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- ¹ **Running head:** Age- and size-structured oyster IPM
- ² The demographic consequences of growing older and bigger in oyster populations
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13 ABSTRACT

14 Structured population models, particularly size- or age-structured, have a long history of informing conservation and natural resource management. While size is often easier to measure than age, and is the focus of many management strategies, age-structure can have important ¹⁷ effects on population dynamics that are not captured in size-only models. However, relatively few studies have included the simultaneous effects of both age- and size-structure. To better understand how population structure, particularly that of age and size, impacts restoration and management decisions, we developed and compared a size-structured integral projection model (IPM) and an age- and size-structured IPM, using a population of *Crassostrea gigas* oysters in the northeastern Pacific Ocean. We analyzed sensitivity of model results across values of local retention that give populations decreasing in size to populations increasing in size. We found that age- and size-structured models yielded the best fit to the demographic data and provided more reliable results about long-term demography. Elasticity analysis showed that population growth ²⁶ rate was most sensitive to changes in the survival of both large (> 175 mm shell length) and small $27 \leq C \leq 75$ mm shell length) oysters, indicating that a maximum size limit, in addition to a minimum size limit, could be an effective strategy for maintaining a sustainable population. In contrast, the purely size-structured model did not detect the importance of large individuals. Finally, patterns in stable age and stable size distributions differed between populations decreasing in size due to ³¹ limited local retention, and populations increasing in size due to high local retention. These patterns can be used to determine population status and restoration success. The methodology described here provides general insight into the necessity of including both age- and ³⁴ size-structure into modeling frameworks when using population models to inform restoration and management decisions. ans volses and an anomia resource management. While
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KEYWORDS

- integral projection model, *Crassostrea gigas*, age-structure, size-structure, demographic
- modeling, oyster demography, size-frequency distribution

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INTRODUCTION

 Structured population models have a long history of informing conservation and natural resource management (e.g. Crouse et al., 1987). This is due to the often direct link between state-specific transition rates and management actions that can allow researchers to evaluate the relative efficacy of alternative management choices (Beissinger and Westphal, 1998). These structured population models take various forms, and can include discretely structured traits, such as age, stage, or gender, and continuously structured traits, such as size.

 Here, we focus on the role of both age- and size-structure. For many organisms, it is often easier ⁴⁷ and less destructive to measure the size of an individual, rather than age, and numerous 48 management decisions are most directly tied to size, such as fishery catch restrictions (Punt et al., 2013). Additionally, for organisms that routinely experience fragmentation or breakage, size-structured models provide a better descriptor of demographic processes (Hughes, 1984; Hughes and Connell, 1987). Conversely, the dynamics of fluctuating populations are often best captured by including age-structure in population models (Bjornstad et al., 2004; Botsford et al., 2014), while the effectiveness of metabolic and cellular processes often decline with age, independent of size (Ivanina et al., 2008; Abele et al., 2009). Notwithstanding these distinctions, in many cases age and size are used interchangeably, with one variable serving as a predictor for the other (e.g. von Bertalanffy growth models). Entrancesse Crosso et an, 1997). This is doet to allo the other uniformation rafes and management enforces (Beissinger and Westphal, 199
Is take various forms, and can include discretely structured transformative managemen

 Far less common are studies that include both age- and size-structure simultaneously. Although age and size may be correlated, there are often independent and interactive effects of age and size. For example, Hughes and Connell (1987) and Babcock (1991) both found that age- and size-structure were necessary to model the demography of several coral species. The relative importance of age-dependence and size-dependence on demographic rates has been shown to

 vary based on the species under study, how far the population is from its steady state conditions, ⁶³ and the degree of correlation between size and age (see Hughes and Connell (1987), Law and ⁶⁴ Edley (1990), and references therein).

 In many taxonomic groups, such as mollusks, crustaceans and fish, the relationship between age and size is highly variable, whereby individuals of a given age can vary greatly in size and vice versa (Lorenzen, 2016). One such globally-distributed group that exhibits substantial variation in the relationship between age and size is the Ostreidae, which includes oysters in the genera *Ostrea*, *Crassostrea* and *Saccostrea*. In these genera, survival, growth, and fecundity are both age- and size-dependent. For instance, larger females have an exponentially greater gonadal mass and egg production than smaller females, yet they can be of the same age, depending on environmental factors such as temperature (Choi et al., 1993; Kennedy et al., 1996; Cardoso et al., 2007, 2013). Mortality is also age- and size-dependent, with larger, older oysters more susceptible to diseases, whereas juveniles are much more vulnerable to predation (Kennedy et al., 1996; Anderson and Connell, 1999; Carnegie and Burreson, 2011). Age-dependent changes in oxidative stress markers and cellular defense proteins can influence the effectiveness of metabolic processes (ultimately leading to senescence and death), as well as the ability of the organism to deal with environmental stressors (Ivanina et al., 2008). Finally, in populations of oysters located τ ⁹ in regions contaminated with heavy metals, concentrations of zinc, copper, and cadmium vary with age (Mackay et al., 1975), and long-term exposure to these metals can influence oyster 81 metabolism and responses to environmental stressors (Luo et al., 2014). Consequently, one must 82 model both size and age to describe population dynamics accurately. ny taxonomic groups, such as mollusks, crustaceans and fish
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83 In addition, oysters provide a good case study due to the current focus on oyster restoration and management. Oyster reefs have deteriorated globally due to coastal development, overfishing, and

 pollution (Airoldi and Beck, 2007; Beck et al., 2011). Specifically, native oyster species, which ⁸⁶ are dominant ecosystem engineers that provide a suite of ecosystem services (Coen et al., 2007; 87 Grabowski et al., 2012), have been reduced to less than 15% of their historical extent along the 88 Pacific and Atlantic coasts of the United States (Rothschild et al., 1994; Beck et al., 2011; Zu Ermgassen et al., 2012). Major efforts are underway to restore and protect native and naturalized oyster species (Laing et al., 2006; Beck et al., 2011), and there have been successful restoration efforts in isolated cases with the eastern oyster along the mid-Atlantic coast and the Gulf of Mexico (Taylor and Bushek, 2008; Powers et al., 2009; Schulte et al., 2009; Puckett and Eggleston, 2012; Lipcius et al., 2015). Though these successes are promising, the scientific 94 community has yet to reach agreement on the most effective means for achieving such success (Kennedy et al., 2011; but see Baggett et al. (2014) and Lipcius et al. (2015)).

 Here, we use the Pacific oyster, *Crassostrea gigas*, as a model species to investigate population 97 structure. Specifically, we develop an integral projection model (IPM) that allows for the simultaneous inclusion of both discrete age structure and continuous size-structure (Easterling et al., 2000; Ellner and Rees, 2006; Coulson, 2012; Rees et al., 2014; Merow et al., 2014). We use this model to address several important questions. First, we assess whether predictions of ¹⁰¹ long-term demography vary depending upon whether only size, or both age and size, are included as structuring variables. Second, while IPMs have most often been applied to size-structured terrestrial populations in which the size of an organism can both increase (e.g. through growth) or decrease (e.g. through starvation), the size of an oyster is often measured along the hard shell structure, which usually does not decrease in size. We fit the IPM with a growth kernel that only allows for positive growth, and investigate the consequences of describing growth in this way. Finally, we explore how the long-term size-distributions, recently proposed as a means of c and **Atlantic** coasts of the United States (Rothschild et al., meassen et al., 2012). Major efforts are underway to restore dized overster species (Laing et al., 2006; Beck et al., 2011), a ation efforts in isolated case

¹⁰⁸ monitoring restoration success (Baggett et al., 2014, 2015), vary depending upon whether ¹⁰⁹ populations are declining, stable, or increasing in size.

110 METHODS ¹¹¹ *Model*

112 Age- and size-based IPMs describe a population where $n_a(x,t)dx$ is the number of individuals 113 aged *a* in the size range $[x, x + dx]$ at time *t*. We consider $n_a(t)$ to include both male and female ¹¹⁴ oysters. Though there is some evidence that growth rate differs between males and females ¹¹⁵ (Baghurst and Mitchell, 2002), for simplicity we consider the two sexes to have equal growth ¹¹⁶ rates. Individuals transition between sizes and ages according to an age-specific projection kernel $K_a(y, x)$, which describes the infinitesimal contribution of size *x* individuals of age *a* to size *y* 118 individuals of age $a+1$. The projection kernel K_a is here expressed as ¹¹⁹ $K_a(y,x) = S_a(x)[G_a(y,x) + F_a(y,x)]$, where $S_a(x)$ is the annual survival probability of individuals 120 of size *x* and age *a*, $G_a(y, x)dy$ is the infinitesimal probability of surviving individuals of size *x* 121 and age *a* growing to size *y* and age $a + 1$, and $F_a(y, x)dy$ is the expected number of offspring of 122 size *y* produced by surviving individuals of size *x* and age *a*. In the most general form, the Model

and size-based IPMs describe a population where $n_a(x,t)dx$

in the size range $[x, x + dx]$ at time t. We consider $n_a(t)$ to is.

Though there is some evidence that growth rate differs be

urst and Mitchell, 2002), for si

¹²³ dynamics of the population are expressed as

$$
n_1(y, t+1) = \sum_{a=2}^{A} \int_0^L S_a(x) F_a(y, x) n_a(x, t) dx,
$$
\n(1)

$$
n_{a+1}(y,t+1) = \int_0^L S_a(x)G_a(y,x)n_a(x,t)dx,
$$
\n(2)

 124 where *L* is the maximum size of an individual, and *A* is the maximum age of an individual. By ¹²⁵ setting a maximum size for individuals, there is the possibility that large individuals can grow past ¹²⁶ this upper limit and be "evicted" from the population (Williams et al., 2012). This phenomenon

127 artificially increases the mortality of the larger size classes and lowers the population growth rate. 128 To avoid this issue, a discrete size class is added to the model for individuals of size $x > L$. The ¹²⁹ kernels for survival and fecundity of this discrete class are set equal to kernels for individuals of 130 size $x = L$ (Easterling et al., 2000; Williams et al., 2012).

 In Oregon, *C. gigas* populations reproduce once during the summer months (Lannan et al., 1980). 132 Thus, we modeled the census as occurring immediately following summer recruitment (Figure 1). ¹³³ We assumed that oysters must first survive and grow throughout the majority of the year prior to reproduction. Following reproduction, larvae experience growth and mortality prior to the census. Here, we consider a single, closed population with no external recruitment; all new oyster recruits are a result of local retention of larvae.

137 To model the fecundity kernel conditioned on survival, $F_a(y, x)$, we consider oysters that first survive and grow from size x to their final end-of-year size x' before reproducing. During reproduction, the total number of larvae produced for a given age class, $f_a(x')$, is equal to the ¹⁴⁰ number of eggs produced that survive and successfully establish. We estimated this function as a 141 product of three terms 1) the proportion of size x individuals in the population that are female, $v(x)$, 2) the total number of eggs produced, $h(x')$, which we assume is dependent upon the size, ¹⁴³ but not the age, of the parent, and 3) the fraction of eggs produced that survive and join the census 144 population, *p* (i.e., local retention). Thus, $f_a(x') = v(x)h(x')p$. The sizes of the newly recruited 145 oysters are assumed to be normally distributed with density $z(y)$. Thus, the overall fecundity ¹⁴⁶ kernel can be expressed as = *L* (Easterling et al., 2000; Williams et al., 2012).

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sumediately following reproduction, larvae exp

$$
F_a(y, x) = z(y) \int_0^L [G_a(x', x) f_a(x')] dx'.
$$
 (3)

Data

 We estimated kernels for survival, growth, and fecundity using data collected from *C. gigas* populations in the Pacific Northwest (Stick, 2011). A full description of the rearing procedure is given in Stick (2011), which we summarize as follows. Juvenile oysters were bred from adults at the Molluscan Broodstock Program (MBP) hatchery (Hatfield Marine Science Center, Newport OR). Adults were crossed to maximize phenotypic and genetic variance. Juveniles were transferred at 80 days of age to growout units held under flow-through raceway conditions at the MBP facility for an additional 50-75 days. When oysters reached approximately 30 mm in length, at an average age of 140 days and weight of 2.4 g, they were randomly assigned in pairs to each of 120 pearl oyster panel net pockets and planted subtidally at two locations in Yaquina Bay, OR. Shell length (measured from anterior hinge to posterior shell margin) and survival were recorded for a total of 1,440 oysters in October 2005, May 2006, February 2007, and January 2008. Although the data were not collected in exact one-year intervals, we assumed that census occurred at approximately the same point in the oyster life cycle each year. Additional data on the relationship between dry tissue weight, size, and number of eggs was obtained from Kang et al. (2003) and Ren et al. (2003). As oysters are protandric hermaphrodites, with most individuals 163 born male and becoming female later in life, we obtained size-specific sex ratios from Buroker (1983). in Sirek. 2011), The same about the summarize as follows. Juvenile of olluscan Broodstock Program (MBP) hatchery (Hatfield Ma
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Statistical fitting

 *Growth kernel.—*Past applications of IPMs typically estimate the growth kernel for a given age, *a*, 167 by fitting a linear regression of size at time $t + 1$ against size at time t , assuming that for each size *x* the probability distribution of growth into size *y* is normally distributed (Easterling et al., 2000). However, as the size of an oyster (measured as shell length) will not decrease in size between

¹⁷⁰ years, regardless of whether the nutrient requirements of the oyster are met, we instead estimated, 171 for a given age, the log change in size from time *t* to $t + 1$ using the size at time *t*. This ¹⁷² methodology ensures that growth is positive, and is thus more realistic for our application. We 173 compared the fit of this kernel to the traditional normally distributed growth kernel using AICc 174 criteria (Anderson, 2007). For both model types, we tested whether including only size, only age, ¹⁷⁵ both age and size, or the interaction between age and size led to a better fit. Since we are ¹⁷⁶ evaluating the use of IPMs, not matrix models, and since most oyster management decisions are ₁₇₇ based on size, rather than age, we did not evaluate the results of an age-only model. For 178 simplicity, all models assume that variance is constant across all ages and sizes.

¹⁷⁹ *Survival kernel.*—For established individuals, we fit the survival kernel, $S_a(x)$, using logistic 180 regression of survival between years. As with the growth kernel, we compared models that ¹⁸¹ included only size, only age, both age and size, and the interaction between age and size using 182 AICc criteria, but did not include an age-only model in model analysis.

Fecundity kernel.—We estimated the total number of eggs produced, $h(x')$, using a linear regression of log egg number against parent size at time *t*, using the pre-spawning relationship between shell length and dry tissue weight obtained from Ren et al. (2003), and the relationship between dry tissue weight and total number of eggs obtained from Kang et al. (2003). Individual oysters are likely to switch from male to female as they grow older and larger. We thus estimated 188 the proportion of female oysters at each size, $v(x)$, by fitting a linear regression using data 189 obtained from Buroker (1983). Local retention (p) , the fraction of eggs that survive from fertilization to the successful settlement and establishment of the larvae, is composed of fertilization success, survival during the pelagic larval stage, the probability of larvae encountering suitable settlement substrate, and the probability of successful metamorphosis. In ared the fit of this kernel to the traditional normally distribut
a (Anderson, 2007). For both model types, we tested whethe
ge and size, or the interaction between age and size led to a
ting the use of IPMs, not matrix m

 marine environments, these values are notoriously difficult to estimate (Cowen and Sponaugle, 2009). Past structured models of marine invertebrates have approximated these values by applying relationships obtained from other species (e.g., Levitan (1991)'s estimate of density-dependent fertilization success for urchins is widely applied), fitting models to data and selecting recruitment values that provide the best fit, or examining patterns under varying assumptions of recruit origination (e.g. Gotelli, 1991; Dudas et al., 2007; Yau et al., 2014; Puckett and Eggleston, 2016). 199 Here, we explored population dynamics using a range of values for p , chosen such that 1) the amount of local retention was insufficient to sustain the population, causing the population to decrease in size; 2) the amount of local retention was sufficient for population persistence, but not $_{202}$ growth; or $\overline{3}$) the amount of local retention was sufficient to sustain the population, causing the population to increase in size. Finally, we estimated the distribution of larval sizes at the time of census, $z(y)$, using a normal distribution. We obtained this distribution using the mean and 205 standard deviation of oyster sizes at the first time step of collected data (age ≈ 150 days). zation success for urchins is widely applied), fitting models that provide the best fit, or examining patterns under varyin ation (e.g. Gotelli, 1991; Dudas et al., 2007; Yau et al., 2014 we explored population dynamics u

Model analysis

₂₀₇ Evaluating the IPM, we calculated the long-term population growth rate, reproductive values, and 208 stable age and size distributions. The dominant eigenvalue of the integral operator, λ , describes 209 the long-term population growth rate. If $\lambda < 1$ the population is decreasing, while if $\lambda > 1$ the population is increasing. The dominant left and right normalized eigenfunctions describe the reproductive values and the stable distributions across all sizes and ages, respectively. Reproductive values give an indication of the lifetime contribution of an individual in a particular age and size class to the population size in future generations, and stable distributions give the long-term size and age distribution of oysters within the population. We also computed the 215 elasticity of λ to determine how proportional changes in the contribution of size *x* to size *y*

 individuals of a particular age (through either survival or fecundity) lead to proportional changes $_{217}$ in λ (Caswell, 2006; Ellner and Rees, 2006). To assess the importance of including age-structure in the IPM, we compared model results from an IPM that includes both age- and size-structure to results from an IPM that includes only size-structure.

 To approximate the integral operators, we used the midpoint rule with 300 equally sized bins from size 0 to 300 mm, for each age class from 0 to 15 years. As noted above, we also included an extra discrete size class to account for individuals growing outside the range of the integration limits. Model implementation and data analysis were conducted in R (R Core Team, 2015; Bolker and Team, 2014). 225 RESULTS *Statistical fits* This article is protected by copyright. All rights 12 reserved Author Manuscript

²²⁷ Within the data set, oyster size ranged from 10.2 mm to 169.0 mm, while oyster ages ranged from 147 days to 2.7 years. In the implementation of the IPM we extrapolated both size and age past 229 the minimum and maximum values in the data, with size ranging from $L = 0$ to $L = 300$ mm and 230 age from $A = 0$ to $A = 15$ years. This allowed us to capture maximum sizes generated by the model (Appendix S1). While *C. gigas* oysters can live longer than 15 years, if the maximum size 232 and age are set sufficiently high (\geq 250 mm and \geq 10 years, respectively), qualitative model output is not highly sensitive to the maximum size or age chosen (see Appendix S2).

 The growth model that included age, size, and the interaction between age and size provided the best fit (lowest AICc; Appendix S3), suggesting that all of these parameters are important for modeling growth. Additionally, all models that forced growth to be positive were selected by ²³⁷ AICc criteria over the commonly used models that allowed for both positive and negative growth.

 Overall, growth trajectories also differed between growth models. In models that allowed for negative growth, individuals were unable to reach large sizes, and on average decreased in size approximately 42% of the time (Appendix S1), a phenomenon never observed in the data. In models that forced growth to be positive, there was a positive relationship between the size of an oyster and the log change in size between years in the two youngest age classes. For the older age classes, this relationship became negative (Figure 2A). This leads to larger oysters becoming more likely to experience little to no growth between years, compared to smaller oysters of the ²⁴⁵ same age (Figure 2B). Note that, at small sizes ($<$ 50 mm), the growth model predicts that older oysters can grow upwards of 150 mm in a single year. This is biologically unrealistic, and is an artifact of the statistical extrapolation. As there is a very low chance that in the model an oyster 248 older than \approx 3 years will be smaller than 100 mm, this effect had little impact on model results. A second artifact, due to the need to extrapolate the growth of oysters past age 3, was the substantial $_{250}$ difference in growth of an age 1 oyster and an age 15 oyster at large sizes ($>$ 200mm). Again, as $_{251}$ it is unlikely that an age 1 oyster will be > 100 mm, this effect had little impact on the results. Similar to growth, oyster survival was dependent upon size, age, and the interaction between age and size (Appendix S3). Above a threshold of approximately 80 mm, oysters had a high probability of survival, regardless of age (Figure 2C). For older individuals below this size threshold, survival increased sharply with size, whereas for younger oysters, the increase was more gradual. Is that foreed growth to be positive, there was a positive related and the log-ethange in size between years in the two younges, this relationship became negative (Figure 2A). This leads likely to experience little to no

 The proportion of females in the population increased sigmoidally as a function of size (Figure 3A). For simplicity, we fit this data using a piecewise linear function, as model results were not highly sensitive to the specific function used. Log number of eggs increased linearly as a function $_{260}$ of female size (Figure 3B), while the size of new recruits was normally distributed (mean $= 30.6$

 $_{261}$ mm, *sd* = 6.4 mm; Figure 3C).

262 In the age- and size-structured model, setting local retention, *p*, to 2.44×10^{-15} , 1.00×10^{-11} , ²⁶³ and 3.97 × 10⁻¹⁰ yielded long-term population growth rates $\lambda = 0.506$, $\lambda = 1.003$, and $\lambda = 1.499$, respectively. In the size-only model, setting *p* to 3.74 × 10⁻¹³ and 6.68 × 10⁻¹² 264 ²⁶⁵ yielded $\lambda = 1.009$ and $\lambda = 1.508$, respectively. For all values of $p \ge 0$, the population growth 266 rate λ was greater than 0.9 in the size-only model. As such, for the size-only model we did not ²⁶⁷ evaluate the case when $\lambda = 0.5$.

²⁶⁸ Final models and parameter estimates for growth, survival, and fecundity are given in Table 1 for ²⁶⁹ the age- and size-structured model, and in Appendix S4 for the size-only model.

²⁷⁰ *Model analysis*

 In the age- and size-structured model, for all values of λ larger oysters had higher reproductive values than smaller oysters, while younger oysters had higher reproductive values than older ones (Figure 4A, B). The difference in reproductive values between the youngest and oldest oysters was greatest when local retention and λ were low. When age was excluded from the model, the difference in reproductive values between the smallest and largest oysters was greatest when local 276 retention and λ were high. For $\lambda > 1$ the largest individuals had the highest reproductive value, while when $\lambda \approx 1$ the values were more evenly distributed across all size classes (Figure 4C). 27 A to gradied only term population grownt rates $\lambda = 499$, respectively. In the size-only model, setting p to 3.74 : 499, respectively. In the size-only model, setting p to 3.74 : was greater than 0.9 in the size-only m

278 In a declining population with limited local retention and $\lambda < 1$, the stable size and age ²⁷⁹ distributions from the age- and size-structured model were unimodal and skewed to larger sizes ²⁸⁰ and older ages (Figure 4D, E). Most individuals in the population were between 150-250 mm and $_{281}$ \geq 10 years of age. When $\lambda \approx 1$, the stable size distribution shifted toward smaller sizes and ²⁸² became bimodal, with peaks at approximately 40 mm and 200 mm. Individuals were distributed

²⁸³ roughly equally across all age classes. In a growing population with high local retention and $284 \quad \lambda > 1$, the stable size distribution was nearly unimodal and skewed to smaller sizes. Most 285 individuals were approximately 40 mm and $<$ 4 years old. The slightly smaller peak to the right ²⁸⁶ of the primary mode was likely due to the ample numbers of oysters in the second age class.

²⁸⁷ When age was excluded from the statistical fitting and only size included in the IPM, much of the ²⁸⁸ information about the value of larger oyster sizes was lost. For instance, in the size only model, ²⁸⁹ the stable size distribution was unimodal with a major peak at small sizes , whereas the age- and 290 size-structured model produced size distributions skewed toward larger oysters as λ decreased $_{291}$ (Figure 4E vs. F).

²⁹² The survival of younger oysters had a higher elasticity than that of older oysters in the age- and ²⁹³ size-structured model, with this difference becoming more pronounced with high local retention 294 and $\lambda > 1$ (Figure 5A). Across sizes, survival of the smallest and the largest oysters had the ²⁹⁵ highest elasticity (Figure 5B), while only changes in the fecundity of oysters approximately 296 150-250 mm had an impact on λ (Figure 5E). However, the fecundity of older individuals had a 297 higher elasticity than that of younger oysters (Figure 5D). As local retention increased and λ ²⁹⁸ increased from 0.5 to 1.5, the fecundity of the younger ages became more important. Relative changes in growth and survival across all ages and sizes had a greater impact on λ than changes ³⁰⁰ in fecundity (Figure 5). primary mode was likely due to the ample numbers of oyste
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³⁰¹ There were large differences in elasticity between the age- and size-structured model and the size-only model. The peaks at larger sizes in the size-specific survival elasticities of the age- and size-structured model were absent in the size-only model (Figure 5C), whereas size-specific fecundity elasticities of the size-only model never peaked, but only increased monotonically with size (Figure 5F).

306 Finally, for the size-only model the population growth rate λ was greater than 0.9 for all values of $307 \ p \geq 0$. At large sizes, survival of oysters increased to almost 100%, while the mean change in size ³⁰⁸ between time steps continued to increase as oysters got larger, rather than decreasing to 0 309 (Appendix S4). As such, when λ was low most oysters were in the discrete size class of oysters 310 \geq 300 mm (62.2% when $\lambda \approx 1$). Because these individuals have a high probability of survival, 311 the long-term population growth rate will still be close to 1, even in the absence of successful ³¹² recruitment. If we assume that all oysters die after reaching the maximum size, a long-term 313 population growth rate of $\lambda = 0.5$ is possible. Even in this case, however, model output failed to 314 capture the peaks at larger sizes that were observed in the age- and size-structured model.

315 DISCUSSION

 We found substantive differences in the importance of large and small oysters to population dynamics between an IPM using age- and size-structured and one using only size-structure. In general, the importance of large oysters to population dynamics was clear from the age- and size-structured model, but absent from the size-structured model. In addition, the age- and size-structured model yielded differences in size distributions between growing populations with ³²¹ high local retention and declining population with low local retention that were not apparent in the size-only model. endix S4). As such, when λ was low most oysters were in the mm (62.2% when $\lambda \approx 1$). Because these individuals have a ge-term population growth rate will still be close to 1, even interned. If we assume that all oyste

 For the age- and size-structured model, most individuals were large and old in declining populations, whereas most individuals were small and young in populations with positive population growth. Intuitively, in declining populations with low local retention, few juveniles are 326 added to the population. As such, size distributions are skewed towards the older, larger sizes. ³²⁷ Alternatively, for populations with high local retention leading to positive growth, there is a substantial influx of small juveniles each year. This leads to the right-skewed stable size and age

329 distributions when $\lambda > 1$. Finally, the joint age- and size-structure was required to detect the 330 importance, measured by elasticity, of both small and large individuals to population growth. ³³¹ With the size-only model, elasticity analysis indicated that survival of the smaller individuals was ³³² most important to population growth.

333 The differences in results between the size-only model and the age- and size-structured model ³³⁴ likely arose due to the differences in individual growth rate at large sizes. In the size-only model, 335 individual growth rate continued to increase as individuals grew, rather than declining to no ³³⁶ growth, as with the age- and size-structured model. Biologically, continued increases in 337 individual growth rate as size increases makes little sense for organisms such as oysters ³³⁸ characterized by indeterminate growth. Moreover, in the size-only model there was no maximum ³³⁹ age at which all individuals die. When local retention was low, this led to a majority of 340 individuals growing beyond the set maximum size and entering the discrete size class of sizes $341 > 300$ mm. The accumulation of individuals in that size class was not evident in the age- and 342 size-structured model. imporiant to population growth.
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343 Model results from the age- and size-structured model are supported by population patterns observed in wild *Crassostrea spp.* populations. For example, in three *C. gigas* populations along the west European coast (Cardoso et al., 2007), the distribution of sizes within each age class matches that predicted by the model. In the Lower Saxony Wadden Sea, Germany, populations of *C. gigas* experiencing significant increases in population size have size distributions characterized $_{348}$ by a major peak in the smaller (> 55 mm) sizes, with some populations also exhibiting a smaller 349 peak in size ranges between 55 − 100 mm (Schmidt et al., 2008). These size distributions are fairly consistent across the three years of the study, and match IPM predictions for populations experiencing positive population growth. Other populations of *C. gigas* in the North Wadden

 along the coast of Denmark and Germany also exhibit right skewed distributions when population densities are increasing (Diederich et al., 2005). In these populations, however, size distribution 354 are more variable over the ten years of the study due to inconsistent recruitment. In upper Chesapeake Bay, where recruitment is limited, *C. virginica* populations outplanted as juveniles become dominated by large, old oysters after 2-4 years due to extremely low recruitment in the years subsequent to the outplant (Paynter et al., 2010). These populations eventually go locally extinct without further transplants of young juveniles. In lower Chesapeake Bay, where recruitment is not limiting, persisting populations of *C. virginica* with multiple year classes are characterized by two major peaks, one for younger, smaller oysters up to 2 years old, and a second one of larger oysters ranging in age from 3-6 years old (Schulte et al., 2009; Lipcius et al., 2015). This pattern was also observed in *C. virginia* populations located in no-take reserves in North Carolina where recruitment was not limiting (Puckett and Eggleston, 2012, 2016). peake Bay, where recruitment is limited, *C. virginica* popular of dominated by large, old oysters after 2-4 years due to extrabsorption to the outplant (Paynter et al., 2010). These population to the outplant (Paynter et

 Importantly, these examples represent populations in which recruitment occurs through a combination of local retention and larval subsidies from external sources, though in many cases the precise source of new recruits is unknown. Our model assumes a closed population with recruitment only occurring through local retention. However, due to the way in which we used p , the amount of local retention, as a tuning parameter to yield populations with various population 369 growth rates, we expect that qualitative stable age and size distribution would not differ significantly if we were to incorporate a mix of local and external recruitment, though 371 implications for management strategies might vary if one is considering a single closed 372 population, or open local populations within a metapopulation.

 In a recent review, Baggett et al. (2015) proposed size-frequency distributions as a "universal metric" for monitoring oyster restoration success. Our results support this proposal, and indicate

 that certain patterns in size distributions can point to populations in need of restoration, or can be indicative of restoration success or failure. If populations exhibit a skewed distribution with most individuals found in the larger, older age groups, this could point to a declining, 378 recruitment-limited population, in which case restoration efforts should focus on broodstock enhancement and incorporating metapopulation dynamics to identify optimal locations for restoration and increased management protection (e.g., marine reserves) (Lipcius et al., 2008; North et al., 2010; Lipcius et al., 2015; Puckett and Eggleston, 2016). If a bimodal size 382 distribution is observed, this could indicate a population with $\lambda \approx 1$, in which case monitoring, and perhaps limited restoration, are sufficient. Finally, if populations exhibit a skewed distribution 384 with substantial numbers of individuals in the smaller, younger age groups, as well as abundant adults, this could point to a successful population with sufficient recruitment and broodstock (Schulte et al., 2009; Lipcius et al., 2015). Such locations where populations are increasing in abundance may be ideal candidates for additional habitat restoration to expand the footprint of successful populations to ensure habitat limitation is not the bottleneck preventing population 389 recovery. tment-limited population, in which case restoration efforts slement and incorporating metapopulation dynamics to identation and increased management protection (e.g., marine reserved, and increased management protection (

 To assess restoration success, it is necessary to monitor changes in the size distribution of a 391 population over time to differentiate between stable population patterns, and transient dynamics or patterns that emerge as a result of external recruitment (e.g. Diederich et al., 2005). Model results showed that, in a closed population started with a few small, young individuals, patterns in 394 population size structure approached the stable distribution in as little as 5 years if the population 395 was doing well ($\lambda > 1$). However, model simulations required 10-15 years to distinguish between 396 stable ($\lambda \approx 1$) and declining ($\lambda < 1$) populations (Appendix S5). Post-restoration is often characterized by distributions skewed towards small individuals. Our results indicate that, in a

 closed population, subsequent monitoring over at least 5 years will inform if the distribution remains skewed toward small individuals, indicating possible population persistence, or becomes skewed toward larger individuals, indicating insufficient local retention and necessitating additional intervention. However, it is important to recognize that if the population is open, size distributions could be misleading, as even a sink population could exhibit a bimodal distribution given sufficient amounts of external recruitment. If this is the case, then additional data is needed to assess persistence of local populations, as well as the entire metapopulation.

405 Once there is information about whether a population is increasing or decreasing, one must then 406 understand which individuals are most important to the growth of that population, and on which ages or sizes efforts should focus to have the greatest positive impact on the population growth rate. Patterns in elasticity can be used to inform these decisions. Our results indicate that, for the modeled population of *C. gigas*, increasing the survival of both small (< 50 mm) and very large $_{410}$ ($>$ 175 mm) oysters had the greatest impact on λ . This suggests several strategies to assist protected or harvested oyster populations. For example, by enhancing the abundance of broodstock (large oysters) in source habitats (*sensu* Lipcius et al., 2011; Puckett and Eggleston, 2016), one could achieve the dual objective of increasing abundance of very small and very large oysters, since in subsequent years the offspring of the broodstock would recruit throughout the metapopulation and consequently increase recruitment of young, small oysters (Lipcius et al., 2008, 2015). Additionally, instead of only establishing a minimum size limit to protect small and ⁴¹⁷ intermediate sizes, as is often done, our results suggest that an additional maximum size limit to harvest would be beneficial. onal *intervention*. However, it is important to recognize that
tutions could be misleading, as even a sink population could
sufficient amounts of external recruitment. If this is the ease
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 Finally, our results show that growth kernels that restrict growth to be positive between years produced a better fit relative to more commonly used growth kernels allowing for reduction in

 size with age. Many sessile marine organisms, such as oysters, grow by forming a calcified, protective shell. As such, fitting growth kernels by performing a standard least squares linear regression of size at time $t + 1$ against size at time t is not appropriate, as it allows for organisms ⁴²⁴ to decrease in size between time steps. This indicates the importance of developing appropriate models of individual growth for the focal organism.

Limitations and challenges

⁴²⁷ While IPMs have been applied extensively to terrestrial plants and mammals, only a handful of examples exist of IPMs applied to a marine system (Bruno et al., 2011; Madin et al., 2012; Edmunds et al., 2014; Yau et al., 2014). Our results further demonstrate that IPMs can be a powerful tool for modeling population dynamics of marine species. However, several challenges remain.

 First, long-term datasets must be developed that include trait-specific information on individuals (not just cohorts) through time. The size-only model and the age- and size-structured model produced similar results across a narrow size range (10-100 mm length) and for which data were 435 available. Past a size of 100 mm, the results of the two models became disparate. Consequently, emphasis should be on acquisition of data across the full size and age range of a focal species, not ⁴³⁷ just on the early years, although the necessary number of years of data collection will vary from species to species. For *C. gigas* populations, our analysis suggests that 4 years of data produces informative patterns. However, we had to extrapolate the statistical demographic kernels upwards of 7 years and 140 mm length, so the specifics of the results should be interpreted with caution. Additional years of data are likely necessary to better tease apart the age- or size-dependence of different vital rates, and to accurately inform on-the-ground decisions about specific populations. Given these limitations, we also need methods to assess how much data is needed to yield rease in size between time steps. This indicates the importate of individual growth for the focal organism.

Limitations and challenges

IPMs have been applied extensively to terrestrial plants and

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 accurate, realistic results, such as examining sensitivities of key response variables to sub-sampling of the collected data.

446 Due to our limited dataset, we were not able to parameterize an age-only model for comparison. Future work could utilize an extended dataset that contained enough years of data to fit an age-only model and assess whether this model is able to capture important patterns in the population, or if the model including both age and size is still essential.

 Another challenge of applying IPMs to marine systems is in obtaining an accurate estimate of recruitment. This parameter can be difficult to estimate, particularly for broadcast spawners, and ⁴⁵² can display a high degree of spatial and temporal heterogeneity (Cowen and Sponaugle, 2009). However, even when this parameter is unknown or highly uncertain, our results show that ⁴⁵⁴ investigating patterns in population structure over a range of recruitment scenarios can provide insight into the current state (e.g., decreasing, stable, increasing) of a population. Our model assumes a closed population, whereby recruitment occurs via local retention of larvae and not from immigration via connectivity from external larval sources. This assumption is reasonable when local retention is high relative to connectivity because recruitment is driven by local reproduction (Figueira, 2009; Carson et al., 2011; Puckett and Eggleston, 2016). However, when local retention is low relative to external recruitment, accounting for this external recruitment is important as it can affect size and age distributions, as well as management strategies (Yau et al., 2014). Acquisition of this necessary data, which likely involves temporal variability in recruitment, and incorporating these features in our models, is a key challenge for the future. Finally, additional factors that are relevant to oyster populations could be incorporated into the IPM, including size-specific susceptibility to disease, size-specific harvest and size limits, and temporal variability in harvest. board manners and actors. We were not does to parameterize an egual work could utilize an extended dataset that contained enoughly model and assess whether this model is able to capture in ation, or if the model including

Conclusion

 Using demographic data from a population of the Pacific oyster, *C. gigas*, in Oregon, our modeling analysis demonstrates the utility of IPMs for understanding the relative importance of including age- and size-structure for understanding population dynamics. We show that 471 simultaneous inclusion of both age and size, as well as limiting growth to positive changes, is necessary to parameterize an IPM of *C. gigas* population dynamics. This type of modeling 473 framework can also be used to assist with management decisions involving restoration and conservation of sensitive and important marine species. However, more long-term datasets are 475 needed that include both age- and size-dependent information on population demographic rates for this tool to be truly effective.

477 ACKNOWLEDGMENTS

 Support for J.L. Moore was provided by an NSF Graduate Research Fellowship, award number DGE-0940903, and an NSF GK-12 Fellowship under DGE grant #0841297 to S.L. Williams and B. Ludaescher. Support for R.N. Lipcius was provided by NSF award DMS-1313093 and NOAA Chesapeake Bay Office award NA13NMF4570205. Support for B. Puckett was provided by NSF award OCE 1155628 and NC Sea Grant award 14-HCE-9. Support for S.J. Schreiber and J.L. Moore was provided by NSF Grants DMS-1022639 and DMS-1313418. *Crassostrea gigas* 484 growth and mortality data were provided by David Stick and Chris Langdon at the Hatfield Marine Science Center, in concert with the Oregon State University Molluscan Broodstock Program. This article is protected by convention and size of the set and size and size structure for understanding population dynamic
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 3393–3400, 2012. This article is protected by copyright. All Taptis reserved 660 Appendix S1. Maximum age and size of individuals. Includes a figure showing the results of individual growth trajectories using both lognormal growth fitting and normal growth fitting.

 Appendix S2. Sensitivity of model output to maximum age and size. Includes figures showing differences in reproductive values, stable age and size distributions, and elasticities for different values of maximum size and maximum age.

 Appendix S3. Model comparisons for growth and survival functions. Includes AICc comparisons of different growth and survival models.

667 Appendix S4. Size-only demographic functions. Includes a figure and table showing statistical fits used for the size-only model.

 Appendix S5. Time to stable size distribution. Includes figures showing how long the age- and size-structured IPM, when started with a single individual at age 1, take to reach the stable size ⁶⁷¹ distribution. Brack and a global control of the maximum age and
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eners in reproductive values, stable age and size distribution
of maximum size and maximum age.
Adix \$3. Model compa

⁶⁷² Metadata S1. Description of data and code. Provides a brief description of all code and data ⁶⁷³ required to run the simulations and generate the figures in the manuscript.

⁶⁷⁴ TABLES

Table 1: Age- and size-dependent demographic functions. Statistical models and parameter estimates for age- and size-structured models used to describe *Crassostrea gigas* demography.

Demographic process	Model
Growth	$\hat{y} = 2.961(0.047) + 0.18(0.027)a + 0.005(0.001)x - 0.002(0.0004)ax$
	standard deviation about the growth curve, $\sigma = 0.402(0.005)$
Survival	$logit(s) = 4.003(0.395) - 0.016(0.010)a - 1.625(0.223)x + 0.018(0.004)ax$
Sex ratio	$v(x) = 0.0311(0.050) + 0.0044(0.0004)x$
Fecundity (number of eggs)	$h(x) = 12.568(0.601) + 0.053(0.006)x$
Distribution of larval size	Gaussian with mean = 30.575 , variance = 40.73
Recruitment success	$\lambda = 0.506$: $p = 2.44 \times 10^{-15}$
	$\lambda = 1.003$: $p = 1.00 \times 10^{-11}$
	$\lambda = 1.499$: $p = 3.97 \times 10^{-10}$
	Notes: All models are functions of age, a , and/or size, x . Values in parentheses are standard errors of parameter
	estimates. Predicted values for growth (y) are the log change in size given current age and size. Models and
	parameter estimates for the size-only model are given in Appendix S4.
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FIGURE LEGENDS

 Figure 1. Modeled life cycle of *Crassostrea gigas*. Census occurs immediately following ⁶⁷⁷ summer recruitment. Oysters then must survive and grow for the majority of the year prior to reproduction. Following reproduction, new oyster recruits experience a separate growth and survival event before joining existing oysters immediately prior to the next census.

 Figure 2. Age- and size-dependent growth and survival functions. Statistical fitting of age- and size-dependent growth (A-B) and survival (C) functions. A) Growth functions are fit using linear regression on the log change in size against size and age. B) Growth functions are 683 translated to generate the age-dependent relationship between size at time $t + 1$ and size at time t . The dotted (black) diagonal line is the 1:1 line. Note that, at small sizes ($<$ 50 mm), the growth model predicts that older oysters can grow upwards of 150 mm in a single year, and that at large sizes (> 200 mm), there is a large difference in the growth of young and old oysters. This result is an artifact of the statistical extrapolation, and has little impact on model results. C) Survival functions are fit using logistic regression of survival between time points. All functions are extrapolated past the collected data (black and gray points) to the minimum and maximum sizes. Parameters of the models are given in Table 1. Example to solve the mass of the dual given by the transfer dual duction. Following reproduction, new oyster recruits experies al event before joining existing oysters immediately prior to e 2. Ape-and size-dependent grow

 Figure 3. Fecundity functions. A) The proportion of females as a function of size (adapted from Buroker, 1983). For simplicity we fit the data using a linear function, as model results are not sensitive to the function used. B) The log number of eggs produced as a function of parent size (from Kang et al., 2003; Ren et al., 2003). C) The distribution of offspring size, fit to the first time step of the *C. gigas* dataset (shown grouped in size bins of 5 mm). Parameters of all model fits are given in Table 1.

697 Figure 4. IPM model output. Model output for $\lambda = 0.5$ (black line and points), $\lambda \approx 1.0$ (dark

698 gray line and points), and $\lambda = 1.5$ (light gray line and points). A) Age-specific reproductive values for the age- and size-structured model. B) Size-specific reproductive values for the age- and size-structured model. C) Reproductive values for the size-only model. For (A) - (C) , reproductive values for each λ are scaled such that the sum of all values = 1. D) Stable age distributions for the age- and size-structured model. E) Stable size distributions for the age- and size-structured model. F) Stable size distributions for the size-only model. For the size-only $_{704}$ model, when $\lambda \approx 1$, and $\lambda = 1.5$ approximately 62.17%, and 1.81%, respectively, of the population is contained in the discrete size class of individuals greater than 300 mm (not shown on graph). Additionally, for the size-only model it was not possible to simulate a population with $707 \quad \lambda = 0.5$. As such, only relationships for $\lambda \approx 1$ and $\lambda = 1.5$ are shown.

 Figure 5. IPM elasticity analysis. Elasticity analysis for when $\lambda = 0.5$ (black line and points), $709 \text{ A} \approx 1.0$ (dark gray line and points), and $\lambda = 1.5$ (light gray line and points). A) Age-specific survival elasticities for the age- and size-structured model. B) Size-specific survival elasticities for the age- and size-structured model. C) Size-specific survival elasticities for the size-only $_{712}$ model. D) Age-specific fecundity elasticities for the age- and size-structured model. E) Size-specific fecundity elasticities for the age- and size-structured model. F) Size-specific fecundity elasticities for the size-only model. For the size-only model, it was not possible to $_{715}$ simulate a population with $\lambda = 0.5$. As such, only relationships for $\lambda \approx 1$ and $\lambda = 1.5$ are shown. ductive values for each λ are scaled such that the sum of all valutions for the age- and size-structured model. E) Stable size
tructured model. E) Stable size distributions for the size-only
turning and $\lambda \ge 1$, and

