,

$$E_y = \sum_{l=l_{min}}^{l_{max}} N_{b,y,l} \times f_l \times r_l \times z_b$$

where b is an index of each of the 1,132 oyster bars, l is oyster length in 5 mm bins from 10-180 mm, $N_{b,y,l}$ is the abundance of oysters on bar b in year y in size class l , f_l is the number of eggs produced by a female oyster at length l , r_l is the ratio of female to male oysters in size class l , and z_b is the fertilization rate as a function oyster density on bar b .

Female fecundity at length (f_L) was calculated as

$$f_L = 0.008 \times L^{2.41}$$

where L is oyster length in mm (from Choi et al. 1992).

Sex ratio (i.e., percentage of the population that is female) at length (r_L) was calculated as

$$r_L = \begin{cases} -0.0645 + L \times 0.0066, & \text{if } L < 112 \\ 0.6724, & \text{if } L \geq 112 \end{cases}$$

where L is oyster length in mm.

Fertilization rate as a function of oyster density on a given bar (z_b) was calculated as

$$z_b = 0.01 \times 10^{(0.72 \times \log_{10}(D_{b,y}) + 0.49)}$$

where $D_{b,y}$ is the density of oysters on bar b in year y .

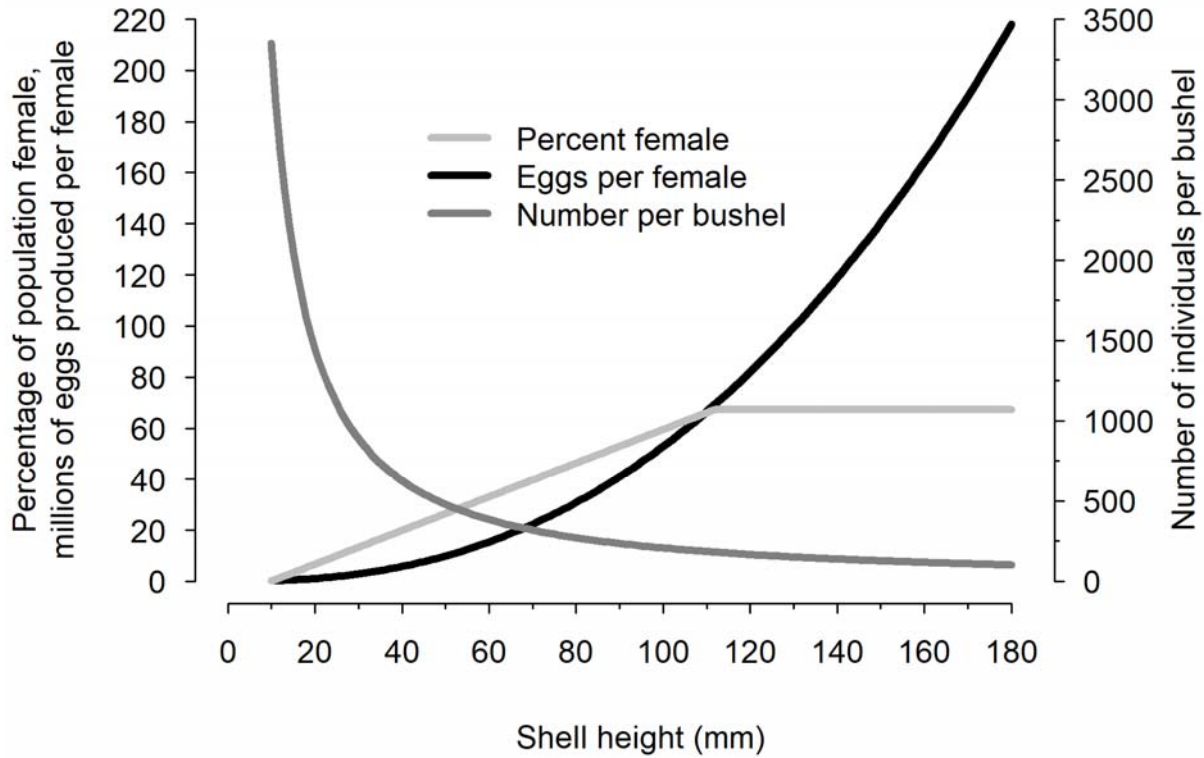


Figure 2. Percent female, female fecundity, and number of oysters per bushel as functions of shell height.

Recruitment

Recruitment in year y on bar b was modeled as a function of egg production, larval transport, larval and post settlement survival, and the number of planted oysters as

$$R_{y,b} = \sum_{bars} E_y T_b S e^{((-DM_{larval}) - \varepsilon_{M_{larval}})} M_{postsettlement} + N_{plant_{y,b}}$$

Where E_y is the total number of eggs produced on all bars in year y , T_b is the probability of transport of larvae to bar b from larvae produced at all other bars, S is the probability of settlement once a larvae reaches a given bar, M_{larval} is the daily instantaneous larval mortality over the larval period (D), $\varepsilon_{M_{larval}}$ is random error in daily larval mortality, $M_{postsettlement}$ is post settlement mortality, and $N_{plant_{y,b}}$ is the number of spat planted in year y on bar b .

The random error in daily larval mortality was calculated as

$$\varepsilon_{M_{larval}} = N(0, \sigma_{M_{larval}})$$

where $N(0, \sigma_{M_{larval}})$ is a normally distributed random variable with mean zero and standard deviation and an assumed standard deviation of daily larval mortality. Larval transport was estimated using a larval transport model and was included as proportion of propagules produced on each bar that ended up on each other bar.

If recruitment was greater than the carrying capacity for spat on a given bar b in year y ($R_{max,y,b}$) then recruitment was set to the carrying capacity, which was calculated as

$$R_{max,y,b} = H_{y,b} \times A_b \times m_{spat} \times F_{surv} \times \varepsilon_R$$

where $H_{y,b}$ is the volume of habitat, A_b is the area of a given bar, m_{spat} is the proportional relationship between the volume of habitat and maximum spat density, F_{surv} is the increase in spat survival when planted on fresh shell, and random error in recruitment calculated as

$$\varepsilon_R = N(0, 1) \times \sigma_{Dspat_{max}} + \frac{\sigma_{Dspat_{max}}^2}{2}$$

Change in volume of habitat (H) over time was calculated as

$$H_{(y+1),b} = H_{y,b}(1 - b) + D_{y,b} (H_{growth} + \varepsilon_{H_{growth}}) + S_{plant,y,b}$$

where b is the fraction of habitat volume lost each year due to all sources (e.g., sedimentation, dissolution), $D_{y,b}$ is the density of oysters in year y on bar b , H_{growth} is the proportional relationship between shell produced each year and density of oysters per m^2 , S_{plant} is the volume of shell planted on bar b in year y , and $\varepsilon_{H_{growth}}$ is the random error in habitat growth calculated as

$$\varepsilon_{H_{growth}} = N(0, \sigma_{H_{growth}})$$

where $N(0, \sigma_{H_{growth}})$ is a normally distributed random variable with mean zero and standard deviation of $\sigma_{H_{growth}}$ for habitat growth. If habitat was calculated to be < 0 then it was set to zero. Initial habitat on each bar was based on sonar habitat maps.

Age structured population dynamics of oysters after fishery removals included adjustments for natural mortality,

$$N_{(y+1),b,a} = N_{y,b,a} e^{M_{y,b,(a-1)}}$$

where $M_{y,b,a}$ is a year, bar, and age specific natural mortality rate that was calculated as

$$M_{y,b,a} = \bar{M}_{r,a} \times e^{(\varepsilon_{M_{y,b,a}} + \varepsilon_{M_y})}$$

where $\bar{M}_{r,a}$ is the mean natural mortality rate in region r and year y , $\varepsilon_{M_{y,b,a}}$ is a year, bar, and age specific random error calculated as

$$\varepsilon_{M_{y,b,a}} = N(0, \sigma_{M_{y,b}})$$

where, $N(0, \sigma_{M_{y,b}})$ is a normally distributed random variable with mean zero and standard deviation of $\sigma_{M_{y,b}}$, and ε_{M_y} is a first order autoregressive, year-specific, random error for natural mortality calculated as

$$\varepsilon_{M_y} = \rho_{M_y} N(0, \sigma_{M_y})_{y-1} + N(0, \sigma_{M_y})_y$$

where ρ_{M_y} is the autocorrelation between natural mortality in adjacent years, $N(0, \sigma_{M_y})$ is a normally distributed random variable with mean zero and standard deviation σ_{M_y} .

Mean length (\bar{L}_a) at age (a) followed a von Bertalanffy growth curve,

$$\bar{L}_a = L_\infty (1 - e^{-K(a-t_0)})$$

The parameters of the von Bertalanffy growth curve, mean L_∞ (asymptotic maximum length), K (growth coefficient), and t_0 (theoretical age at length zero) were estimated from known age oysters from plantings that were monitored for one to 10 years ($L_\infty=109.1$ mm, $K = 0.58$, $t_0 = -0.397$). The coefficient of variation (CV) in size at age was assumed to be 14.8% based on the data in Liddell (2008).

The distribution of length at age followed a normal distribution about mean length-at-age,

$$P(l | a) = \Phi(l | L_a, \sigma_a^2) - \Phi(l - 1 | L_a, \sigma_a^2)$$

The amount of nitrogen (N_{meat}) in the oyster meats was calculated as

$$N_{meat} = 0.000003 \times L^{1.837}$$

where Length (L) here is the midpoint of the length bin.

Nitrate removal associated with oyster reefs was modeled as a function of oyster biomass on each reef,

$$\begin{aligned} \text{Nitrate Removal} &= \text{days} \times (a + b \times DW) \\ a &= 7474.6 + 2046.1 \times \varepsilon \\ b &= 15.98 + 5.44 \times \varepsilon \end{aligned}$$

where $\text{days} = 244$ and ε is normally distributed random variable. The dry weight (DW) of oysters length followed a power relationship of shell height (L)

$$\begin{aligned} DW_L &= a \times L^b \times e^{(0.5 \times 0.21)} \\ a &= -10.23 + 0.217 \times \varepsilon \\ b &= 2.29 + 0.0486 \times \varepsilon \end{aligned}$$

Fishery model

Bushels per oyster was calculated for each shell height bin, where L is the midpoint of the length bin

$$\text{Bushels per oyster} = \frac{1}{54075 \times L^{-1.208}}$$

Selectivity

Selectivity at length for compliant trips was modeled as a double logistic curve

$$S_L = \left(\frac{1}{1 + e^{(-b_1(L-b_2))}} \right) \left(1 - \frac{1}{1 + e^{(-b_3(L-b_4))}} \right)$$

where b_1 is the slope of the increasing limb, b_2 is the length with selectivity of 0.5 for the ascending limb, b_3 was the slope of the descending limb, and b_4 was the length with a selectivity of 0.5 for the descending limb.

Selectivity at length for non-compliant trips was modeled by a single logistic curve

$$S_L = \frac{1}{1 + e^{(-b_5(L-b_6))}}$$

where b_5 is the slope of the increasing limb and b_6 is the length with selectivity of 0.5 for the ascending limb.

Calculating harvest

The model included five fishing fleets (hand tong, power dredge, sail dredge, diver, and patent tong). Fishery harvest was modeled using a simplified approach that assumed that all oysters that were profitable to harvest would be harvested accounting for fixed and variable costs of fishing for each fleet,

$$\text{Cost}_{b,f} = D(2C_{\text{mile}}) + C_{\text{fixed}}$$

where D is the distance to the bar from the nearest port, C_{mile} is the cost per mile for one fishing trip, and C_{fixed} is a fixed cost per trip for each fleet. The cost per mile was multiplied by two to account for the round trip to and from the oyster bar.

The CPUE needed to obtain zero profit (Critical CPUE) on a particular bar for each fleet was calculated as,

$$\text{Critical CPUE}_{b,f} = \text{Cost}_{b,f} / BP / H$$

where BP is mean price per bushel received by commercial harvesters and H is mean number of hours for a single harvesting trip.

The harvestable density of oysters was calculated as the product of selectivity and abundance-at-length,

$$HD_{y,b} = S_L N_{y,b,L}$$

where harvestable density on a particular bar in a given year ($HD_{y,d}$).

The maximum density needed to obtain zero profit (Critical Density) was calculated as

$$CD_{b,f} = \frac{\text{Critical CPUE}_{b,f}}{q_f}$$

where critical density is a function of critical CPUE in a given year for a given bar ($\text{Critical CPUE}_{b,f}$) and catchability of each fleet q_f . The q was estimated by finding a value for the parameter that allowed the model to reproduce harvest patterns in 2015 and 2016.

Options for Management

The model included a number of potential management options that could be set up in the options.dat file including sanctuaries, shell/substrate addition, spat on shell addition, rotational harvest, and enforcement/compliance.

Performance measures

The model produced a range of performance measures including abundance, harvest, shell, nitrogen removal, value of harvest, and value of nitrogen removal (Table 1).

Table 1.

Performance metric	Units
Adult oyster abundance	
Abundance of spat	
Harvest	1,000's bushels
Revenue	1,000s of dollars
Licenses	
Full time harvesters	
Habitat	(Liters/sq. m)
N_2 removed	
Social value of N_2 removed	
N_2 removed from harvest (in meat)	
