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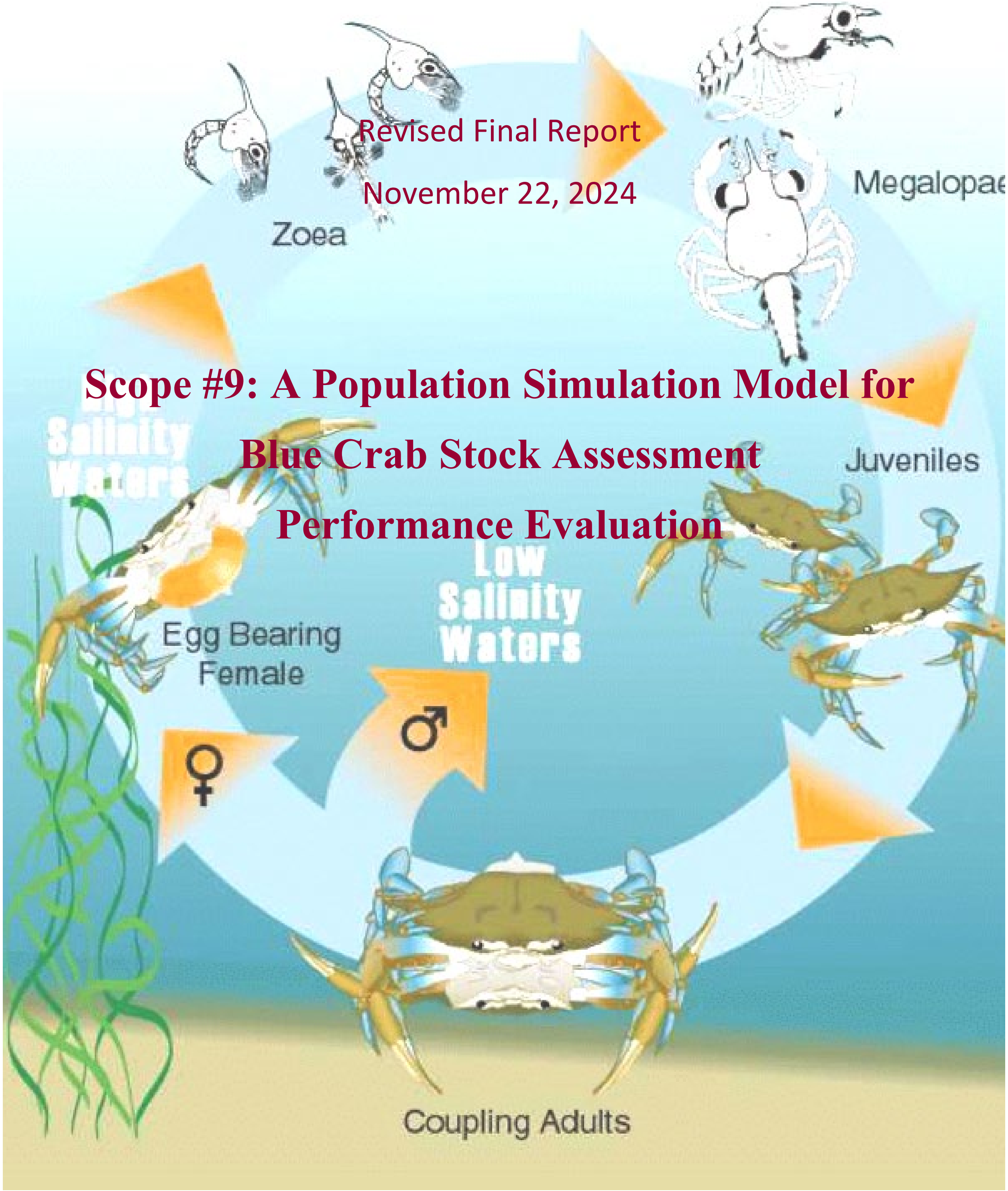
CHESAPEAKE BIOLOGICAL LABORATORY



Revised Final Report

November 22, 2024

Scope #9: A Population Simulation Model for Blue Crab Stock Assessment Performance Evaluation

[UMCES] TS-815-24

Final Report

Scope #9: A Population Simulation Model for Blue Crab Stock Assessment

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Project Dates	**July 1, 2022 – June 30, 2024** **(24 onths)**

Section 1

Background

The blue crab (*Callinectes sapidus*) is widely distributed in estuarine and coastal lagoonal habitats from Argentina to Maine (Williams 1974). It occupies an important trophic link within ecosystems throughout its native range (Baird and Ulanowicz 1989, Frisk et al. 2011, Allen 2022). Blue crab also supports important commercial and recreational fisheries in many of these ecosystems. More recently, blue crab have invaded ecosystem outside of its natural range. The most high profile of these invasions is in the Mediterranean basin (Türeli et al. 2016). Blue crab was first observed in the early years of the 20th Century close to Mediterranean terminal of the Suez Canal. Since then, the species has spread widely throughout the basin, disrupting native ecosystems and affecting fisheries (Mancinelli et al. 2017).

Blue is an iconic species in the Chesapeake Bay. Its physiology, ecology and phenology in the Chesapeake have been extensively studied. Growth rates have been determined in laboratory (Brylawski and Miller 2006), mesocosms (Ju et al. 2001b) and field studies (Davis et al. 2005). It is an important epibenthic predator, potentially serving as a keystone species in seagrass and oyster reef habitats (Mansour and Lipcius 1991, Eggleston et al. 1992, Seitz et al. 2003, Lipcius et al. 2005). Tagging studies have revealed the timing of sex-specific seasonal movements (Semmler et al. 2021).

As in other regions, the blue crab supports important commercial and recreational fisheries in the Chesapeake Bay (Fogarty and Lipcius 2007). Management of these fisheries in the Chesapeake Bay has advanced dramatically in the last 25 years. During this period, the winter dredge survey (WDS), which is the principal tool for estimating the abundance of blue crabs of all ages in the Bay, has matured(Sharov et al. 2003), and its analysis was enhanced(Liang et al. 2017). The first stock assessment was conducted in the late 1990s (Rugolo et al. 1997, Rugolo et al. 1998). Rugolo and colleagues attempted to fit surplus production models and DeLury depletion models to estimate stock status. But at this time, fishery independent surveys were too limited in duration to allow for reliable estimation. Miller developed stage-based models (Miller and Houde 1999, Miller 2001, 2003) that used a discrete size classes to model crabs for the first time. These authors also developed target and threshold reference points for management. Miller et al. (2005) developed a catch-multiple survey model that built on from the previous stage-based models. These authors parameterized the models by fitting them to the Maryland trawl survey, the Virginia Institute of Marine Science (VIMS) trawl survey and the WDS. Reference points were developed using an individual-based yield per recruit model (Bunnell and Miller 2005). This model served as the basis for management for six years. Miller et al (2011) extended the previous assessment to include a sex-specific catch multiple survey model and integrated estimation of reference points. This was also the first assessment that underwent external peer review with the Center for Independent Experts. This model has provided the foundations for management of blue crab for the last 12 years. It utilizes survey data from the Maryland summer trawl program, the VIMS trawl program and the WDS as well as commercial catch data from all three jurisdictions to estimate the abundance of juvenile, adult male and adult female crabs. The model also estimates management reference points, thereby providing a foundation for the determination of stock status. This assessment was updated in 2017.

Despite the substantial progress in the management of blue crab made in the last 25 years, we still lack the ability to assess the performance of previous and future stock assessments. Are the estimates produced by the stock assessment reliable? Are they accurate? Such questions can be answered by developing an operating model (Butterworth and Punt 1999 - Figure 1).

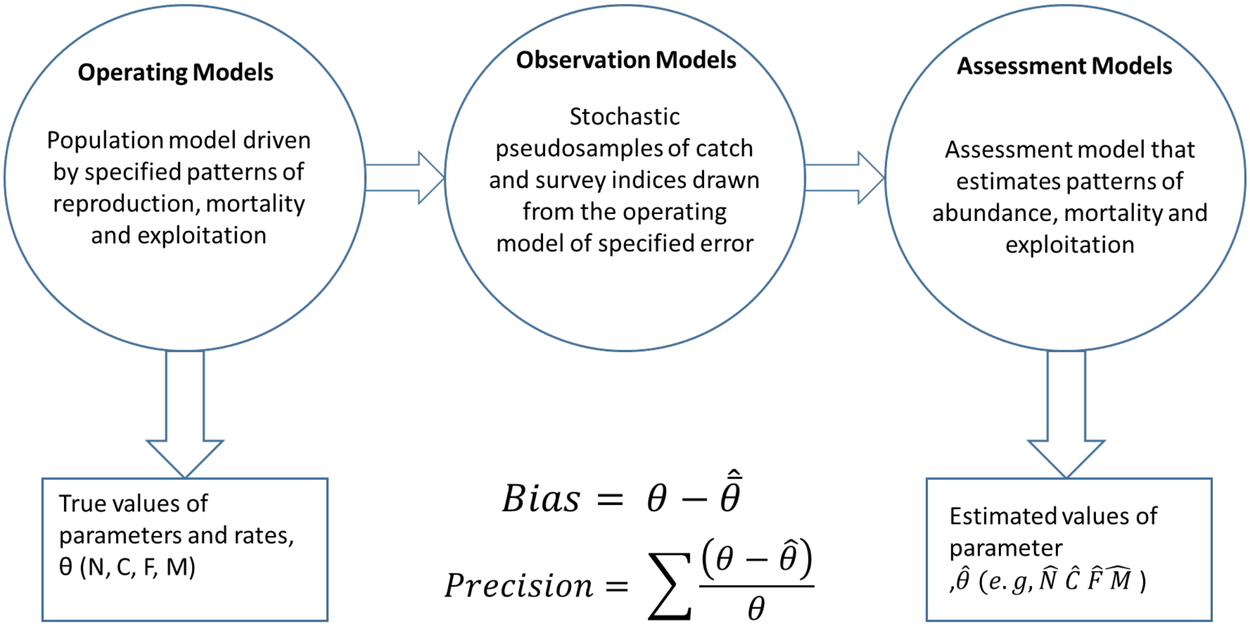

Figure 1. Relationship between operating, observation and assessment models in assessing the performance of an assessment model

Operating models are mathematical representations or hypotheses reflecting the dynamics of the exploited population. The operating model is parameterized with known values of vital rates of the species such as natural mortality and reproductive output and estimates of the action of fisheries thought be exploiting the stock including the pattern of fisheries selectivity and mortality. Indeed, the prior stage-based models (Miller 2001, 2003) can be thought of as operating models. Importantly however, an observation model is also developed. The observation model “samples” abundances, survey indices and catches from the operating model (Butterworth and Punt 1999). These sampled datasets can be used as inputs into the assessment model. Estimates of abundances, survey indices and catches from the assessment model can be then compared to the “true” values of these parameters from the operating model to estimate both the bias and precision of estimates from the assessment model.

Here we summarize our work to develop and evaluate operating models for the blue crab fishery in Chesapeake Bay. Our objectives are

Objective 1. Prepare an open, fully documented population model for blue crab that can serve as an operating model to test the performance of any subsequent stock assessment and to evaluate the potential impacts of sources of error in input data sources.

Objective 2: Conduct extensive simulation testing of the operating model to validate parameterization and model performance to ensure it provides a suitable foundation from which to evaluate the performance of current and future stock assessment models under different suites of assumptions regarding the state of nature, uncertainties in specific input data and management uncertainty.

First, we describe a general operating model that can be used to assess performance of the current stock assessment models. This general operating model must be of sufficient flexibility such that the observation model can draw pseudo samples appropriate to the different assessment models that have been used since 1997. Subsequently, we built upon this general operating model to include additional temporal and spatial complexity that has been envisioned in the next generation of blue crab assessment models. It is possible to develop operating models of any desired level of complexity. However, it is a best practice to consider whether the structure this complex model can yield observations that can be provided to an assessment model to produce estimable parameter values. Accordingly in the second phase of this report we present complex operating models and assess the extent to which they yield estimable parameters.

Section 2

Data Sources

The research team entered into binding data confidentiality agreements with two state agencies and one inter-state program to access data required for development and testing of the operating model. Specifically, we requested the following information on available surveys and harvest data streams.

Surveys:

1. Winter dredge survey data:

The winter dredge survery (WDS) has been conducted collaboratively by the Maryland Department of Natural Resources and the Virginia Institute of Marine Sciences. Designed and initially implemented by Rothschild and colleagues (Volstad et al. 2000, Sharov et al. 2003) , the baywide winter dredge survey has been conducted cooperatively by the states of Maryland and Virginia since the winter of 1989/1990. The survey is designed as a stratified random sample. Stations are allocated randomly each year in proportion to stratum area. Sampling is restricted to waters > 1.5 m depth. On average about 1200 stations are visited each winter. A single tow of 1.83-m wide Virginia crab dredge is taken at each station. The dredge is towed along the bottom at a fixed speed and the beginning and ending coordinates are recorded with a differential GPS. All crabs collected during a tow are measured for carapace width and sexed. Crabs are categorized as age-0, or age-1+ based on size-age conventions. Temperature, salinity and water depth are recorded. During each survey year, trials are conducted to estimate vessel- and year-specific catchability coefficients. These catchability coefficients are used, together with tow-specific area, to estimate the absolute density of crabs caught at each station. Standard design-based statistical approaches are used to expand station abundances to a total baywide abundance (Sharov et al. 2003).

The data are managed by Glen Davis (Maryland Department of Natural Resources, MDNR). WDS data are central to the management of blue crab in the Bay. The time series is at the heart of annual Chesapeake Bay Stock Assessment Committee status of the stock updates.We have used these data in a number of analyses (Jensen and Miller 2005) We have accessed these data in a previous Fisheries GIT-funded projects (Liang et al. 2017, Liang et al. 2021). Accordingly, we were familiar with the data structure, data dictionary and many of the inherent concerns in using these data. We submitted a data request to Mr. Davis on 2022.11.23. The formal data request is provided in Appendix 1.1. Data were provided in a spreadsheet format for the years 1990-2022. Requested data included tow ID, date, time, strata, latitude, longitude, #crabs (by carapace width, sex, and maturity), depth, temprerature, and salinity.

2. Maryland summer trawl survey

Beginning in 1977, Maryland DNR instituted a trawl survey of Eastern Shore sites and tributaries. The survey was expanded in 1984 to include the Patuxent and Chester Rivers, and again in 2003 to include the Nanticoke, and Little Choptank Rivers as well as Fishing Bay. The survey is conducted from May - November. However, coverage is inconsistent temporally and spatially from year to year. Sites within each stratum are fixed and were selected based on patterns of commercial activity and habitat. The survey has used a consistent gear throughout: a 16’ semi-balloon otter trawl. The trawl has 1 1/4” stretch mesh body, a 1 1/8” stretch mesh cod end with a ½” stretch mesh liner. Additionally, the trawl has a 3/16” footrope and a 3/16” tickler chain. Data from the survey were recorded in two different ways. Prior to

1989, crabs caught in a tow were counted and binned into predetermined size categories representing age-0, age-1 and age-2+ crabs. No size measurements were taken. From 1989 onward, size measurements of individual crabs were taken.

A request for data was submitted to Mr. Glenn Davis at Maryland DNR on 2022.11.23 at the same time as we requested the WDS data (Appendix 1.1). We received data in two spreadsheet files. One file covered the period 1977-2009 and included data on tow ID, date, time, location, latitude, longitude, #crabs (by age group, sex, and maturity), depth, tempreraturе, and salinity. A second file includes the years 1989-2021 and included data on tow ID, date, time, location, latitude, longitude, #crabs (by carapace width, sex, and maturity), depth, tempreraturе and salinity

3. Viriginia juvenile finfish and blue crab survey

Since 1955, the Virginia Institute of Marine Sciences (VIMS) has conducted a trawl survey to monitor abundance trends in selected finfish and invertebrate species in the southern portion of Chesapeake Bay. Originally, the survey sampled only the York River, but it has expanded steadily. Currently, seven strata are recognized that cover an area from the mouth of the Bay to the VA/MD border, and up to the freshwater interfaces of the York, James and Rappahannock Rivers. Samples are collected monthly from about 60 stations within the strata. Both fixed and random station assignments have been employed. All blue crabs collected in the VIMS survey are enumerated, sexed and measured. The trawl used in the survey has changed over the survey time series. The most important changes were the addition of a tickler chain and a net liner in 1973 and 1979, respectively. Published calibration factors are available (Hata 1997).

The trawl survey data were used in both the 2005 and 2011 benchmark stock assessments and all subsequent updates. The data are managed by Dr. Troy Tuckey (VIMS). We submitted a data request on 2023.11.23 that included a request for detailed meta-data and data dictionaries (Appendix 1.2). The data request was approved by and data were supplied in a spreadsheet that included tow ID, date, time, location, station (fixed or random), gear, effort (e.g., tow distance or time), latitude, longitude, #crabs (by carapace width, sex, and maturity), depth, temperature, and salinity.

4. Chesapeake Bay Multispecies Monitoring and Assessment Program (ChesMMAP).

The Chesapeake Bay Multispecies Monitoring and Assessment Program, ChesMMAP, began in 2002 and was developed to assist in filling data gaps, and ultimately to support Bay-specific, stock-assessment modeling activities at both single and multispecies scales. ChesMMAP was designed to maximize the biological and ecological information collected for several recreationally, commercially, and ecologically important species in Chesapeake Bay. The survey uses a large-mesh bottom trawl to sample juvenile-to-adult fishes from the head of Chesapeake Bay at Poole's Island, MD to the mouth of the Bay just outside the Chesapeake Bay Bridge Tunnel. The principal goals of the survey are to estimate population sizes for priority species and quantify their geographic and seasonal distribution. The survey has not been used in previous assessments.

The data are managed by Dr. Robert Latour (VIMS). We submitted a data request on 2023.11.23 that included a request for detailed meta-data and data dictionaries (Appendix 1.3). The data request was approved, and data were supplied in a spreadsheet that included tow ID, date, time, location, gear, effort (e.g., tow distance or time), latitude, longitude, #crabs (by carapace width, sex, and maturity), depth, tempreraturе, and salinity.

Harvest time series

1. Maryland

The state of Maryland recognizes both commercial and recreational fishery sectors. This executive function is devolved to the Maryland Department of Natural Resources. Currently, in the commercial fishery Maryland prescribes seven legal methods for harvesting blue crab: scrapes, dipnets, trotlines, handlines, seines, bank traps and pots. However, the fishery is dominated by the hard crab pot fishery, and the trotline fishery. There are numerous temporal and spatial regulations that limit when, where and how these gear types can be used.

Maryland maintains two data streams that were of potential utility for this study. The first is the commercial harvest report. Licensed watermen are required to submit harvest reports to DNR. These reports include the region fished, the amount of gear and the number of crabs harvested by market category. Additionally, MDNR has managed a sentinel fishery since 2002. Participants in the sentinel fishery report additional biological characteristics of the catch, including maturity state, sex and condition. We submitted a data request to Ms. Genine Lipkey of MDNR on 2022.11.23 (Appendix 1.4). Data and related meta-data were provided in spreadsheet form for commercial harvest for the period 1985 – 2021. Reported parameters included catch by sex, market category, NOAA code, month, and gear (when non-confidential). The sentinel survey data were provided in spreadsheet format and included parameters for date, location, gear, the size, maturity status, condition and sex of crabs caught.

2. Virginia

Commercial fishing for blue crab in the Commonwealth of Virginia is regulated by the Virginia Marine Resources Commission (VMRC). There are a variety of gear types that can be legally used to harvest crabs within the Commonwealth, but crab pots, peeler pots and dredges predominate. Crab pots can be fished in both the mainstem of Chesapeake Bay and in the tributaries. No person may place, set or fish more than a combined total of 500 hard crab pots in Virginia tidal waters. Peeler pots are fished on a more seasonal basis and can be "baited" with live adult crabs. Crab dredges were restricted historically to the mainstem of the bay during winter months, and have been banned by regulation since 2008.

We submitted a request to Mss Alexa Galvin and Brooke Lowman at VMRC on 2022.11.23 for theVA harvest up through the most recent year (2022). We requested catch data by sex, market category, reporting area, month, and gear (if this ends up being non-confidential). We are requesting the data by reporting area (Appendix 1.5). Subsequent to this informal request, we submitted a formal data request to Ms. Stephanie Iverson at VMRC on 2022.12.18 (Appendix 1.5). VMRC required project staff to sign confidentiality agreements with the Commission (Appendix 1.5). Data confidentiality agreements were in place by early January 2023 (Appendix 1.5). Commission staff provided the data for the 1993-2021 period in a spreadsheet format. Reported data included catch by sex, market category, NOAA code, month, and gear (if non-confidential).

3. Potomac River Fisheries Commission

Under the *Maryland and Virginia Potomac River Compact of 1958* (Compact), fisheries in the Potomac River are managed by the Potomac River Fisheries Commission which is charged with the establishment and maintenance of a program to conserve and improve the fisheries resources in the river. The Commission is responsible for adopting the rules, regulations and licenses for the recreational and commercial taking, catching or attempting to take or catch fish, crabs, oysters and clams from the

Potomac River. Using this authority, the PRFC has established regulations limiting the number of crab pots that can be used in both the hard crab and peeler pot fisheries. The Potomac River was historically closed to crabbing from 1 December to 31 March each year. However, as with other jurisdictions, the PRFC has implemented late season bans on female harvest. Commercial data for blue crab harvested in the Potomac River have been used in previous assessments

Access to Potomac River commercial harvest data was requested from Mr. Marty Gary, Executive Director of the PRFC on 2022.11.23 (Appendix 1.6). Data and full metadata were provided by the PRFC in spreadsheet format at a monthly resolution for the years 1990-2022 for the number of #1, and #2 males and all females estimated in pounds. A second dataset provided annual harvest for 2007-2022 by NOAA code for the same categories.

Data management and archving

The research team gratefully acknowledges the provision of data for development of the operating model. These data have generally been made freely available, although harvest data time series are confidential and we had to enter into confidentiality agreements before we could access information.

The research team undertook QA/QC protocols on the data supplied. We note that data in all of the time series supplied are routinely updated and errors removed, such that it is a strong recommendation that any future analysis re-engage with the original data holders to support new analyses.

We have made the data collected for this project available to the research team undertaking the 2026 benchmark stock assessment.

Section 3

Modelling approach

We adopted a stepwise approach to developing operating models for blue crab. The first step in the sequence of model development sought to develop a sex-specific, length-specific model that operated at a broad, Bay-wide scale. The justification for this decision is based on the need to provide an operating model that can be used to evaluate the current sex-specific catch multiple survey assessment model (SSCMSAM) that is at the heart of the last benchmark assessment (Miller et al. 2011), **and** would permit the evaluation of a new assessment model that had a more highly resolved length structure. We term this model a sex-specific length-based assessment model (SSLAM). These two assessment models differ in the temporal resolution and in the resolution of population structure. The SSCMSAM operates on an annual time step, and represents the population as existing in either a pre-recruit or fully recruited size class. In contrast the target of the SSLAM is to operate on a monthly time step with a more highly resolved population structure. We have been encouraged by management considerations to develop this higher resolution model as it would allow: (i) recruitment to be modeled better, ii) environmental impacts on growth and other life history parameters to be represented, iii) the impacts of differences in the timing of different fisheries to be incorporated and iv) potentially assess the efficacy of size-based management (Chesapeake Bay Stock Assessment Committee 2022).

To meet these two goal, any operating model would have to track the higher resolution dynamics. The operating model can be sampled at a monthly interval in an observation process (Fig. 1). When appropriately specified, these samples become fishery-independent and fishery-dependent data streams that are fed into the SSLAM. Similarly, the operating model could be sampled monthly during the fishing season. When appropriately specified, these samples become monthly harvest data that are aggregated to estimate annual catches used in the SSCMSAM. Samples from the operating model during appropriate months could be converted based on size criteria to counts of pre-recruit and fully recruited that are used in SSCMSAM. Thus the one highly resolved model provides estimates that can used to assess the performance of both assessment models.

A central challenge in developing size-based population models is determining how growth propagates an initial size distribution forward to represent variation. Growth is an inherently multiplicative process (Caswell 2001). An initial state in which all crabs are "recruited" at say 10 mm must elaborate size distributions over time that have the appropriate size distributions observed in real populations. Based on the blue crab data workshop sponsored by the NOAA Chesapeake Bay Office in 2022 (Chesapeake Bay Stock Assessment Committee 2022), managers advised that the model should include the impacts of environmental factors on the rate of increase in mean size and the change in the moments of the distribution. It was felt this was important to account for potential changes in overwinter behavior (Glandon et al. 2019), and what is known about the effects of temperature and salinity on growth (Smith 1997, Brylawski and Miller 2006). We adopted an approach originally developed by Cao et al. (2017a) for Nortern Shrimp.

Thus development of a single region, sex-specific length-based operating model was the highest priority activity in the project. A detailed description of this work is provided in Section 4. Model code is provided in Appendix IX. We have not undertaken thorough testing of the performance of either SSCMSAM or SSLAM based on the operating model.

The 2022 Data workshop identified many processes of interest that have an explicit spatial component (Chesapeake Bay Stock Assessment Committee 2022). We made exploring development of a spatially-explicit operating model the second priority. In this work, we started with state-specific models. We developed a MD operating model that followed male crabs, and a parallel VA operating model that followed female crabs. Our work started off with informing the state-specific operating models with recruitment, a single state-specific fishery independent surveys and state-specific harvest data. This work is described in Section V. Full model code is provided in Appendix IX

Initial work on the state specific operating models generated continuous monthly time series of fishery-independent and fishery-dependent data. These data were sampled through an observation process (Fig. 1). The resultant samples were provided to the proto-SSLAM to determine the precision and accuracy of subsequent results. When we had satisfied ourselves with the performance of the operating / assessment model combination when perfect information was available, we moved to challenge the operating / assessment model with data more representative of the real world. Our goal was to build incrementally from the single survey starting point to one in which multiple surveys were generated by the observation process and fit according to the assessment model. Ultimately, we sought to link the two state-specific models into a single Bay-wide model that would allow us to represent reproductive movements of female crabs to spawning areas.

Section 4

General Blue Crab Operation Model

Model structure

The core of the operating model is a length-specific, sex-specific population model operating on a monthly time step. This general blue crab operating model can be observed to provide length-specific, sex-specific monthly samples of abundance, survey indices and catches. Observations can also be aggregated to provide annual estimates of abundance, survey indices and catches. The length structure and separation of sexes can be aggregated to provide the pre-recruit and recruited abundances and survey indices required by the catch-multiple survey assessment model (Miller et al. 2005). Alternatively, discrete sex-specific data can be retained, while the length data are aggregated into the pre-recruit and recruited stages required by the sex-specific catch multiple survey model (Miller et al. 2011). Finally, the operating model can be observed as a fully sex-specific, length specific population which will be the likely starting point for future stock assessments.

The operating model simulates the population abundance-at-length in three sex categories: males, immature females, and mature females. The model is flexible such that it can represent the different life history and fishery dynamics. The model can simulate any number of years of blue crab dynamics. It is currently specified for a 10-month year in which January-March are pooled as the first month to represent the overwinter period. All other months are kept as individual calendar months. This aggregation of winter months can be relaxed in future operating models, given the expectation that climate change-driven warming of the Bay will reduce the likelihood that blue crab will overwinter by the end of the 21st Century (Glandon et al. 2019).

Recruitment

The model is initiated through recruitment of young blue crab. Recruitment at length (R_l) in each year (y) and sub-annual time step (t) will be the product of the proportion at length for recruits (p) and the estimated total recruitment ($R_{y,t}$), $R_{l,y,t} = p_{l,t} R_{y,t}$. We used the sex-specific Ricker stock-recruitment function from Miller et al. (2011),

$$R_{y,t} = \omega_t \alpha S_f e^{-\beta(S_{f,y}+S_{m,y})+\varepsilon_y},$$

where $S_{f,y}$ is female spawners, $S_{m,y}$ is adult males, ω_t is the proportion of recruits in month t, α and β are parameters, and ε_y is a normally distributed random error. We used the stock-recruitment parameter estimates from the 2011 stock assessment so that the recruitment would match the observed recruitment in the WDS. Similar to the 2011 stock assessment, we assumed that recruitment occurred at the time of the WDS. We note that this initial formulation of recruitment includes strong assumptions about sex ratios (Miller 2001), and as currently parameterized does not incorporate potential sperm limitation (Ogburn et al. 2014, Rains et al. 2016, 2018). The importance of both assumptions on the reliability of assessment results could be evaluated within the framework proposed here.

Abundance at length

The population is divided into three sex-maturity stages (x): male (m), immature female (f), and mature female (*n*). Male abundance by size (*N*) is the sum of recruitment and the abundance of individuals that survive and grow to that size class,

$$N_{m,l',y,t+1} = \kappa_m R_{l,y,t} + \sum_{l} P_{m,t,l,l'} N_{m,l,y,t} e^{-Z_{m,l,y,t}+\delta_{m,l,y,t}} ,$$

where κ_m is the proportion of recruits that are male, *P* is the probability of growing from bin l to l', and *Z* is the total instantaneous mortality rate. This representation follows standard approaches in size-based population models (Caswell 2001). A normally distributed process error (δ) is also included in the population dynamics, $\delta_{m,l,y,t} \sim N\left(0,\sigma_\delta^2\right)$.

Growth in the operating model is discrete and probabilistic. The details of the molt cycle are not represented in the model. Growth for males follows a stochastic von Bertalanffy growth model that uses a normal distribution to estimate the probability of moving from one length bin (i.e., carapace width) to the next,

$$P_{m,l,l'} = \Phi\left(l'-l+w,\Delta_{t,l},\sigma^2_{\Delta,t,l}\right) - \Phi\left(l'-l,\Delta_{t,l},\sigma^2_{\Delta,t,l}\right),$$

Where *w* is the bin width, Φ is the cumulative normal density function, Δ is the mean growth increment for an individual in a size bin with lower limit *l*, $\Delta_{t,l} = \left(L_\infty - l\right)\left(1-e^{-k}\right)$, L∞, is length at maximum size is based on earlier reviews of growth (Miller et al. 2005) and $\sigma^2_{\Delta,t,l}$ is the variance of the growth increment (Cao et al. 2017):

$$\sigma^2_{\Delta,t,l} = \sigma^2_{L_\infty}\left(1-e^{-K_t}\right)^2 + \left(L_\infty - l\right)\sigma^2_{K_t} e^{-2K_t} + \sigma_{L_\infty}\sigma_{K_t}\rho_{L_\infty,K}\left(1-e^{-K_t}\right)\left(L_\infty - l\right)e^{-K_t} .$$

The standard deviation for L∞, $\sigma_{L_\infty} = L_\infty CV_{L_\infty}$, was the product of L∞ and its coefficient of variation (CV). Similarly, the standard deviation of K_t was the product of K_t and its coefficient of variation, $\sigma_{K_t} = K_t CV_K$. Growth intervals decline from their maximum for the smallest size bin, to zero at the L∞. The mean growth increment is shown in Figure 2.

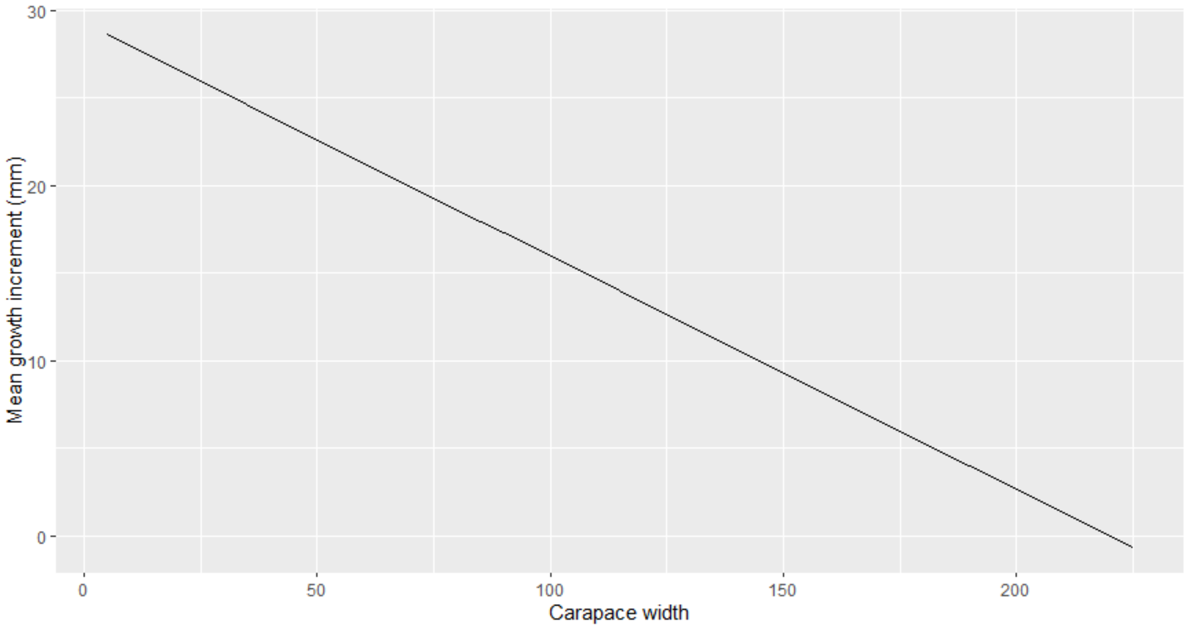

Figure 2 Mean growth as a function of starting length in August for blue crab in Chesapeake Bay

The smallest length bin represents individuals in that range and smaller,

$$P_{m,l} = \Phi\left(w/2, \Delta_{t,l}, \sigma^2_{\Delta,t,l}\right).$$

The largest length bin is a "plus" group representing all individuals that carapace width and larger,

$$P_{m,l,l'} = 1 - \Phi\left(l' - l, \Delta_{t,l}, \sigma^2_{\Delta,t,l}\right).$$

Negative growth (i.e., individuals shrinking in their carapace width) is not allowed.

The total instantaneous mortality (Z) in the operating model is the sum of natural mortality (M) and fishing mortality (F) summed over fleets (ζ), $Z_{x,l,y,t} = M_{x,l} + \sum_{\zeta} F_{x,l,y,t,\zeta}$.

The fishing mortality is the product of length-based selectivity for each fleet (s) and the fishing intensity during each sub-annual time step t for a fleet (F^*), $F_{l,y,t,\zeta} = s_{l,f} F^*_{y,t,\zeta}$.

Currently, two fleets are included in the model: a hard crab and peeler fleets. For now, fishing mortality is constant over time for each fleet, but in future version of the operating model, it can be dynamic over time. In the example results shown, the hard crab fishing mortality rate is 1.05 per year, and the peeler fishing mortality rate is set to zero. Natural mortality of each length bin is set to 0.9 per year to match the assumptions of the 2011 stock assessment (Miller et al. 2011).

The operating model includes a process error, δ. The standard deviation for the process error is set to a small value for these simulations to more clearly show the dynamics of the model. However, the importance of this parameter can be evaluated in subsequent analyses if desired.

The combined dynamics for males described above produces simulated length distributions that reflect what is known about size distributions of males in the population (Figure 3).

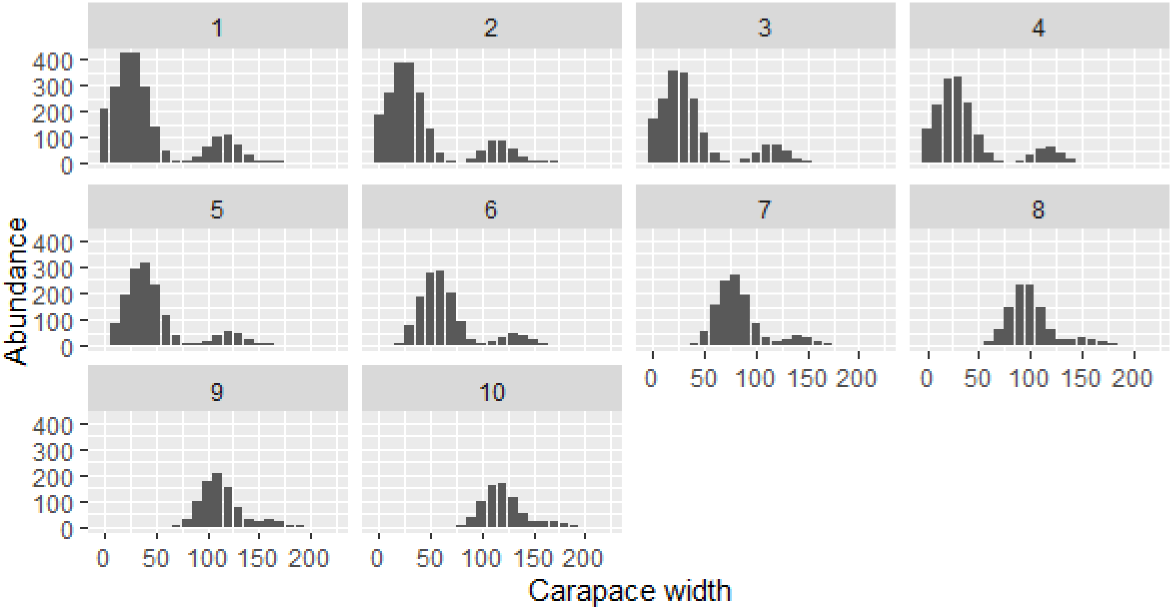

Figure 3. Simulated length composition of male blue crabs during a simulate year by month. The first month represents January-March, and months 2-10 represent April-December.

Females, both immature and mature, are modelled in a broadly similar way as males, except the model has to account for the molt to maturity, which serves as a functional terminal molt (Smith and Chang 2007). For immature females, abundance-at-age follows similar dynamics as males except for the inclusion of maturation in *P*, which causes transition to the category of mature females. For immature females the dynamics of abundance at length is given by,

$$N_{f,l',y,t+1} = \kappa_f R_{l,y,t} + \sum_l P_{f,t,l,l'} N_{f,l,y,t} e^{-Z_{f,l,y,t}+\delta_{f,l,y,t}} \ .$$

The probability of an immature female crab moving from one size bin to another and remaining immature is described by

$$P_{f,l,l'} = \left(\Phi\left(l'-l+w,\Delta_{t,l},\sigma^2_{\Delta,t,l}\right)-\Phi\left(l'-l,\Delta_{t,l},\sigma^2_{\Delta,t,l}\right)\right)\left(1-\psi_l\right),$$

where ψ is the probability of maturation.

For mature females, the model is similar to immature females, but it does not include recruitment, and *P* includes females that mature,

$$N_{n,l',y,t+1} = \sum_{l} P_{n,t,l,l'} N_{n,l,y,t} e^{-Z_{n,l,y,t}+\delta_{n,l,y,t}} + \sum_{l} P_{fn,t,l,l'} N_{f,l,y,t} e^{-Z_{f,l,y,t}+\delta_{f,l,y,t}} \ .$$

Females that mature transition to mature females at length with probability,

$$P_{fn,l,l'} = \left(\Phi\left(l'-l+w, \Delta_{t,l}, \sigma^2_{\Delta,t,l}\right) - \Phi\left(l'-l, \Delta_{t,l}, \sigma^2_{\Delta,t,l}\right)\right)\psi_l \ .$$

This equation is only applied for *l'>l,* which indicates that a female grew during that time step (i.e., a female to grow during the month in which she matures). Once a female reaches maturity, she will no longer grow, which is represented by an identity matrix. The female maturity curve is shown in Figure 4.

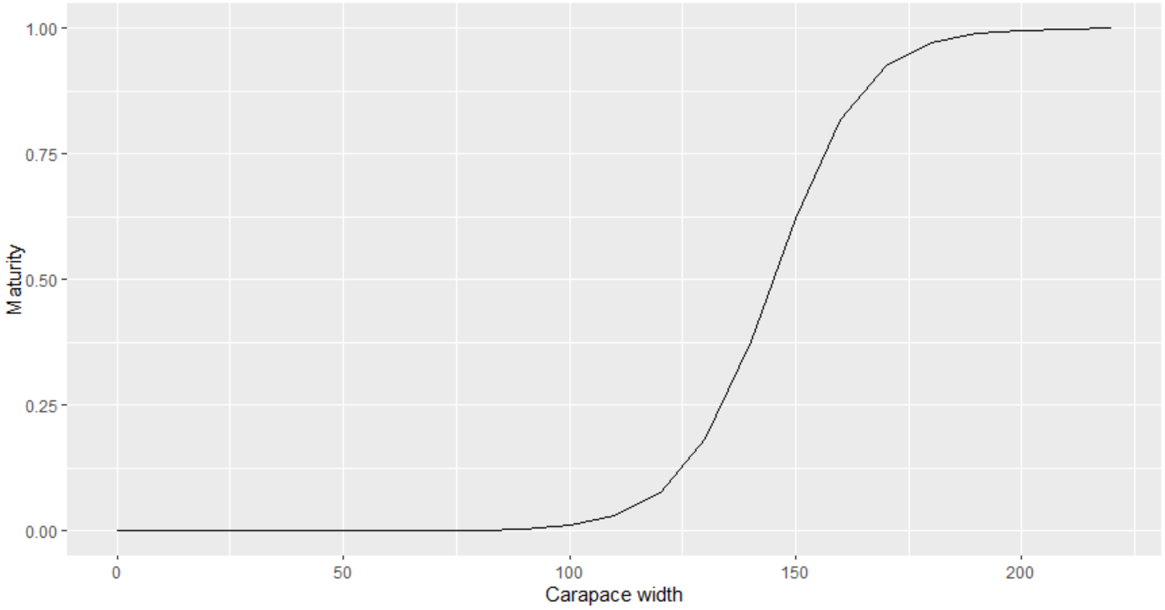

Figure 4. Female maturity-at-length curve used in the operating model.

The operating model explicitly links growth to environmental conditions. The model includes environmental drivers for the growth parameters (*K*) over time,

$$K_{y,t} = g\left(env_{y,t}\right).$$

We are modeling K as a linear function of average cumulative growing degree days during a time step (Figure 5).

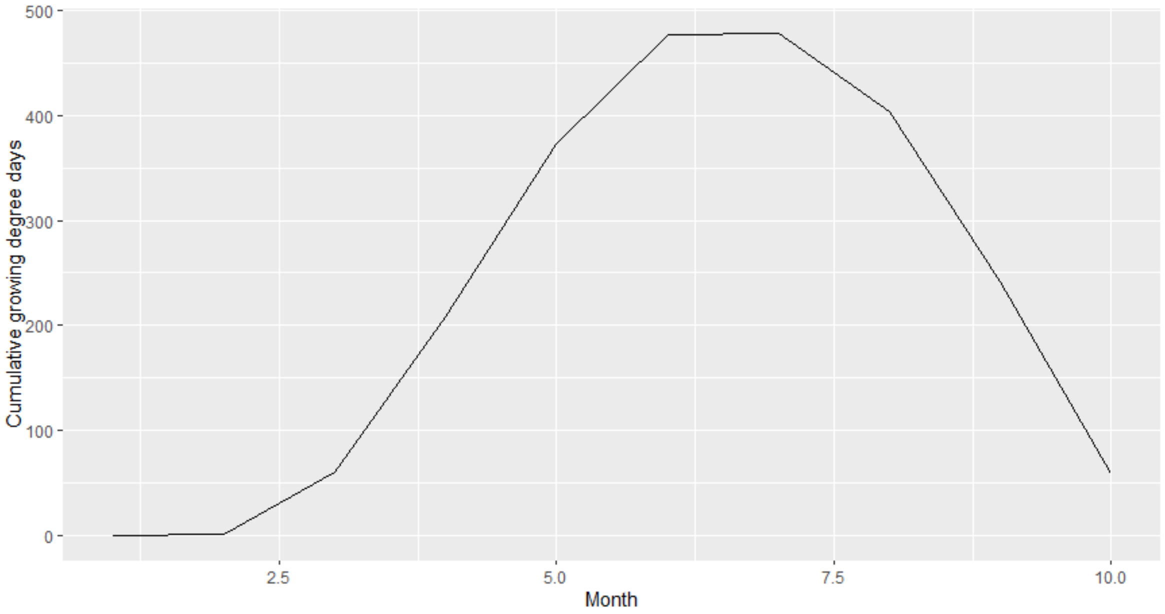

Figure 5. Cumulative growing degree days per month based on interpolated water temperatures in the Chesapeake Bay.

Catch at length

Catches in the operating model are length-, sex-, and time-specific. Catch (C) for each fleet and sex category follows the Baranov catch equation,

$$C_{l,y,t,f} = \frac{F_{l,y,t,f}}{Z_{l,y,t}}\left(1 - e^{-Z_{l,y,t}}\right) N_{l,y,t} .$$

Where all parameters are as described previously.

Indices at length

Expected survey indices (I) are calculated as the product of catchability (q), survey selectivity (s^v), and abundance, $I_{l,y,t} = q s_l^v N_{l,y,t}$. We included surveys to represent the WDS, Maryland Trawl Survey, VIMS Trawl Survey, and the ChesMMAP Trawl Survey. The selectivity functions are shown in Figure 6.

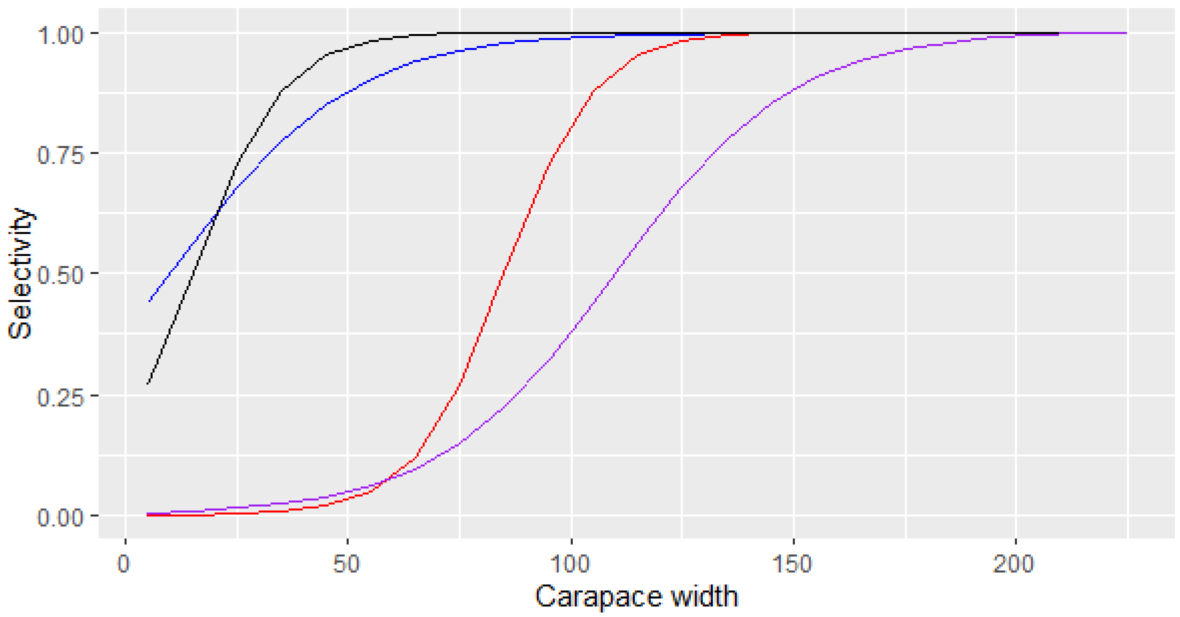

Figure 6. Selectivity curves used in the operating model for the male hard crab fishery (red) and the surveys. The blue line represents the Winter Dredge Survey, the black line represents the Maryland Trawl Survey and the VIMS Trawl Survey, and the purple line represents the ChesMMAP Trawl Survey.

Lognormal errors are applied to generate observed catch and indices, and multinomial error functions are used to generate the size composition data. Size composition in the model is generated.

The model has been implemented in the R programming environment. Full model code is provided in Appendix 2.

Results

The operating model simulated recruitment that matched reasonably well with the range estimated in the 2011 stock assessment (Figure 7), but this is expected because we used the same stock-recruitment parameters as the 2011 stock assessment (Miller et al. 2011).

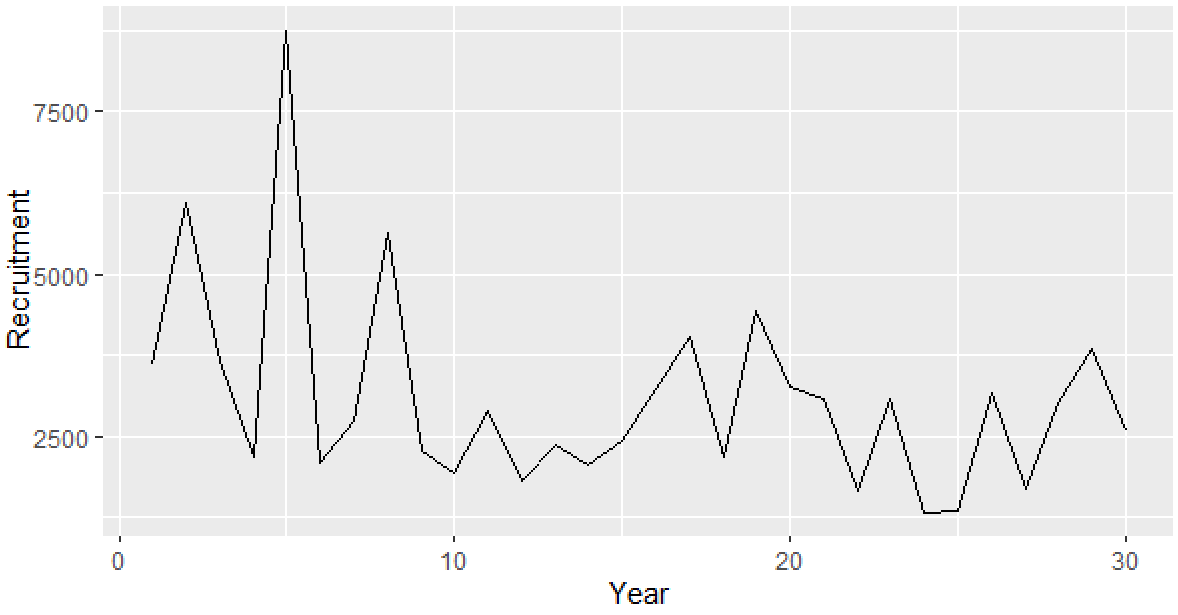

Figure 7. One realization of simulated recruitment during a 30-year period from the operating model.

Total male abundance (Figure 8) and female abundance (not shown) also fluctuated in similar ranges as has been previously observed.

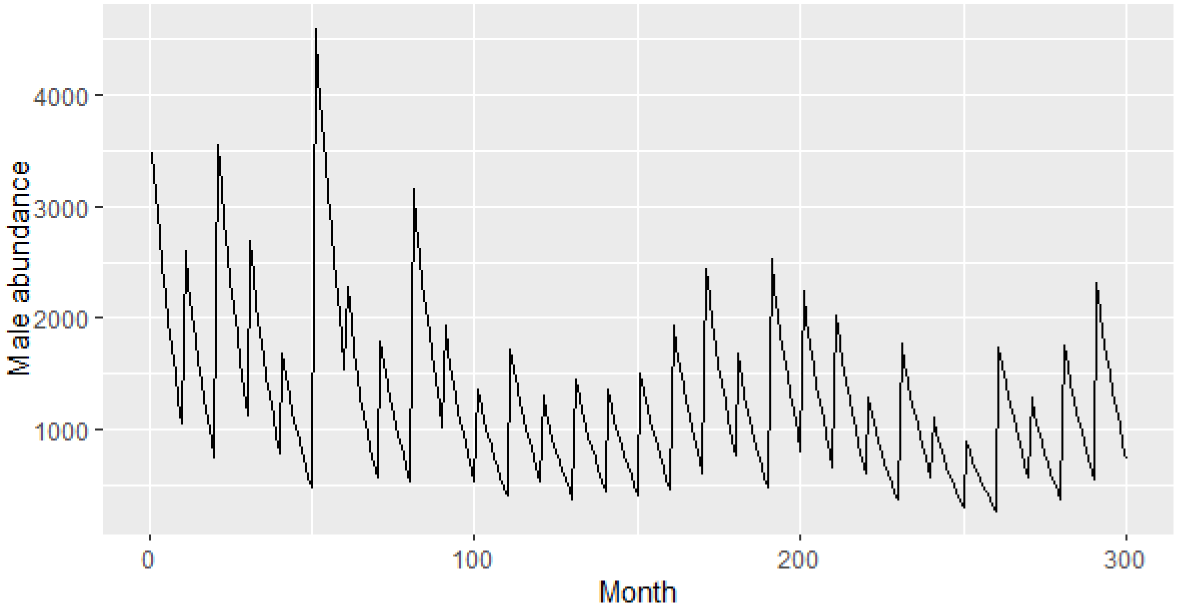

Figure 8. Simulated monthly male abundance during a 30-year period from the operating model.

The pattern of abundance shows annual peaks in recruitment, followed by declines in abundance driven by the combination of natural and fishing mortality. Female abundance demonstrates a similar saw tooth pattern.

The model was able to simulate the length structure of the population observed in the WDS during month 1 very well for mature females, reasonably well for males, and fairly for immature females (Figure 9). The model exhibited one clear peak in the length composition for mature females and two modes for males and immature females. In particular, the operating model had larger age 1+ immature females than the data.

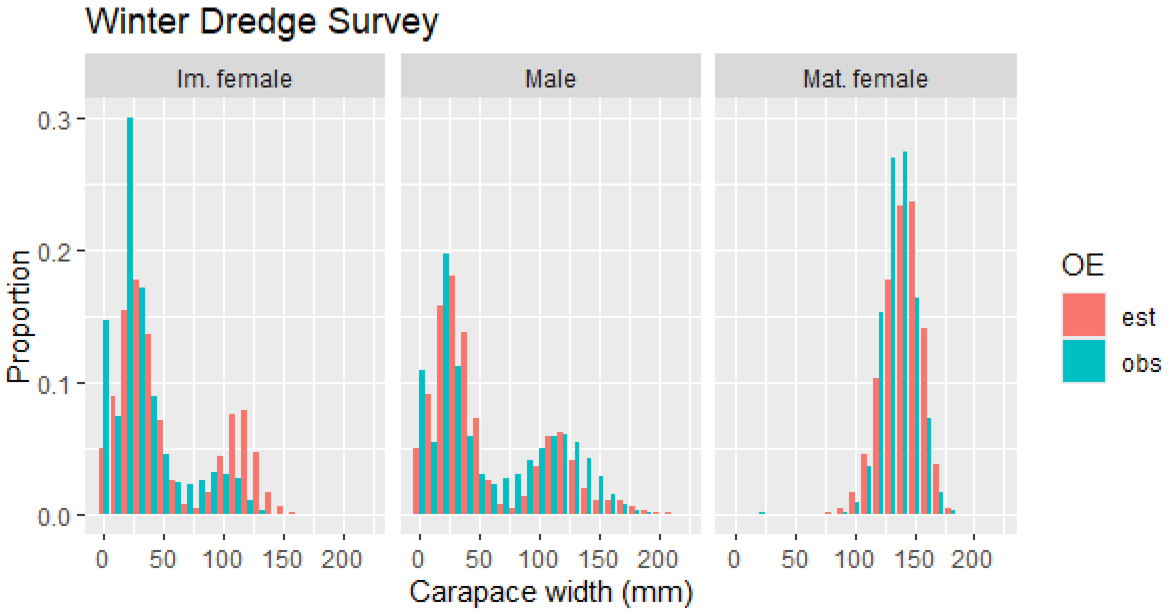

Figure 9. Comparison of operating model simulated length composition to the average length composition of the Winter Dredge Survey. Blue bars are the observed proportions-at-length and the red bars are the simulated proportions-at-length.

We caution that the close similarity of results of the combined operational / observational model does not reflect any sort of statistical fitting of model parameters to data. Rather they closeness reflects judicial choices of parameter estimates in the operating model. Considerable work remains to evaluate parameter values for the operating model and how these affect the potential bias and precision of the assessment model.

For the other surveys, the operating model's ability to match the survey length composition data depended on the sex and month. In all months and surveys, the operating model generated length compositions that were very close to those observed in the surveys for mature females (Figures 10, 13, and 16). For immature females and males, the operating model was able to match the length compositions reasonably well during the spring, fall, and winter, but struggled to match the length compositions during the spring and summer (Figures 11-12, 14-15, 17-18). The fall length compositions only differed because they include small young-of-the year that are observed before our recruitment time in the model. The observed summer length compositions typically became unimodal, whereas our model predicted continued bimodal distributions until the fall. This may indicate that we need to allow for increased growth variability in the model.

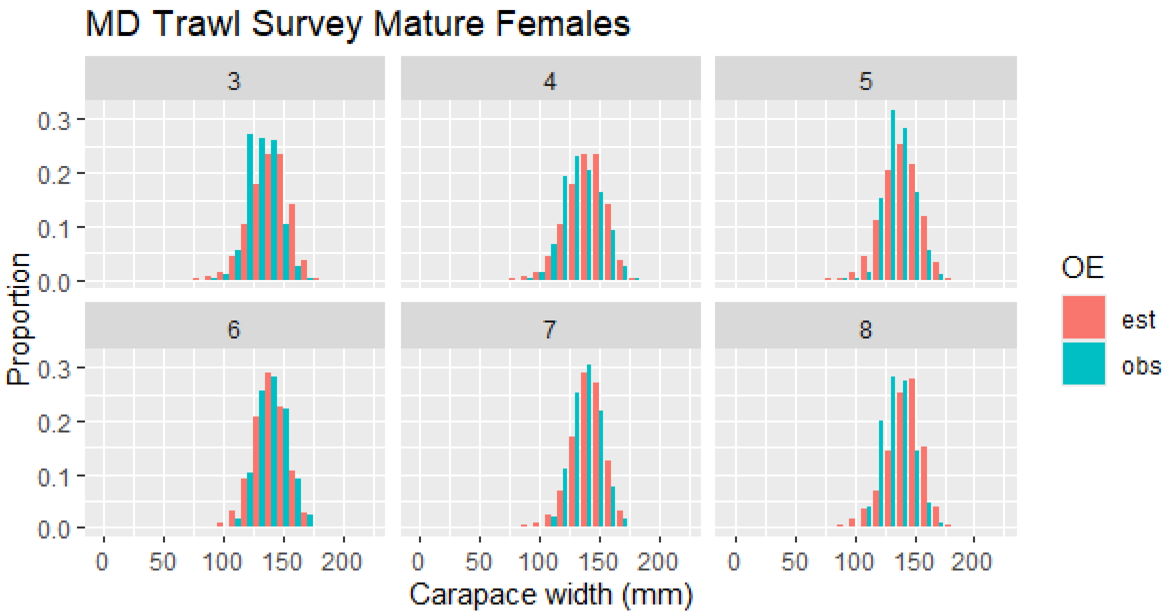

Figure 10. Monthly simulated and observed proportions-at-length from the Maryland Trawl Survey for mature females. Colors are as defined in Figure 9.

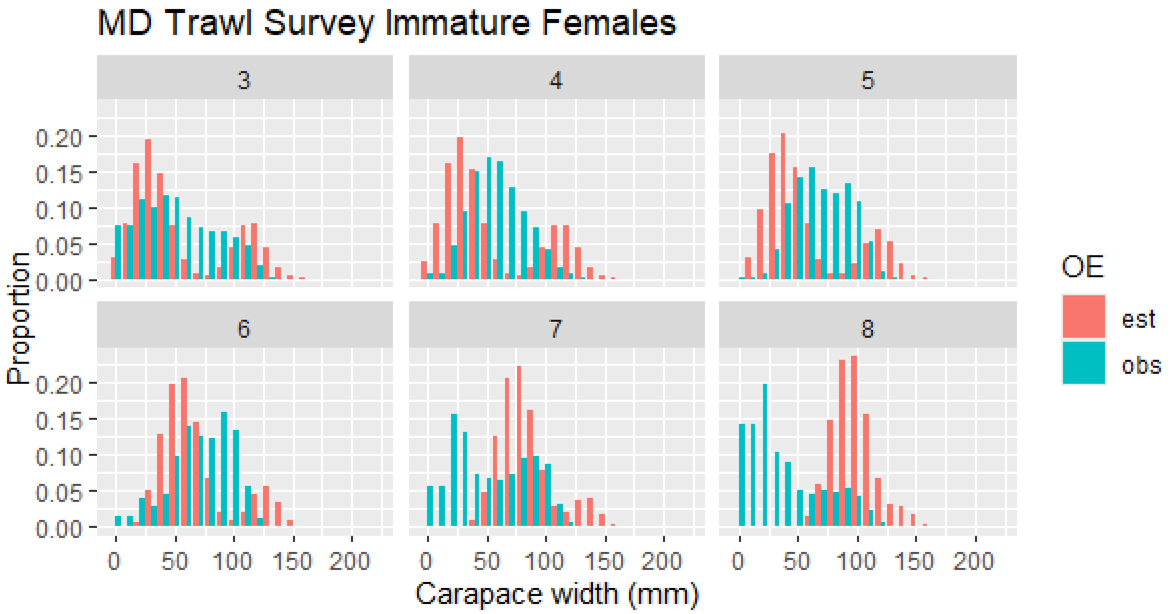

Figure 11. Monthly simulated and observed proportions-at-length from the Maryland Trawl Survey for immature females. Colors are as defined in Figure 9.

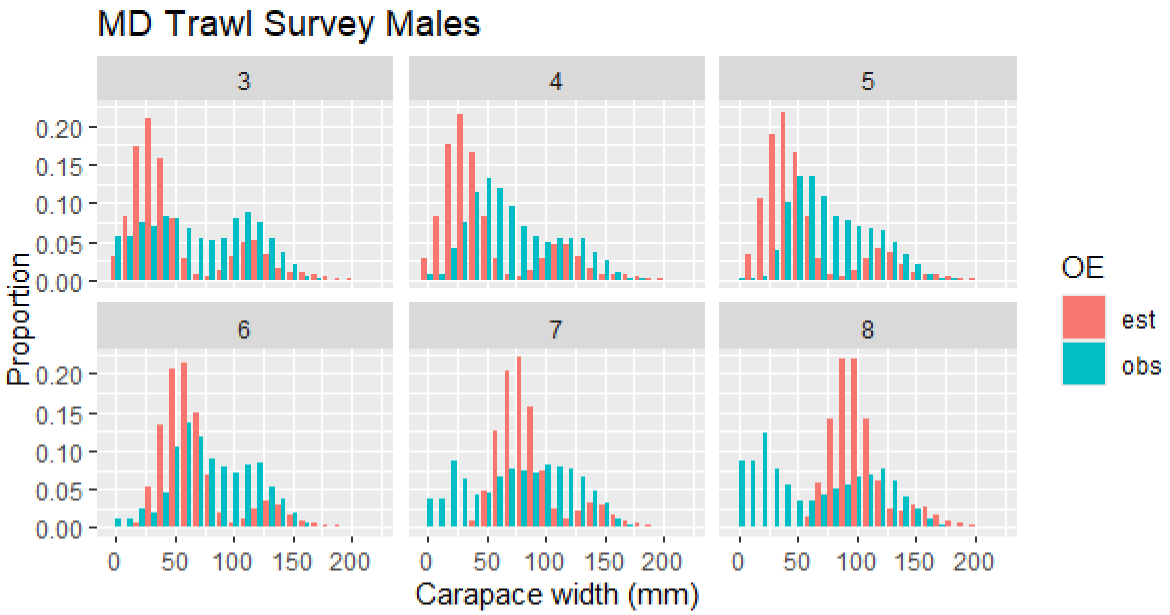

Figure 12. Monthly simulated and observed proportions-at-length from the Maryland Trawl Survey for males. Colors are as defined in Figure 9.

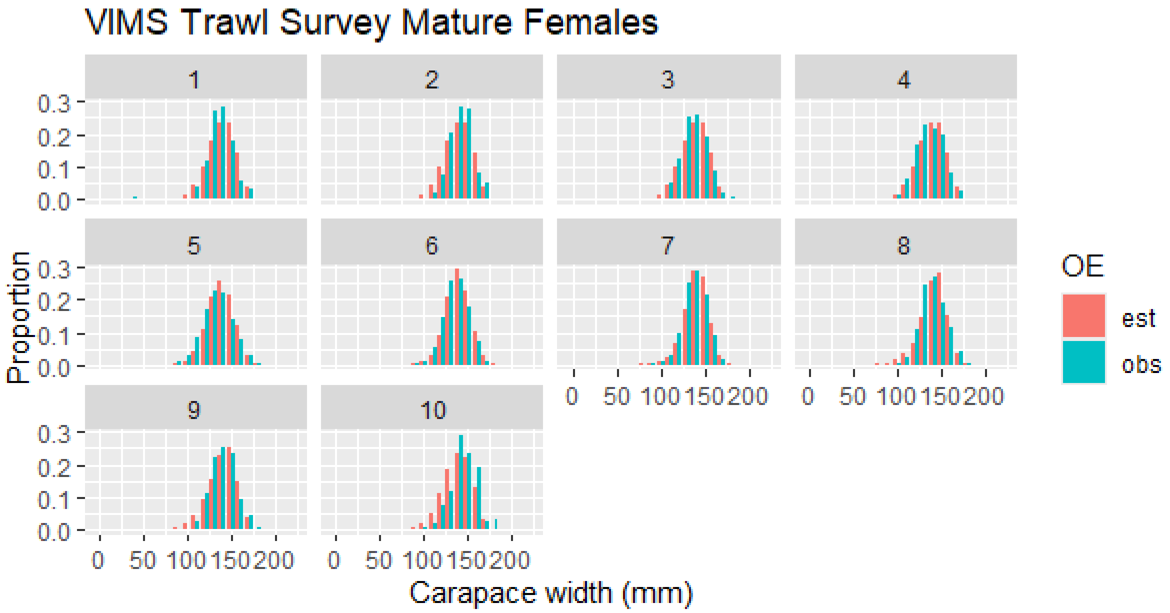

Figure 13. Monthly simulated and observed proportions-at-length from the VIMS Trawl Survey for mature females. Colors are as defined in Figure 9.

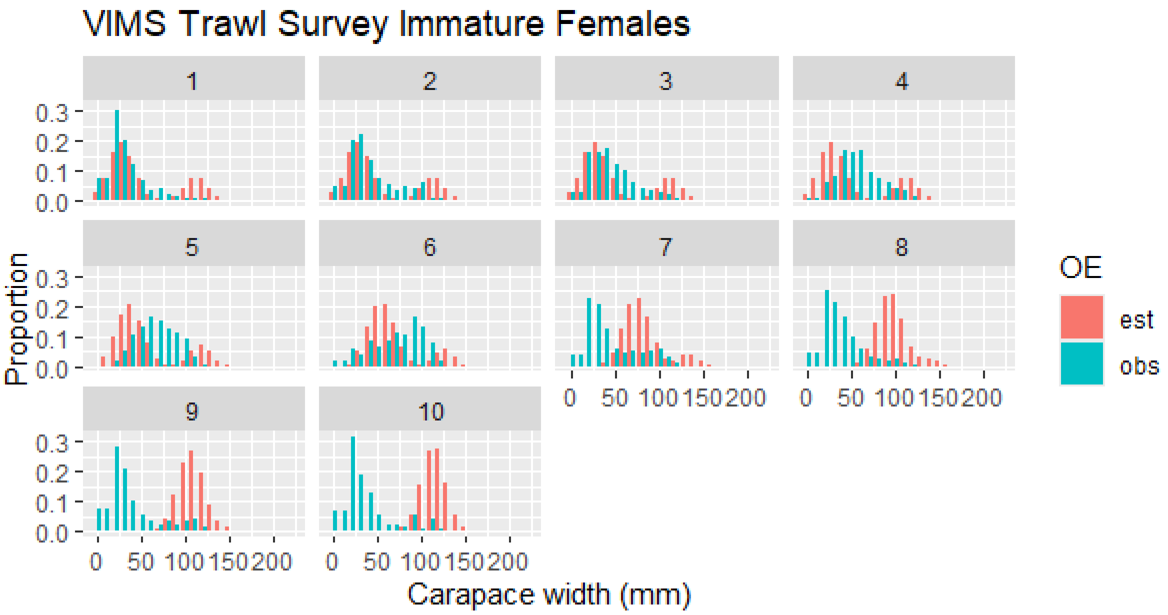

Figure 14. Monthly simulated and observed proportions-at-length from the VIMS Trawl Survey for immature females. Colors are as defined in Figure 9.

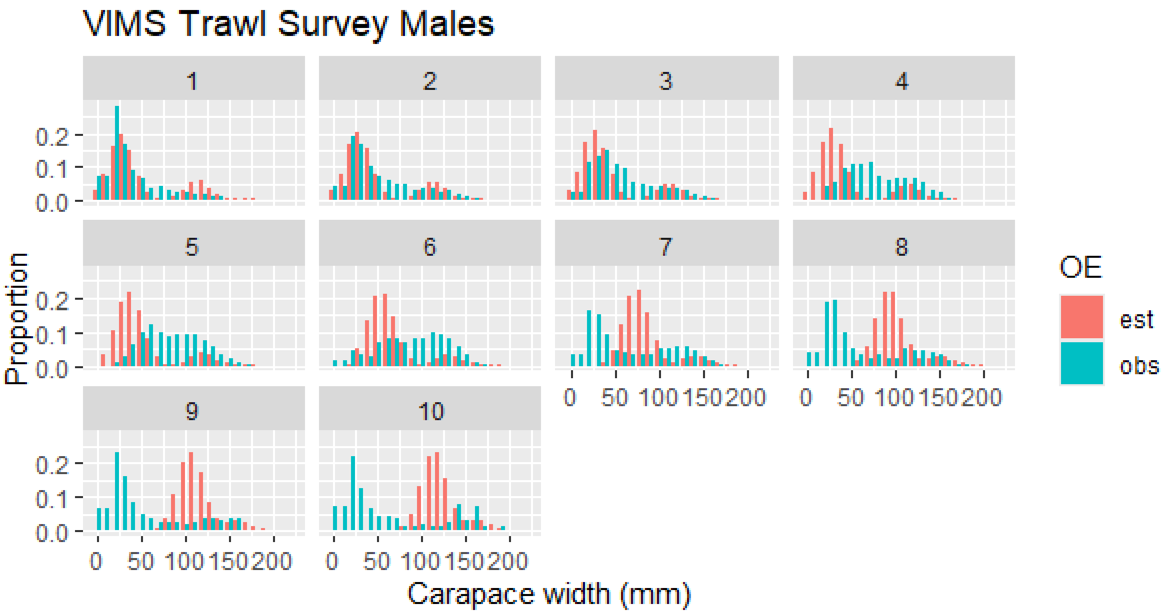

Figure 15. Monthly simulated and observed proportions-at-length from the VIMS Trawl Survey for males. Colors are as defined in Figure 9.

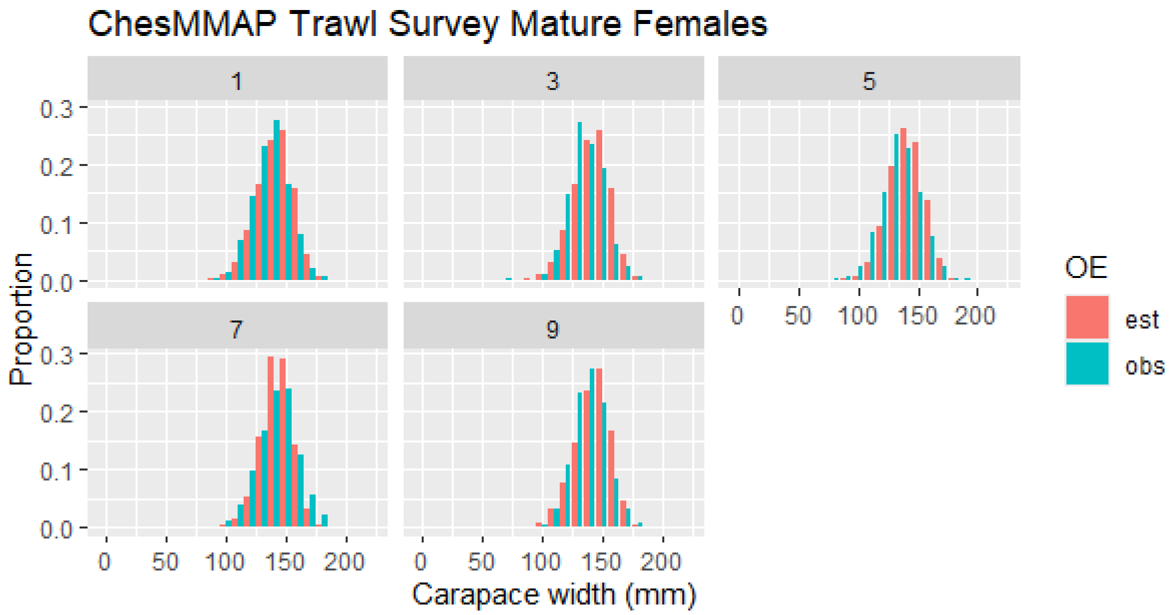

Figure 16. Monthly simulated and observed proportions-at-length from the ChesMMAP Trawl Survey for mature females. Colors are as defined in Figure 9.

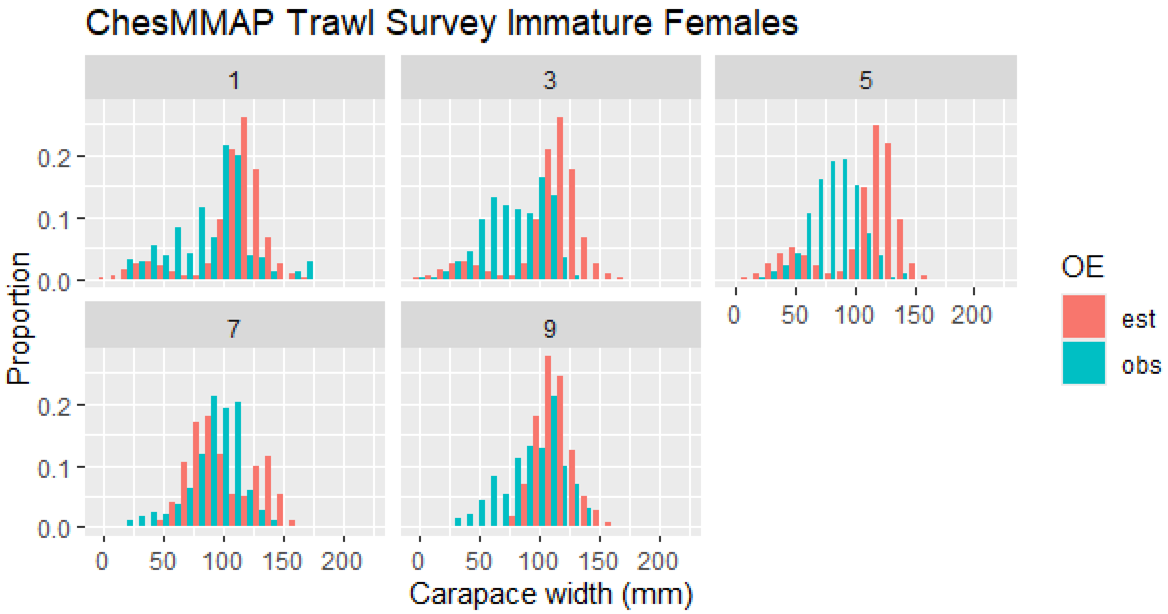

Figure 17. Monthly simulated and observed proportions-at-length from the ChesMMAP Trawl Survey for immature females. Colors are as defined in Figure 9.

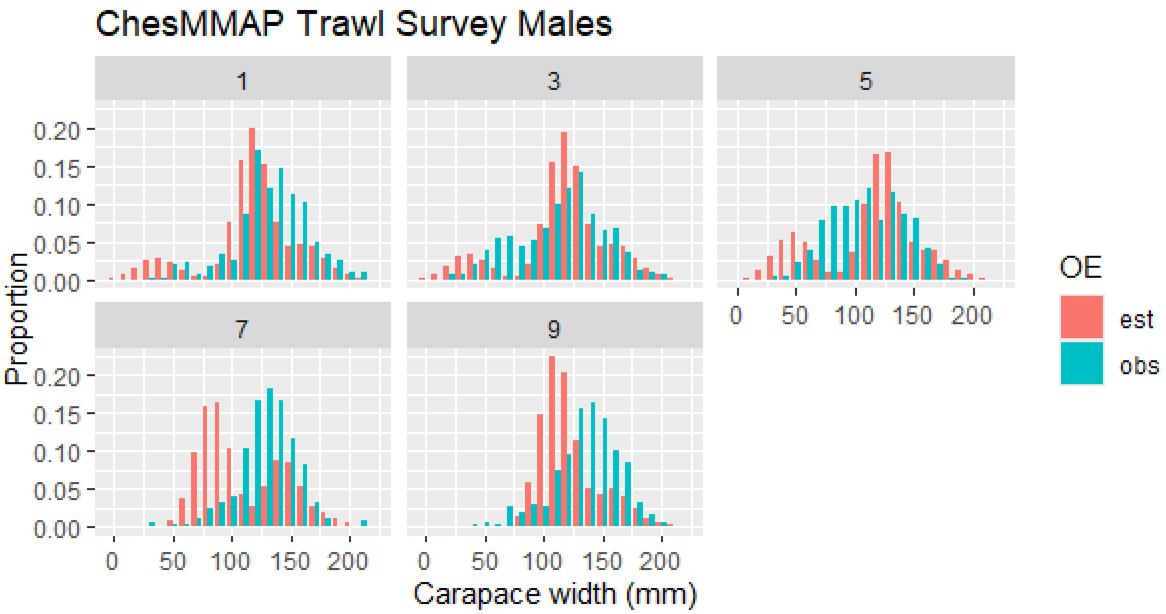

Figure 18. Monthly simulated and observed proportions-at-length from the ChesMMAP Trawl Survey for males. Colors are as defined in Figure 9.

Challenges

We had two main challenges that caused us to deviate from our initial modeling plan. The first challenge was that the length-based dynamics model development took substantially longer than expected. This was partially due to the complexity of the length- and sex-structured model, which required substantially different models for growth of females and males. We attempted to develop statistical fitting approaches to estimate the growth parameters within the population model, which took a considerable amount of time. However, we were unable to find a stable version of the model for estimation of the growth parameters. Additionally, because we were unable to statistically estimate the growth parameters, we also gave up on attempting to statistically estimate movement parameters for a spatial version of the model. That said, this project has allowed us to make substantial progress toward a length-structured blue crab assessment model and a spatial operating model.

Conclusions

We developed an operating model that is able to simulate dynamics of blue crabs in the Chesapeake Bay. The model included recruitment, growth, mortality, and observation processes and can be tailored to represent specific scenarios about growth, recruitment, or mortality. In many ways the model was able to replicate the observed interannual and intra-annual dynamics of blue crabs. It was best at representing mature females, but the current growth model was not able to match the length compositions in the spring-summer. This likely points to a mismatch in our assumed growing degree day threshold, or it may indicate that the effect of temperature on growth changes during the year. These hypotheses will be explored in the upcoming benchmark stock assessment for blue crabs. Additionally, the operating model will be extremely useful for testing versions of stock assessment models to determine their accuracy and bias under known conditions.

Section 5

Toward a spatial blue crab assessment model

We developed also as a part of this project more detailed operating / observation models to support a highly resolved assessment model (Figure 1). These models were used to explore both assumptions underlying the observation model, include more fine-scaled spatial population dynamic processes in the operating model and assess the performance of a prototype assessment model. This assessment model is simpler than the operation model. This effort focuses on development of models that are estimable from the incomplete survey and fisheries data. The resulting model can be expanded into a simulation model and used to test the assessment model. These efforts are not complete, but have provided considerable insight that will guide the upcoming blue crab stock assessment model.

This secondary modelling initiative focused only on male crabs. We made this simplifying assumption because it eases estimation challenges associated with the terminal molt in female crabs. Other than this distinction, the operating model follows closely the format of the general operating model presented in the previous section. The model was parameterized for a number of spatial regions (Fig 19).

Population dynamic model

The model represents the life history and fishery dynamics of the male blue crab in the Chesapeake Bay. It is a discrete model with a monthly time step. As in the general operating model, the months of January – March are combined to represent winter, during which no growth occurs. Thus the model is based on a 10-month year. In all subsequent equations, y is the year, and t is the month

The abundance of crabs is given by the number of crabs in discrete size bins, defined by a parameter l, at time t

Recruitment

Recruitment is modelled to occur from May to November in each year. Some recruitment is possible in each of these months. Each monthly cohort experiences natural mortality between recruitment and the first winter. Recruitment is modeled via the proportion of recruits at length (P_l) and monthly recruitment parameter (R_t):

$$\mathrm{R}_{l,t} = \mathrm{P}_l \, \mathrm{R}_t \qquad (1)$$

There is no stock-recruitment function in the model. R_t is a random variable.

Model initialization

A recursive relationship is used to establish the initial population abundance and distribution at size. The male abundance at length $N_{l,t+1}$ is the sum of the recruitment and the abundance of individuals that survive and grows to a specific size bin. We define a monthly growth matrix $\mathrm{G}_{t,l,l'}$ as the probability of growing from size bin l' to l during month t. The total instantaneous mortality rate is defined as $Z_{l,t}$.

$$N_{l,t+1} = \exp\{\delta_{l,t}\} \sum_{l'} G_{t,l,l'} N_{l',t} \exp\{-Z_{l',t}\} + R_{l,t} \tag{2}$$

A Normally distributed process error $\delta_{l,t} \sim N(0, \sigma_\delta^2)$ is included in the population dynamic. The model assumes growth occurs after mortality.

The population abundance and distribution at length in the initial time step is determined by running Eq. (2) for ten years. During this phase, only natural mortality, $M_{l,t}$ contributes to $Z_{l,t}$. Natural mortality is assumed constant and fixed over time. However, natural mortality is size dependent (Figure 20). There is no fishing mortality ($F_{l,t}$) during this phase. A seasonal growth matrix $G_{m,l,l'}$ is used during the initialization stage.

Growth and Survival

The abundance and size composition are calculated using Eq. 2, but with a variable G matrix and fishing mortality.

Growth for males follows a stochastic von Bertalanffy growth model that uses a normal distribution to estimate the probability of moving from one length bin (i.e., carapace width) to the next,

$$G_{t,l,l'} = \Phi(l' \times w) - \Phi(l \times w), \tag{3}$$

where w is the bin width, l is the length bin, and Φ is a cumulative normal density function with mean $\Delta_{t,l} = (L_\infty - l)(1 - e^{-K_t})$ and variance of the growth increment (Cao et al. 2017b),

$$\sigma_{\Delta,t,l}^2 = \sigma_{L_\infty}^2 (1 - e^{-K_t})^2 + (L_\infty - l)\sigma_{K_t}^2 e^{-2K_t} + \sigma_{K_t,L_\infty}(1 - e^{-K_t})(L_\infty - l)e^{-K_t} \tag{4}$$

where σ_{K_t,L_∞} is the covariance between the L_∞ and K_t parameters in the von Bertalanffy model. The smallest length bin represents individuals in that range and smaller,

$$G_{t,l=1} = \Phi\left(\frac{w}{2}\right) \tag{5}$$

The largest length bin is a "plus" group representing all individuals that carapace width and larger,

$$G_{t,l=L} = 1 - \Phi(L \times w) \tag{6}$$

Negative growth is not allowed. The parameterization of the seasonal growth model is shown in Figure 21

We include an environmental driver for the annual growth coefficient of the von Bertalanffy model over time.

$$K_t = k_p \mathrm{GDD}_t \tag{7}$$

Initially, we are modeling *K* as a linear function of cumulative growing degree days during a time step.

Following initialization, the total instantaneous mortality (Z) is the sum of natural mortality at length (M_l) and fishing mortality at length for a single fleet ($\mathrm{F}_{l,t,f}$) specific to each time step.

$$\mathrm{Z}_{l,t} = \mathrm{M}_l + \mathrm{F}_{l,t,f} \tag{8}$$

The fishing mortality is the product of the length-based selectivity (fsel_l) and fishing intensity (Fmult_t).

$$\mathrm{F}_{l,t,f} = \mathrm{fsel}_l \times \mathrm{Fmult}_{t,f} \tag{9}$$

Fishing occurs between March and November each year. Limited winter catches are ignored in this model.

Catch (*C*) for each fleet and time step follows the Baranov catch equation,

$$\mathrm{C}_{l,t,f} = \frac{F_{l,t,f}}{Z_{l,t}}\left[1 - \exp\left(-Z_{l,t}\right)\right]N_{l,t} \tag{3}$$

Observation model

The WDS is treated as the beginning of the year survey, with no catchability adjustment. Size specific abundances in the WDS is given by,

$$\mathrm{I}_{1,l,t} = \mathrm{ssel}_l \times N_{l,t} \tag{4}$$

The WDS occurs only once in the year during the winter time step.

The Maryland trawl survey is a monthly survey that operates during April – September. The Maryland trawl survey is subject to a constant catchability over time. Size specific abundances in the Maryland trawl survey is given by

$$\mathrm{I}_{2,l,t} = q \times \mathrm{ssel}_l \times N_{l,t} \tag{5}$$

where ssel_l is the survey selectivity at length. Catchability is calculated internally

$$q \propto \sum_{l,t}\left[\log\left(\mathrm{ssel}_l \times N_{l,t}\right) - \log\left(n_{l,t}\right)\right] \tag{6}$$

where the sum is taken over all length bins with a positive catch.

The lognormal likelihood is used for observation errors in total catch from both survey indices,

$$n_{s,t} \sim \mathrm{lognormal}\left(I_{s,t}, w_1\right), \tag{7}$$

where n is the total catch and w_1 is the assumed known standard deviation for each index s.

Multinomial errors are used for size composition data from the survey

$$p_{s,l,t} \sim \text{Multinomial}\left(P_{s,l,t}, n_1\right), \tag{8}$$

where P is the proportion of abundance at length for each time step, and n_1 is the assumed known number of stations for both surveys.

The lognormal likelihood is used for the errors in total fishery catch,

$$c_t \sim \text{lognormal}(C_t, w_2). \tag{9}$$

Size composition in the model is pooled into total catch to match the data source. Additionally, random effects are estimated for the recruitment parameters, and the process error for abundance at length.

Estimation

Parameters from the model were estimated in TMB. The full model code is provided in Appendix 3.

Informative priors were derived for the von Bertalanffy parameters based on literature values(Ju et al. 2001a). The reported L_∞ and K from six studies were re-sampled using bootstrap to derive the lognormal prior distribution for their mean and standard deviation. Informative priors were derived for the survey selectivity parameters based on expert knowledge (Figure 22).

Informative priors were derived for the fishing intensity and recruitment based on cross-validation. An initial set of mean and standard deviations for the lognormal priors on the log standard deviation of the recruitment were selected based on the prior assessment. The priors that lead to optimal cross-validation errors for the WDS index were selected. Detailed prior specifications can be found in the supplementary codes.

The model was fit iteratively to 5-13 years of data. Considerable supervision was required to improve model performance.

Results

In the results, observations and estimates for regions were aggregated at the state level. The Main 1, Main 2, Choptank, Patuxent, Potomac and Tangier 3 regions were defined as Maryland (Figure 19). The Main 3, Main 4, Tangier 5, Rappahannock, York and James regions were defined as Virginia (Figure 19).

Overall, the model demonstrated the ability to generate the pattern and scale of catches in the male fisheries (Figure 23). However, the model rarely predicted catches as high as those observed, and there is some evidence for a mismatch in the timing of peak catch between the modelled and observed catches.

The model was less able to estimate catches in the WDS correctly (Figure 24). There appears no consistent pattern of match of observed and estimated data. This is made more challenging by the fact that the observation model predicts WDS abundance for all 10 months of the year – providing the saw tooth nature of the estimated survey abundance, in which recruitment during summer is acted upon by mortality. A more appropriate comparison might be to compare just estimated survey abundance for the aggregate winter month to that observed in the WDS. This may reflect either incorrect specification of error in the observation model, or problems with estimated uncertainty in the assessment model.

The model also did not estimate the size distribution in the WDS well (Figures 25 - 26). The model did much better in estimating the size distributions in Virginia than in Maryland. We have shown previously that the operating model was able to forecast the size distribution in surveys to a reasonable degree of accuracy. However, the assessment model in our simulations was not able so to do. This suggests tension in the data that are entered into the model.

The model appeared to estimate the scale and pattern of catches in both the Maryland trawl and the VIMS trawl surveys (Figure 27). As was the case with the WDS, the model does not estimate survey indices as high as those observed in the field. This difference is evident most in the later years of the Maryland trawl survey, but is more consistent throughout the VIMS trawl survey. This may reflect either incorrect specification of error in the observation model, or problems with estimated uncertainty in the assessment model.

The model performed better in estimating the size distributions of male crabs in both the Maryland trawl survey (Figure 28) and the VIMS trawl survey (Figure 29). This improvement in model performance relates directly to the greater number of monthly observations in these two surveys providing information to the model that improves the fit of the model to the size distributions. Specifically, the data provide the model more information from which to estimate the G matrices that drive growth.

As noted above, this model does not include any movement among spatial regions. It is possible that a fully spatial model will help resolve some of the patterns observed in the length compositions by allowing for varying temperature in different parts of the Bay. However, from the experience gained in fitting these length-structured models, we are concerned that there is insufficient movement data, at the spatial and temporal resolution of the surveys, to allow us to successfully develop such a spatial model.

There are three main challenges for moving from the current non-spatial length-structured model to a spatial version: 1) spatial patterns of recruitment, 2) spatial patterns of mortality, and 3) movement among regions. Spatial patterns in recruitment is likely the easiest problem to address because the WDS operates in all parts of the Bay and surveys in a consistent manner. Therefore, it should be relatively straightforward to estimate the proportion of age-0 blue crabs in each region of the Bay. But this requires us to include the assumption that recuitment is observed for the first time in the aggregate winter month. The main issue would be if the proportions in each region are changing over time because forcing functions would need to be developed to allow the simulation model to forecast changes in the spatial distribution of recruits. Spatial patterns in mortality are more challenging to deal with than recruitment because a common survey like the WDS does not sample throughout the whole year. Rather, we have surveys that sample large, but often non-overlapping areas. The differences in selectivity and catchability among surveys make it difficult to infer differences in mortality rates from survey data alone. Lastly, movement will likely be the most difficult portion of the model to parameterize. Ideally, movement would be estimated through a large-scale tagging study that marks indiviuals throughout the Bay and has a coordinated and well-designed approach for getting recaptures throughout the whole Bay. To date this kind of study has not been done. Smaller scale tagging studies can help inform movement, but substantial uncertainty will remain because many parts of the Chesapeake were not included in those studies.

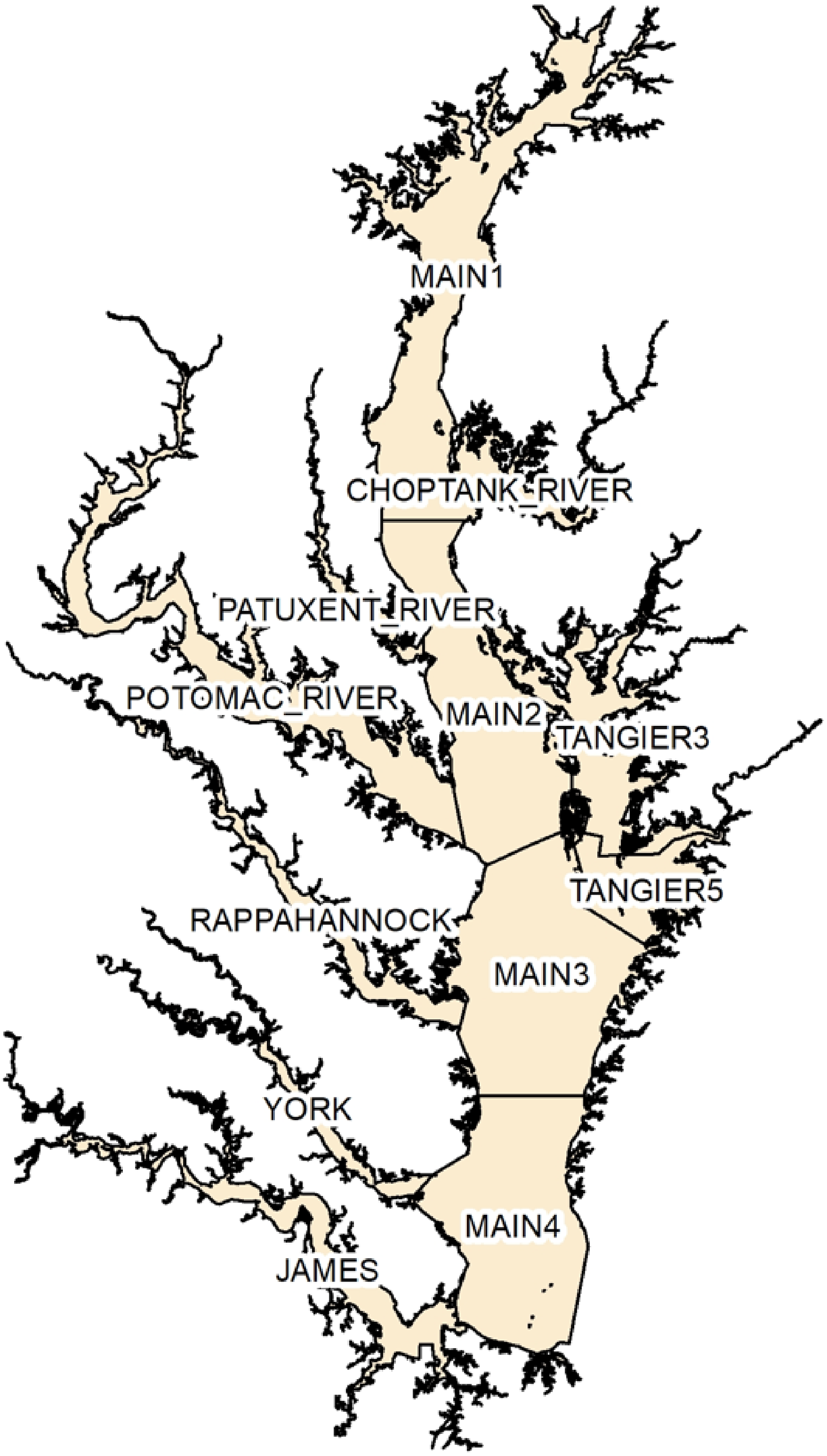

Figure 19. The spatial regions used in the spatially explicit modeling exercise

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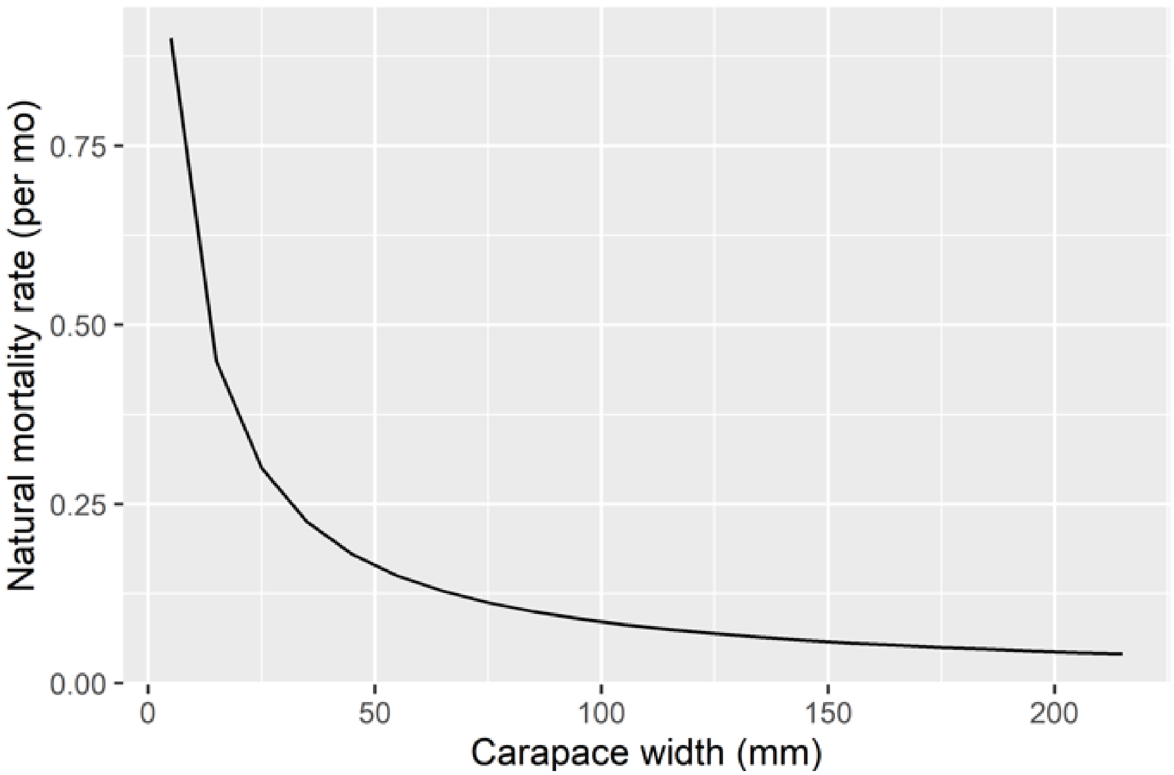

Figure 20. The size dependent natural mortality function used in the model. The overall rate of natural mortality was fixed to M=0.9 / yr or 0.009 / month for the 10 month year

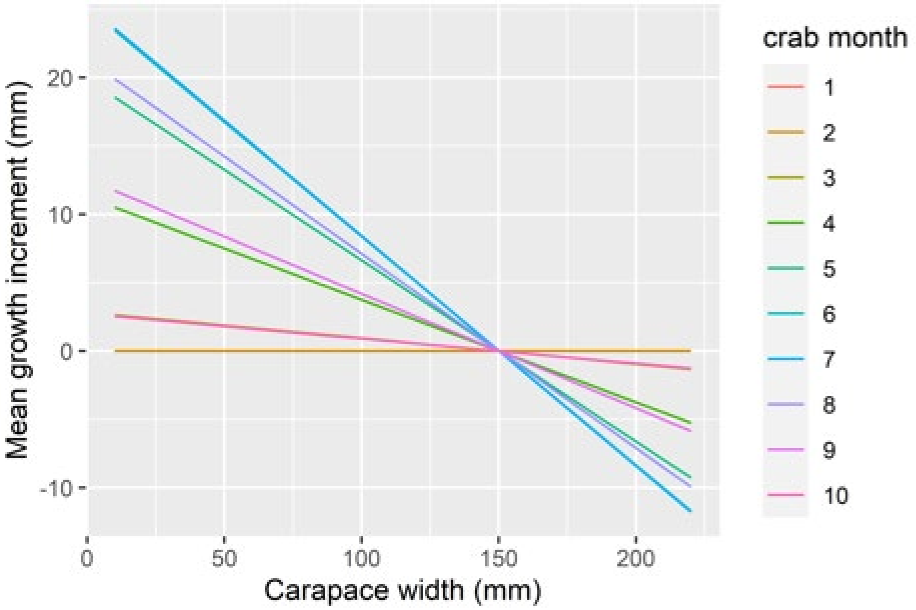

Figure 21. The seasonal growth model used in the operating model. Each line is the linear incremental growth function for a different month

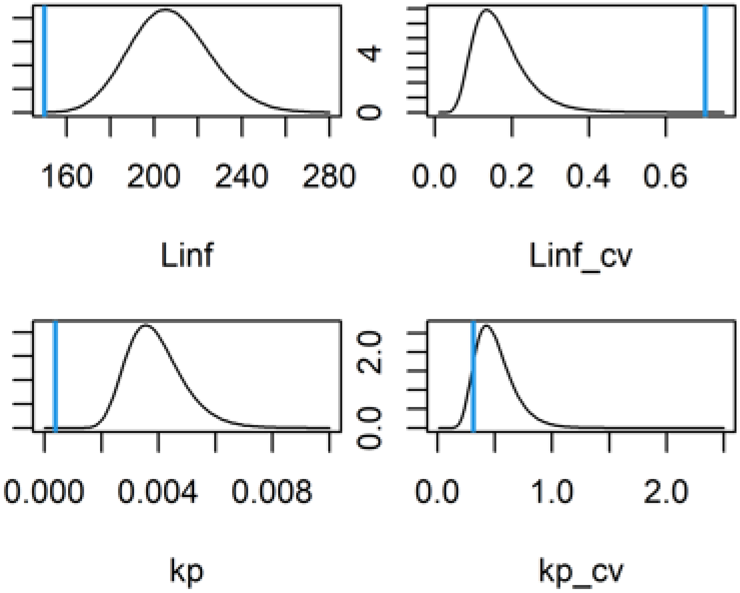

Figure 22. Posterior distributions of parameters for the growth model, together with their initial values (in blue)

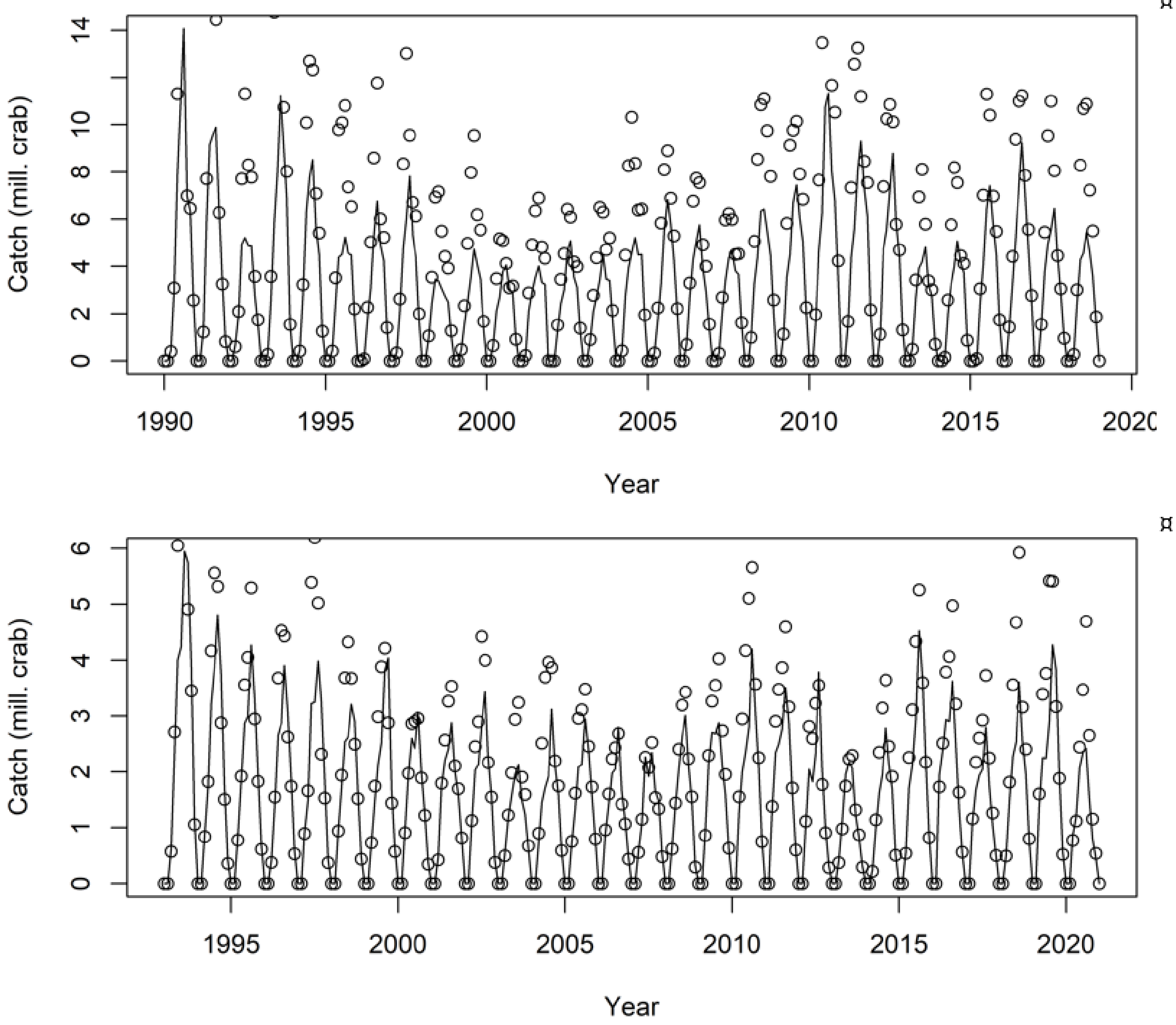

Figure 23. Time series of observed and estimated catch of male crabs in Maryland (upper panel) and Virginia (lower) for the period 1993-2022. The observed catches are shown as open symbols, and the estimated catches as the solid line.

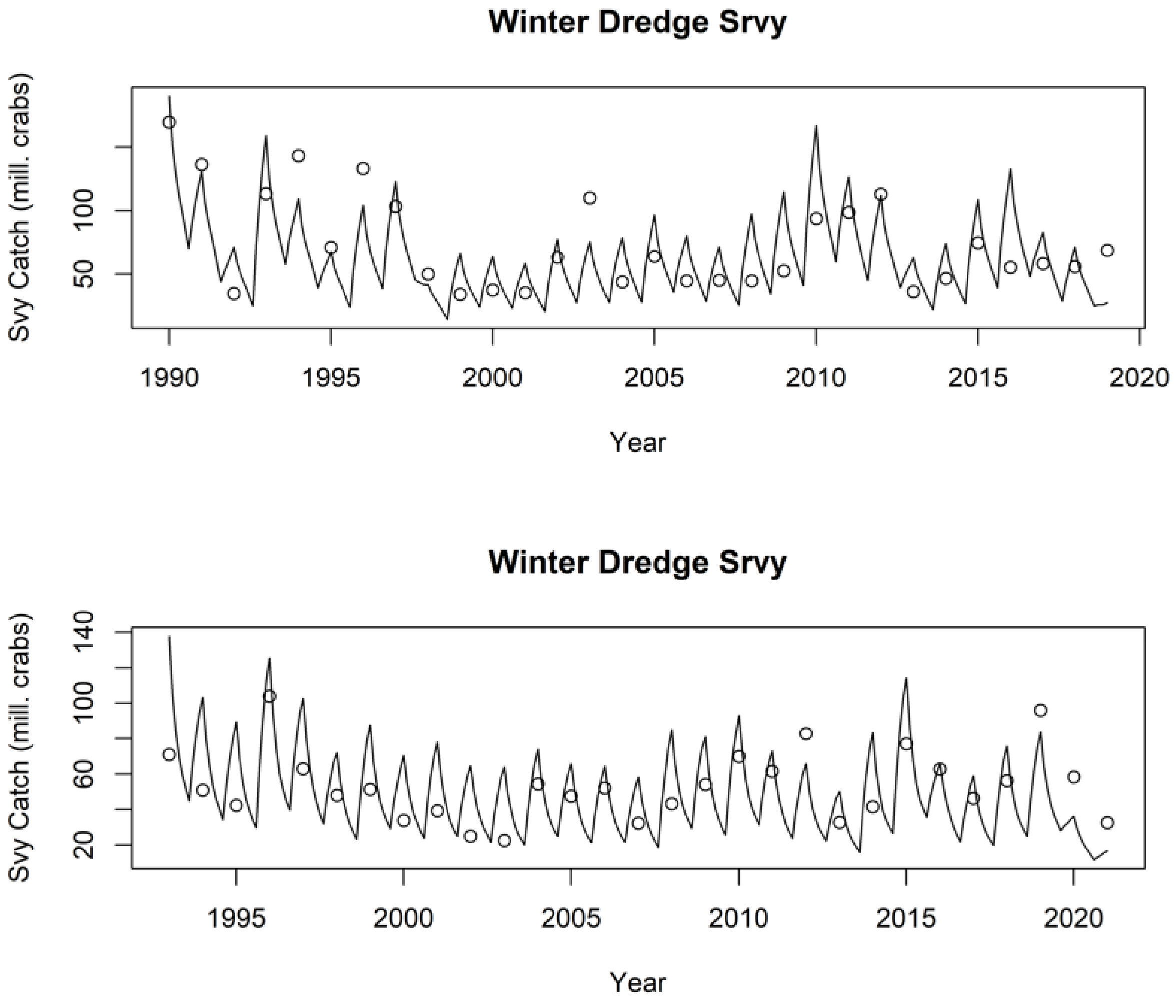

Figure 24. Time series of observed and estimated indices for total male abundance in the winter dredge survey for strata in Maryland (upper panel) and in Virginia (lower) panel for the period 1993 -2022. Both panels show observations as open circles and estimated male abundance as the black line

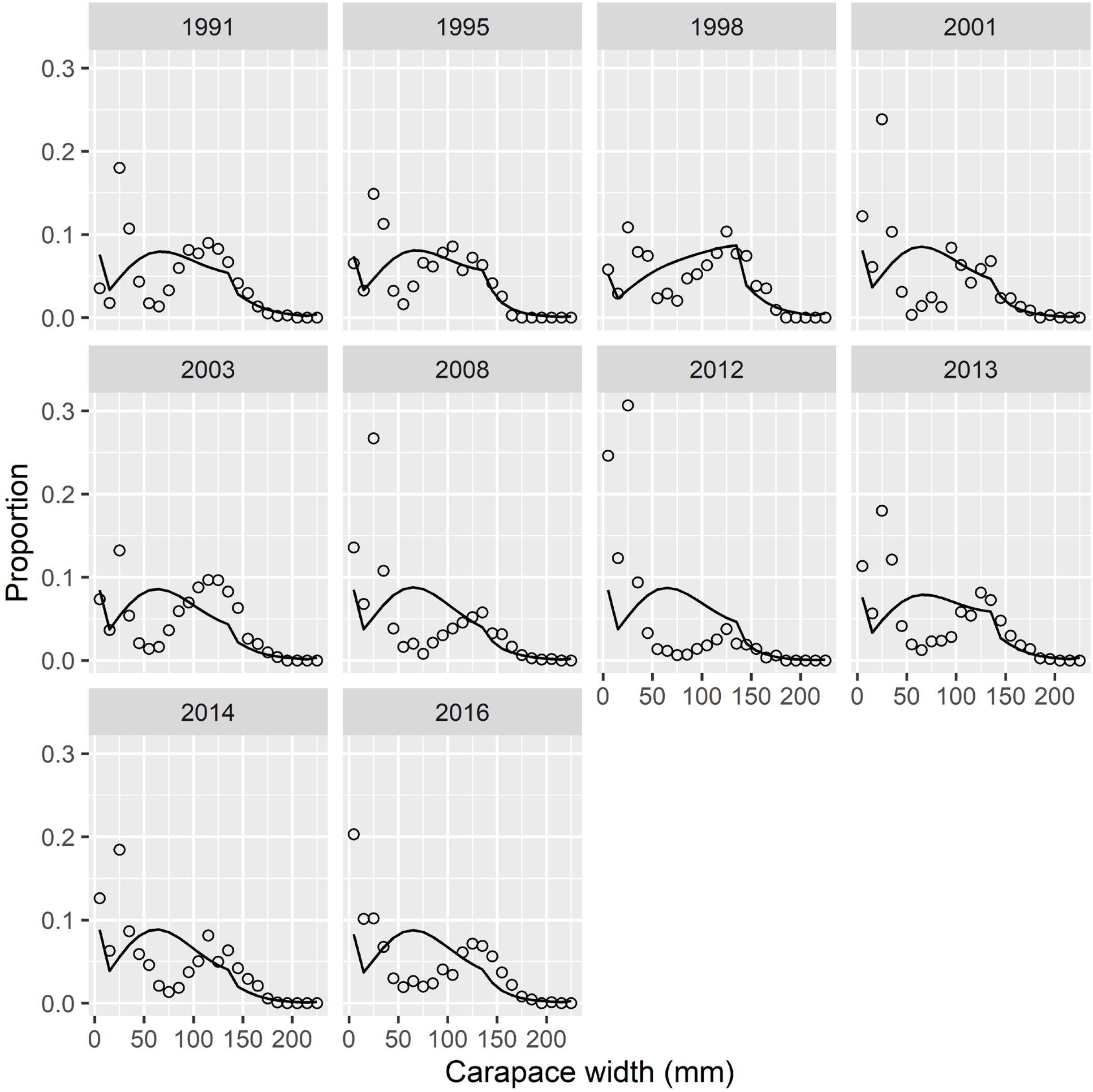

Figure 25. Observed (solid symbols) and predicted (line) size distributions of male crabs in the winter dredge survey from 1991-2016

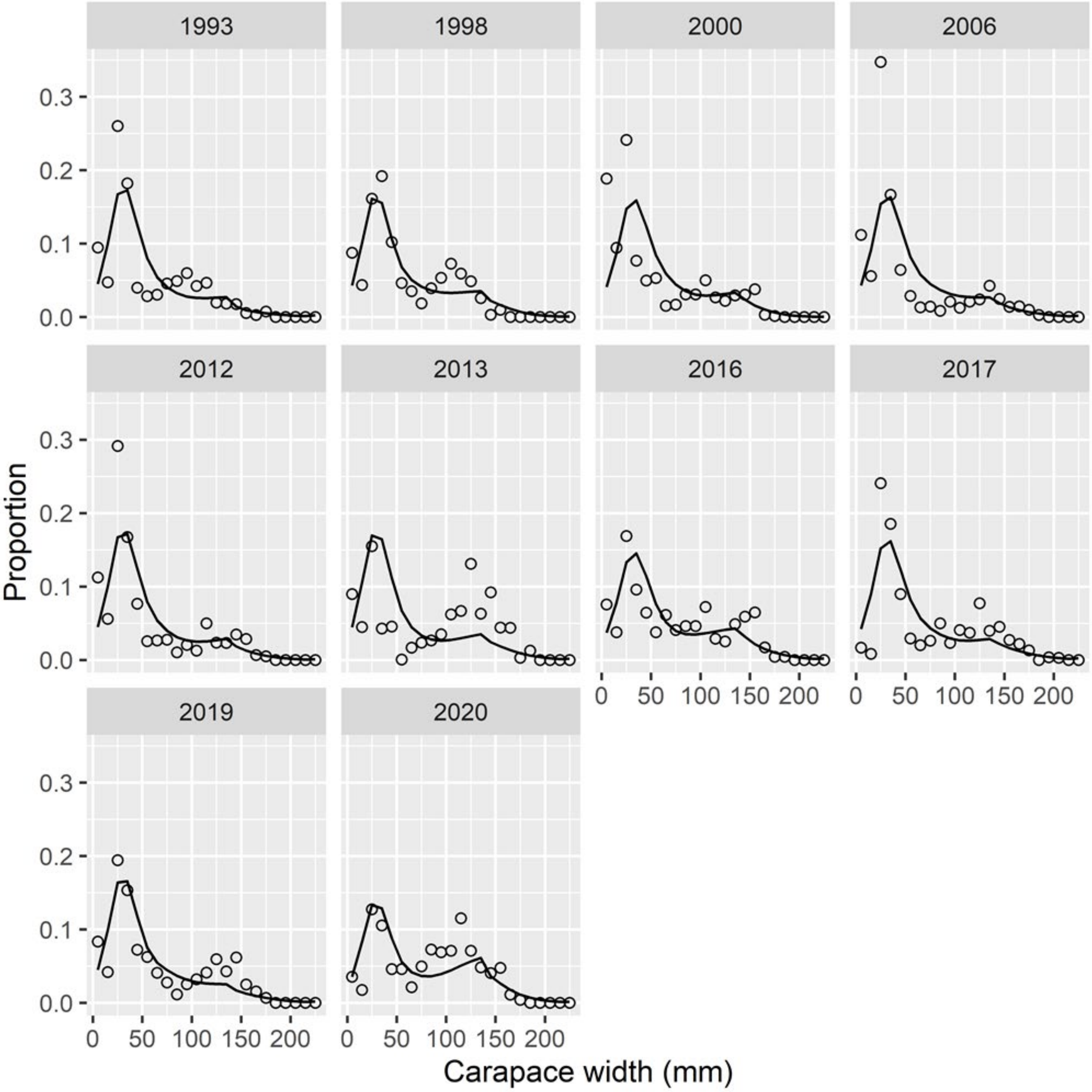

Figure 26 Observed (solid symbols) and predicted (line) size distributions of male crabs in the winter dredge survey from 1991-2016

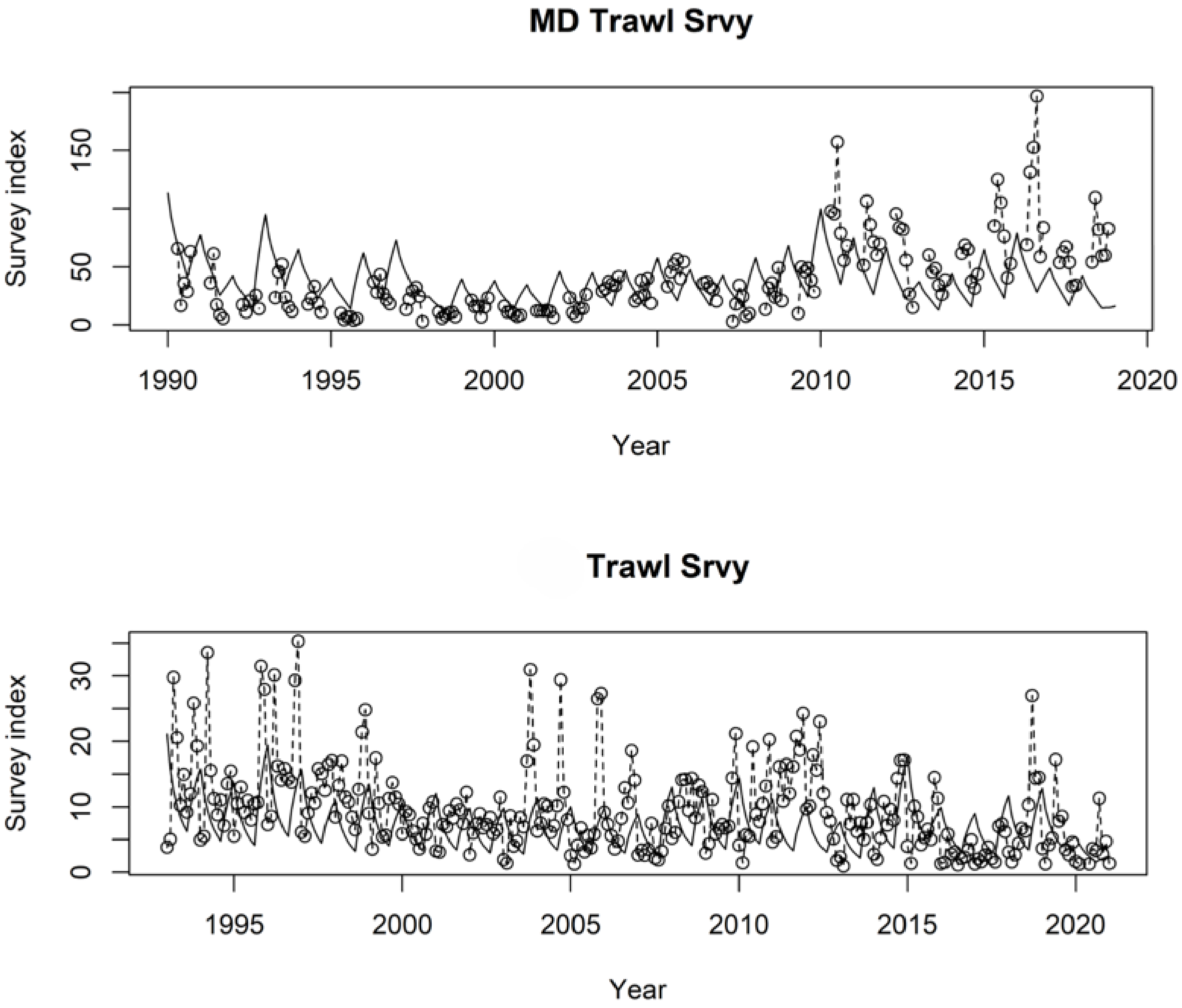

Figure 27. Observed and estimated abundances of male crabs in the Maryland trawl survey (upper panel) and the VIMS trawl survey (lower panel) for the period 1993- 2022. Estimated values are shown as a solid line and observed values as open symbols and a dashed line.

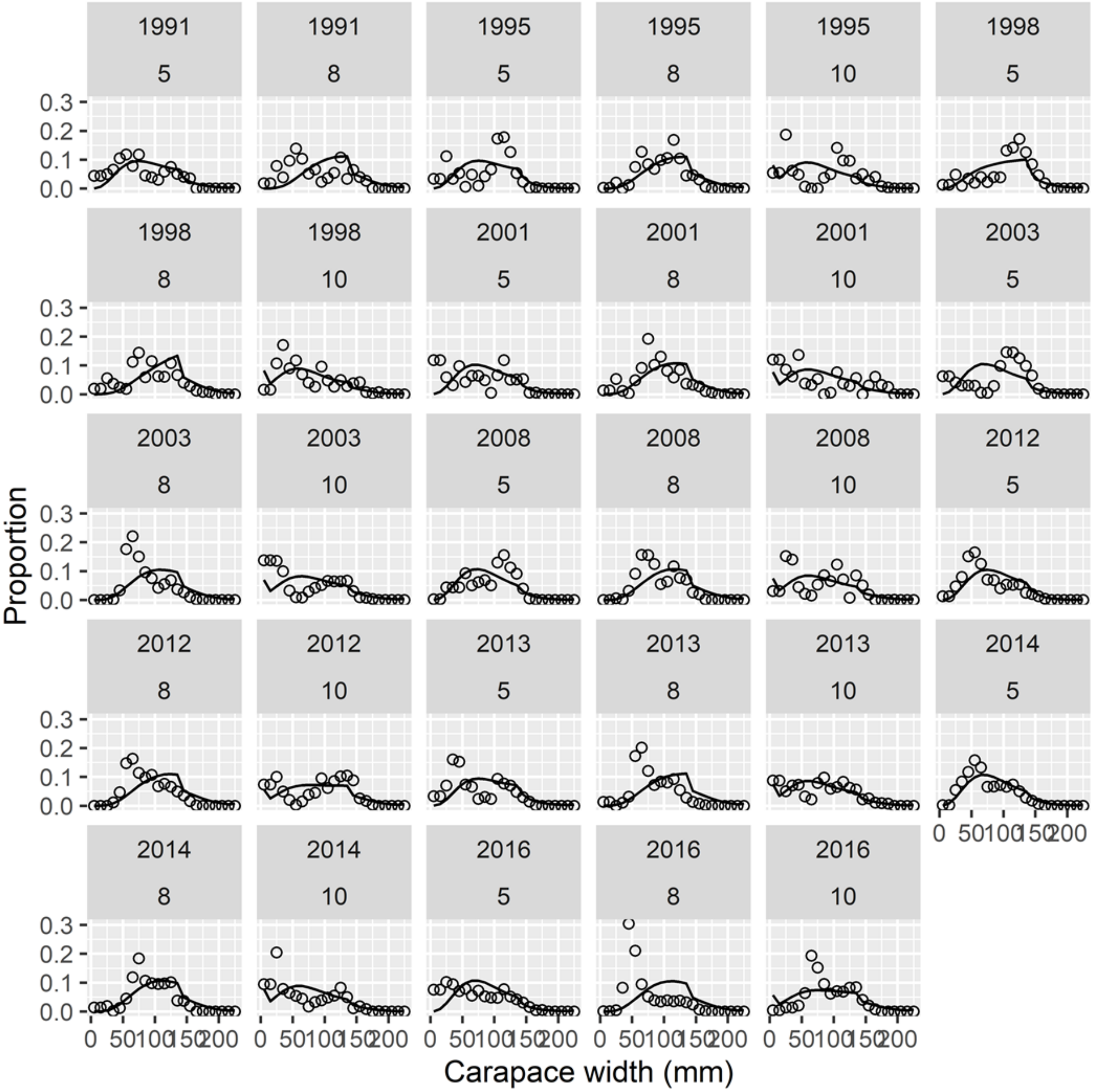

Figure 28. Predicted (solid line) and observed (open symbols) size distributions of male crabs in the Maryland trawl survey for 1991-2016 by month

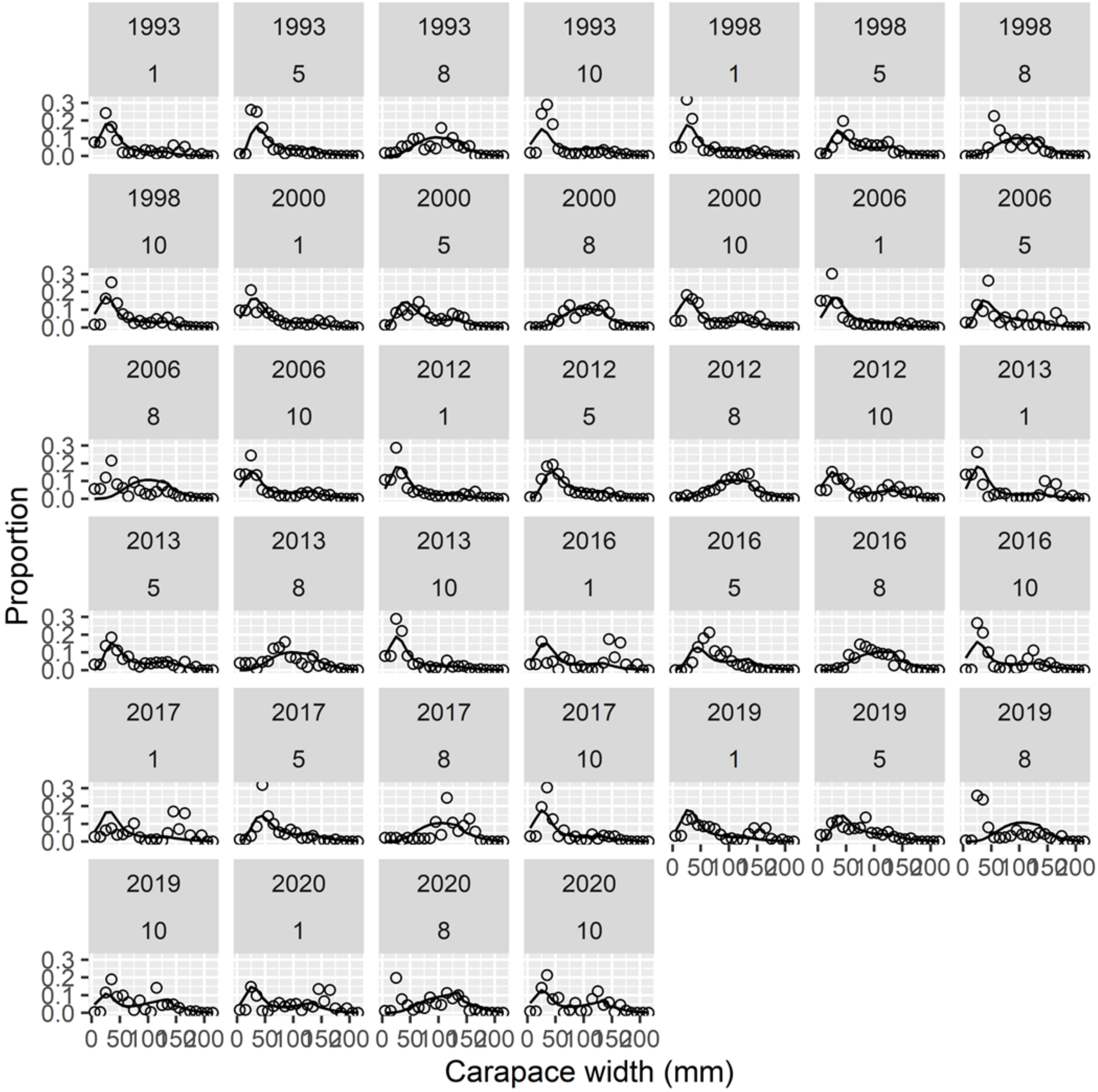

Figure 29. Predicted (solid line) and observed (open symbols) size distributions of male crabs in the VIMS trawl survey for 1993-2020 by month

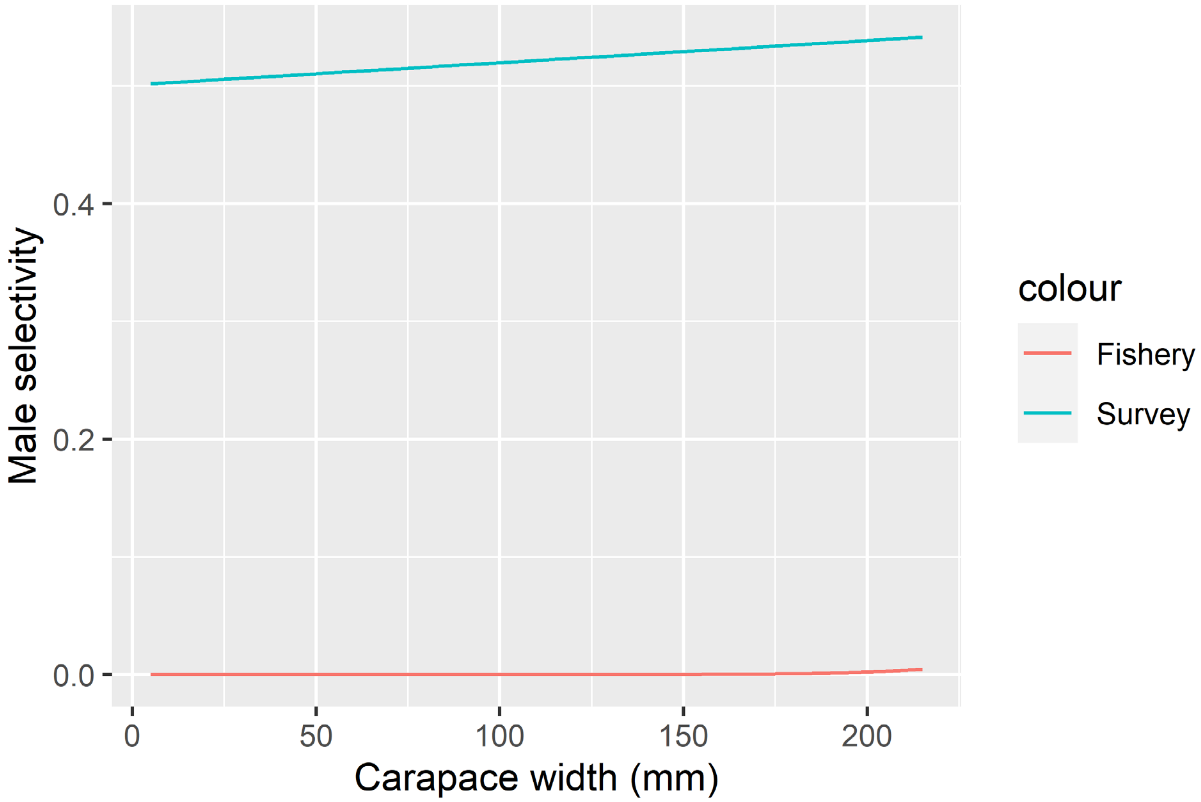

Figure 30. Estimated selectivity curves for the fishery (red) and surveys (blue) for male crabs in Maryland between 1990-1999

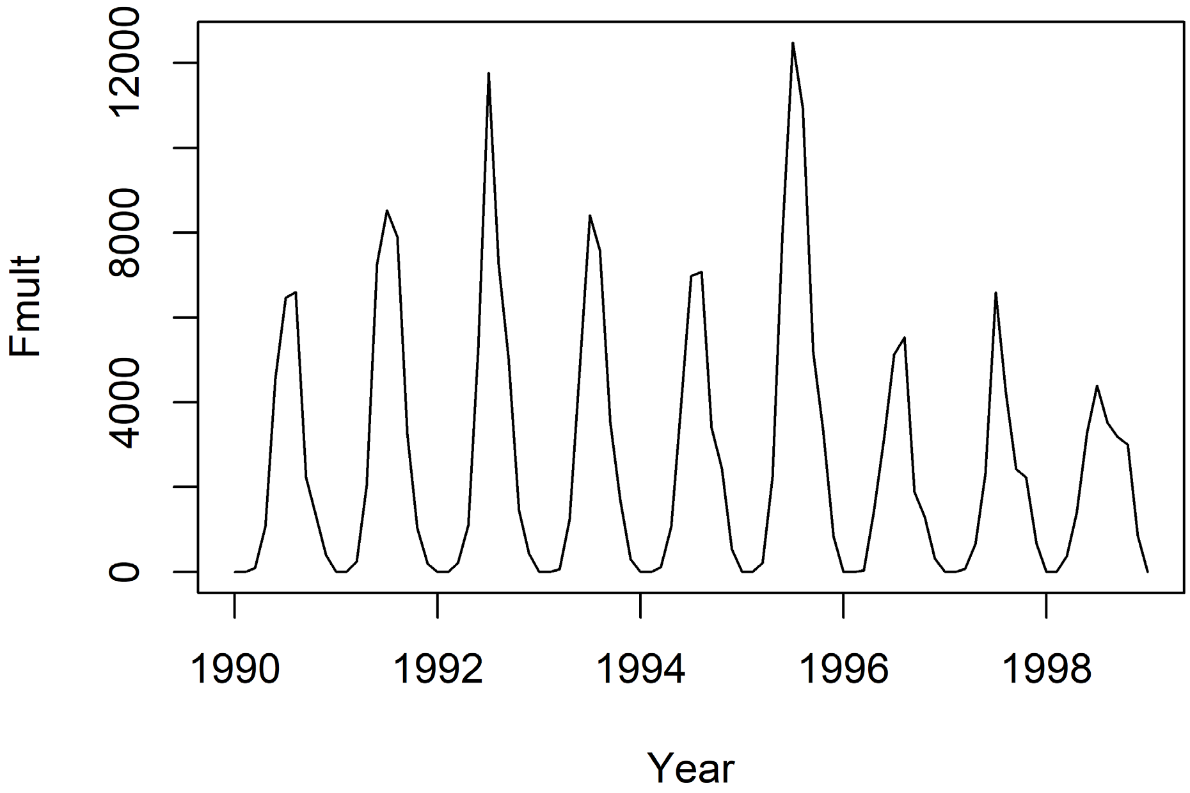

Figure 31. The F multiplier estimated by the stock assessment model for the period 1990-1999 fit to data for male blue crab in Maryland

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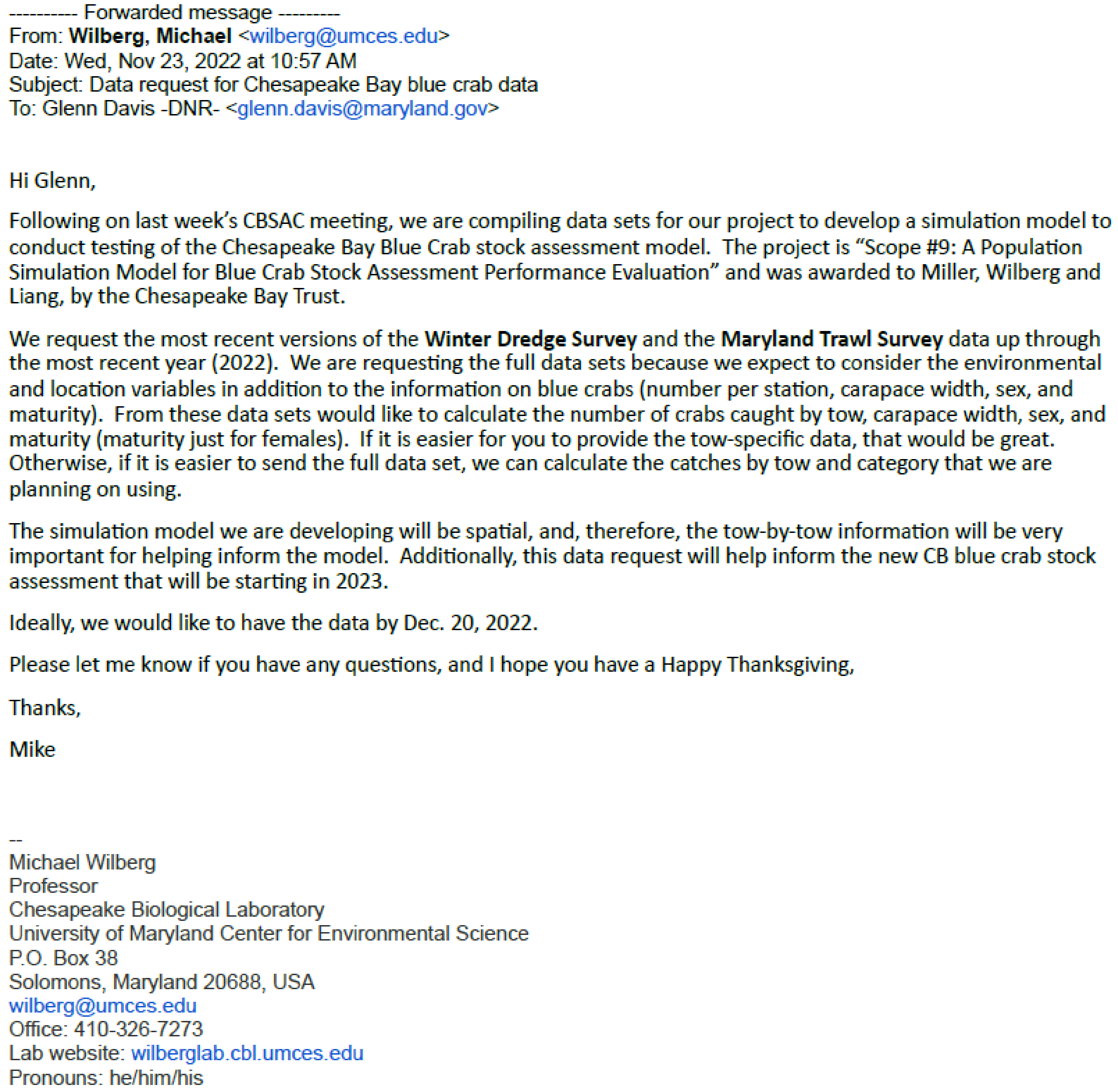
Appendix I

Data requests and agreements

Appendix 1.1. Winter dredge survey



---------- Forwarded message ---------
From: **Wilberg, Michael** <wilberg@umces.edu>
Date: Wed, Nov 23, 2022 at 10:57 AM
Subject: Data request for Chesapeake Bay blue crab data
To: Glenn Davis -DNR- <glenn.davis@maryland.gov>

Hi Glenn,

Following on last week's CBSAC meeting, we are compiling data sets for our project to develop a simulation model to conduct testing of the Chesapeake Bay Blue Crab stock assessment model. The project is "Scope #9: A Population Simulation Model for Blue Crab Stock Assessment Performance Evaluation" and was awarded to Miller, Wilberg and Liang, by the Chesapeake Bay Trust.

We request the most recent versions of the **Winter Dredge Survey** and the **Maryland Trawl Survey** data up through the most recent year (2022). We are requesting the full data sets because we expect to consider the environmental and location variables in addition to the information on blue crabs (number per station, carapace width, sex, and maturity). From these data sets would like to calculate the number of crabs caught by tow, carapace width, sex, and maturity (maturity just for females). If it is easier for you to provide the tow-specific data, that would be great. Otherwise, if it is easier to send the full data set, we can calculate the catches by tow and category that we are planning on using.

The simulation model we are developing will be spatial, and, therefore, the tow-by-tow information will be very important for helping inform the model. Additionally, this data request will help inform the new CB blue crab stock assessment that will be starting in 2023.

Ideally, we would like to have the data by Dec. 20, 2022.

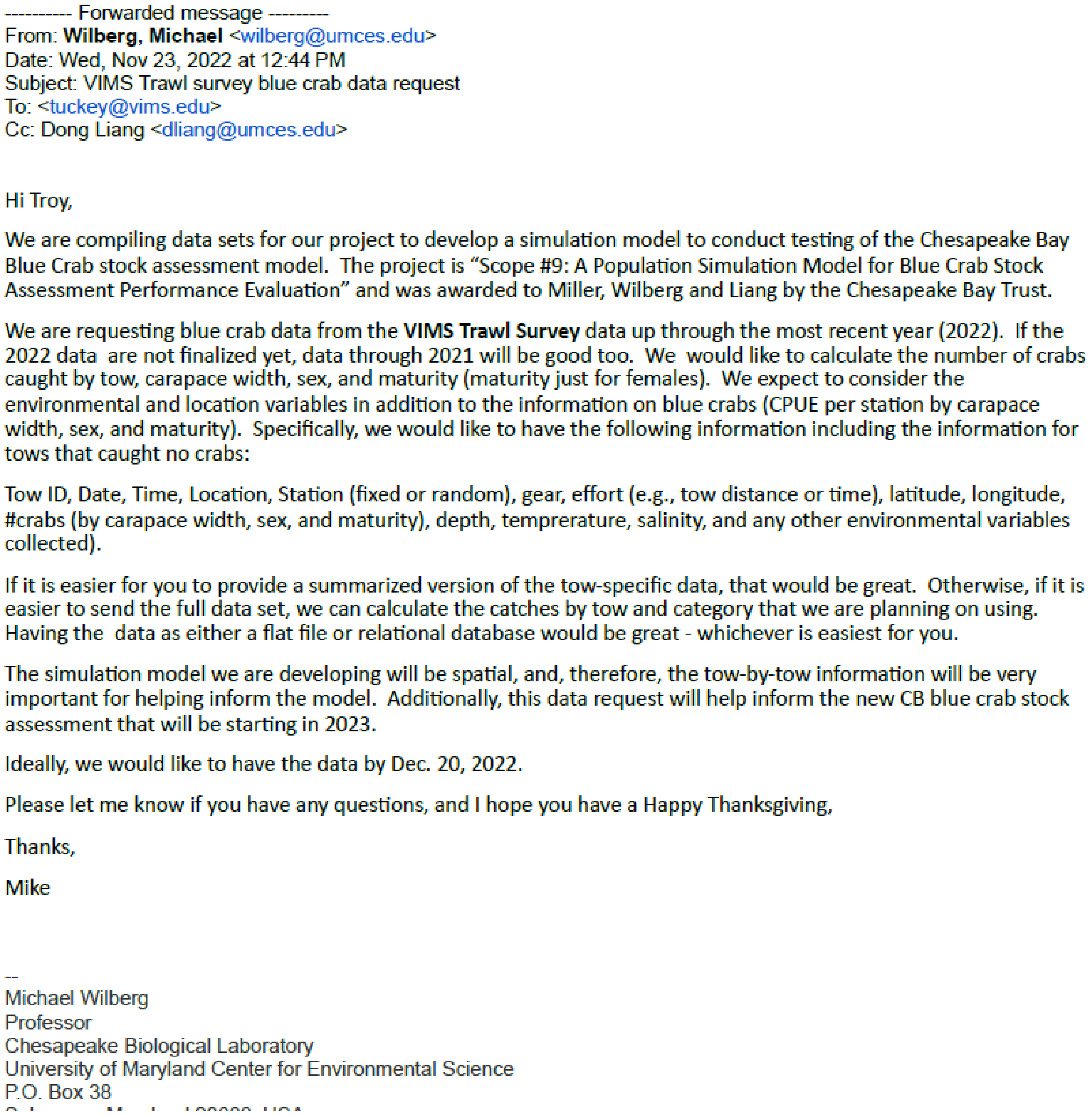
Please let me know if you have any questions, and I hope you have a Happy Thanksgiving,

Thanks,

Mike

--
Michael Wilberg
Professor
Chesapeake Biological Laboratory
University of Maryland Center for Environmental Science
P.O. Box 38
Solomons, Maryland 20688, USA
wilberg@umces.edu
Office: 410-326-7273
Lab website: wilberglab.cbl.umces.edu
Pronouns: he/him/his

Appendix 1.2 Virginia Institute of Marine Science Juvenile Finfish and Blue crab Trawl Survey



---------- Forwarded message ---------
From: **Wilberg, Michael** <wilberg@umces.edu>
Date: Wed, Nov 23, 2022 at 12:44 PM
Subject: VIMS Trawl survey blue crab data request
To: <tuckey@vims.edu>
Cc: Dong Liang <dliang@umces.edu>

Hi Troy,

We are compiling data sets for our project to develop a simulation model to conduct testing of the Chesapeake Bay Blue Crab stock assessment model. The project is "Scope #9: A Population Simulation Model for Blue Crab Stock Assessment Performance Evaluation" and was awarded to Miller, Wilberg and Liang by the Chesapeake Bay Trust.

We are requesting blue crab data from the **VIMS Trawl Survey** data up through the most recent year (2022). If the 2022 data are not finalized yet, data through 2021 will be good too. We would like to calculate the number of crabs caught by tow, carapace width, sex, and maturity (maturity just for females). We expect to consider the environmental and location variables in addition to the information on blue crabs (CPUE per station by carapace width, sex, and maturity). Specifically, we would like to have the following information including the information for tows that caught no crabs:

Tow ID, Date, Time, Location, Station (fixed or random), gear, effort (e.g., tow distance or time), latitude, longitude, #crabs (by carapace width, sex, and maturity), depth, temprerature, salinity, and any other environmental variables collected).

If it is easier for you to provide a summarized version of the tow-specific data, that would be great. Otherwise, if it is easier to send the full data set, we can calculate the catches by tow and category that we are planning on using. Having the data as either a flat file or relational database would be great - whichever is easiest for you.

The simulation model we are developing will be spatial, and, therefore, the tow-by-tow information will be very important for helping inform the model. Additionally, this data request will help inform the new CB blue crab stock assessment that will be starting in 2023.

Ideally, we would like to have the data by Dec. 20, 2022.

Please let me know if you have any questions, and I hope you have a Happy Thanksgiving,

Thanks,

Mike

--
Michael Wilberg
Professor
Chesapeake Biological Laboratory
University of Maryland Center for Environmental Science
P.O. Box 38

Appendix 1.3 Chesapeake Bay Multispecies Monitoring and Assessment Program

---------- Forwarded message ---------
From: **Wilberg, Michael** <wilberg@umces.edu>
Date: Wed, Nov 23, 2022 at 12:38 PM
Subject: ChesMMAP data for blue crab project
To: Robert J Latour <latour@vims.edu>
Cc: Dong Liang <dliang@umces.edu>

Hi Rob,

We are compiling data sets for our project to develop a simulation model to conduct testing of the Chesapeake Bay Blue Crab stock assessment model. The project is “Scope #9: A Population Simulation Model for Blue Crab Stock Assessment Performance Evaluation” and was awarded to Miller, Wilberg and Liang by the Chesapeake Bay Trust.

We are requesting blue crab data from the **ChesMMAP Survey** data up through the most recent year (2022). If the 2022 data are not finalized yet, data through 2021 will be good too. We would like to calculate the number of crabs caught by tow, carapace width, sex, and maturity (maturity just for females). We expect to consider the environmental and location variables in addition to the information on blue crabs (CPUE per station by carapace width, sex, and maturity). Specifically, we would like to have the following information including the information for tows that caught no crabs:

Tow ID, Date, Time, Location, gear, effort (e.g., tow distance or time), latitude, longitude, #crabs (by carapace width, sex, and maturity), depth, temprerature, salinity, and any other environmental variables collected).

If it is easier for you to provide a summarized version of the tow-specific data, that would be great. Otherwise, if it is easier to send the full data set, we can calculate the catches by tow and category that we are planning on using. Having the data as either a flat file or relational database would be great - whichever is easiest for you.

The simulation model we are developing will be spatial, and, therefore, the tow-by-tow information will be very important for helping inform the model. Additionally, this data request will help inform the new CB blue crab stock assessment that will be starting in 2023.

Ideally, we would like to have the data by Dec. 20, 2022.

Please let me know if you have any questions, and I hope you have a Happy Thanksgiving,

Thanks,

Mike

--
Michael Wilberg
Professor
Chesapeake Biological Laboratory
University of Maryland Center for Environmental Science
P.O. Box 38
Solomons, Maryland 20688, USA
wilberg@umces.edu
Office: 410-326-7273
Lab website: wilberglab.cbl.umces.edu
Pronouns: he/him/his

Appendix 1.5 Maryland Harvest Data and Sentinel Fishery Data Request

---------- Forwarded message ---------
From: **Wilberg, Michael** <wilberg@umces.edu>
Date: Wed, Nov 23, 2022 at 1:35 PM
Subject: Maryland blue crab harvest data and sentinel survey data request
To: Genine K Lipkey -DNR- <genine.mcclair@maryland.gov>
Cc: Dong Liang <dliang@umces.edu>

Hi Genine,

As we talked about at the last CBSAC meeting, we are compiling data sets for our project to develop a simulation model to conduct testing of the Chesapeake Bay Blue Crab stock assessment model. The project is “Scope #9: A Population Simulation Model for Blue Crab Stock Assessment Performance Evaluation” and was awarded to Miller, Wilberg and Liang by the Chesapeake Bay Trust.

We are requesting blue crab data from the **Maryland harvest** and the **Maryland Sentinel Survey** up through the most recent year (2022). If the 2022 data are not finalized yet, data through 2021 will be good too.

For the **Maryland Harvest data**, we would like to have catch by sex, market category, NOAA code, month, and gear (if this ends up being non-confidential). We are requesting the harvest by NOAA code because we thought that would be easiest for you. However, if the data are confidential at that level, the regions we are expecting to use in the model are the major tributaries (Patuxent, Chester, and Choptank), three mainstem regions in MD (Above the Bay Bridge (including small tribs); Mid-MD (127, 027, Eastern Bay, all the minor tribs in those regions); and lower-MD (229 and 129)), and Tangier/Pocomoke Sounds (including the tribs).

For the **Maryland Sentinel Survey** data, we would, ideally like to get the raw data that includes date, location, gear, the size and sex of crabs caught, and any other relevant information. We haven't worked with these data previously, so it may be worth a call so that we better understand what is available.

The simulation model we are developing will be spatial, and, therefore, the spatial information will be very important for helping inform the model. Additionally, this data request will help inform the new CB blue crab stock assessment that will be starting in 2023.

Also, if you have a table on the size and season regulations for MD, that would be very helpful.

Ideally, we would like to have the data by Dec. 20, 2022.

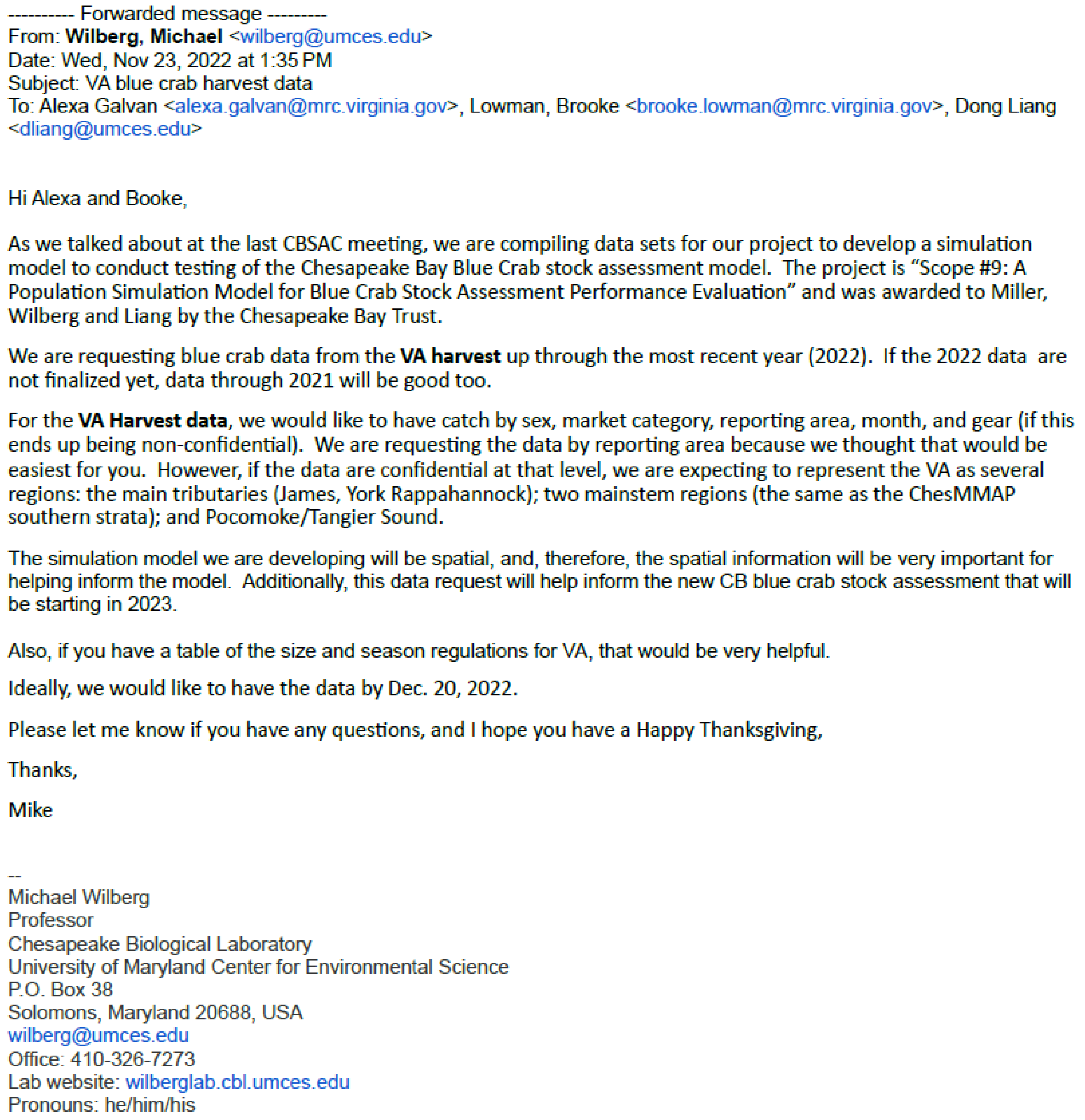
Please let me know if you have any questions, and I hope you have a Happy Thanksgiving,

Thanks,

Mike

--
Michael Wilberg
Professor
Chesapeake Biological Laboratory
University of Maryland Center for Environmental Science
P.O. Box 38
Solomons, Maryland 20688, USA
wilberg@umces.edu
Office: 410-326-7273

1.6 Virginia Marine Resource Commission Data Request and Confidentiality Agreements



---------- Forwarded message ---------
From: **Wilberg, Michael** <wilberg@umces.edu>
Date: Wed, Nov 23, 2022 at 1:35 PM
Subject: VA blue crab harvest data
To: Alexa Galvan <alexa.galvan@mrc.virginia.gov>, Lowman, Brooke <brooke.lowman@mrc.virginia.gov>, Dong Liang <dliang@umces.edu>

Hi Alexa and Booke,

As we talked about at the last CBSAC meeting, we are compiling data sets for our project to develop a simulation model to conduct testing of the Chesapeake Bay Blue Crab stock assessment model. The project is “Scope #9: A Population Simulation Model for Blue Crab Stock Assessment Performance Evaluation” and was awarded to Miller, Wilberg and Liang by the Chesapeake Bay Trust.

We are requesting blue crab data from the **VA harvest** up through the most recent year (2022). If the 2022 data are not finalized yet, data through 2021 will be good too.

For the **VA Harvest data**, we would like to have catch by sex, market category, reporting area, month, and gear (if this ends up being non-confidential). We are requesting the data by reporting area because we thought that would be easiest for you. However, if the data are confidential at that level, we are expecting to represent the VA as several regions: the main tributaries (James, York Rappahannock); two mainstem regions (the same as the ChesMMAP southern strata); and Pocomoke/Tangier Sound.

The simulation model we are developing will be spatial, and, therefore, the spatial information will be very important for helping inform the model. Additionally, this data request will help inform the new CB blue crab stock assessment that will be starting in 2023.

Also, if you have a table of the size and season regulations for VA, that would be very helpful.

Ideally, we would like to have the data by Dec. 20, 2022.

Please let me know if you have any questions, and I hope you have a Happy Thanksgiving,

Thanks,

Mike

--
Michael Wilberg
Professor
Chesapeake Biological Laboratory
University of Maryland Center for Environmental Science
P.O. Box 38
Solomons, Maryland 20688, USA
wilberg@umces.edu
Office: 410-326-7273
Lab website: wilberglab.cbl.umces.edu
Pronouns: he/him/his

VMRC PLANS & STATISTICS DATA REQUEST FORM

NAME: Michael Wilberg PHONE: 410-326-7273
AGENCY: Ches. Biological Lab., UMCES FAX#: 410-326-7318
ADDRESS: P.O. Box 38, Solomons, MD 20688 EMAIL: wilberg@umces.edu

SELECT REPORT BELOW: If one of the reports (1 through 15) cannot fill your request, there are more available upon request. Select the appropriate system (1 through 9), if necessary. Please write your detailed request in the "Additional Comments" section of the form.

REPORTS: 16. Other (Please specify in the "Additional Comments" section)

Systems = A group of water bodies as follows:
- ☐ System 1 = Atlantic Ocean
- ☐ System 2 = Seaside E. Shore
- ☐ System 3 = Misc. Seaside Codes
- ☐ System 4 = Chesapeake Bay
- ☐ System 5 = James River & Tribs.
- ☐ System 6 = York River & Tribs.
- ☐ System 7 = Rappahannock River & Tribs.
- ☐ System 8 = Potomac River & Tribs.
- ☐ System 9 = Other Chesapeake Bay Tribs.
- ☐ Systems 1-3 = Coastal Waters
- ☑ Systems 4-9 = Ches Bay and All Tribs
- ☐ Systems 1-9 = All Virginia Waters

Group = All size classes of a certain species.
This is only available for species commonly marketed in different size classes (i.e. Trout Group includes small, med and large trout).

Be sure to include the following information:
A) **Species**: species group or all species
B) **Year**: range of years or all (1929-Present)
C) **Water body**: a particular one or all in a system
D) Do you want values for species **caught** in VA waters only? (1993 – Present)
E) Do you want values for species **landed** in VA only? (1939 – Present)

Export File Format: .XLSX

PLEASE REMEMBER ALL DATA ARE PRELIMINARY AND SUBJECT TO CHANGE!

Please return this form to:
Virginia Marine Resources Commission
Plans & Statistics - Data Request
380 Fenwick Road, Bldg. 96,
Fort Monroe, VA 23651
Email: Stephanie.Iverson@mrc.virginia.gov
Fax: (757) 247-2264

OFFICIAL USE ONLY

Date Received:
Via:

VIRGINIA MARINE RESOURCES COMMISSION
Individual Statement of Non-Disclosure

This is to certify that:

1. I am a research/state employee working for the UMCES/CBL in that role, it has been determined by Stephanie Iverson that in order for me to carry out my fisheries-related work assignments, I require access to state computer systems and/or VMRC data files that may contain information declared to be held confidential by the VMRC.
2. In using VMRC computers and data I agree to uphold the state's security provisions for preserving the safety and integrity of the systems accessed and protecting against misuse or destruction of the computer systems and data being accessed.
3. I have read Section 28.2-204 of the "Laws of Virginia Relating to the Marine Resources of the Commonwealth," which pertains to the collection and confidentiality of fisheries data.
4. I am fully aware of the civil and criminal penalties for unauthorized disclosure, misuse or other violation of the confidentiality of such data.
5. I will not knowingly disclose any statistics identified as confidential under this agreement to any person or persons, except as authorized by the VMRC Data Supervisor, or the Supervisor's designee, in accordance with the law, as authorized by the Commonwealth of Virginia Attorney General.

DONG LIANG		09/01/22	09/01/24
Name of User	Signature	Begin Date	End Date

VMRC Data Supervisor	Signature	Expiration Date

VIRGINIA MARINE RESOURCES COMMISSION
Individual Statement of Non-Disclosure

This is to certify that:

1. I am a Professor employee working for the UMCES in that role, it has been determined by Stephanie Iverson that in order for me to carry out my fisheries-related work assignments, I require access to state computer systems and/or VMRC data files that may contain information declared to be held confidential by the VMRC.
2. In using VMRC computers and data I agree to uphold the state's security provisions for preserving the safety and integrity of the systems accessed and protecting against misuse or destruction of the computer systems and data being accessed.
3. I have read Section 28.2-204 of the "Laws of Virginia Relating to the Marine Resources of the Commonwealth," which pertains to the collection and confidentiality of fisheries data.
4. I am fully aware of the civil and criminal penalties for unauthorized disclosure, misuse or other violation of the confidentiality of such data.
5. I will not knowingly disclose any statistics identified as confidential under this agreement to any person or persons, except as authorized by the VMRC Data Supervisor, or the Supervisor's designee, in accordance with the law, as authorized by the Commonwealth of Virginia Attorney General.

THOMAS MILLER		1/10/2023	1/9/2024
Name of User	Signature	Begin Date	End Date

VMRC Data Supervisor	Signature	Expiration Date

VIRGINIA MARINE RESOURCES COMMISSION
Individual Statement of Non-Disclosure

This is to certify that:

1. I am a Professor employee working for the UMCES in that role, it has been determined by <u>Stephanie Iverson</u> that in order for me to carry out my fisheries-related work assignments, I require access to state computer systems and/or VMRC data files that may contain information declared to be held confidential by the VMRC.

2. In using VMRC computers and data I agree to uphold the state's security provisions for preserving the safety and integrity of the systems accessed and protecting against misuse or destruction of the computer systems and data being accessed.

3. I have read Section 28.2-204 of the "Laws of Virginia Relating to the Marine Resources of the Commonwealth," which pertains to the collection and confidentiality of fisheries data.

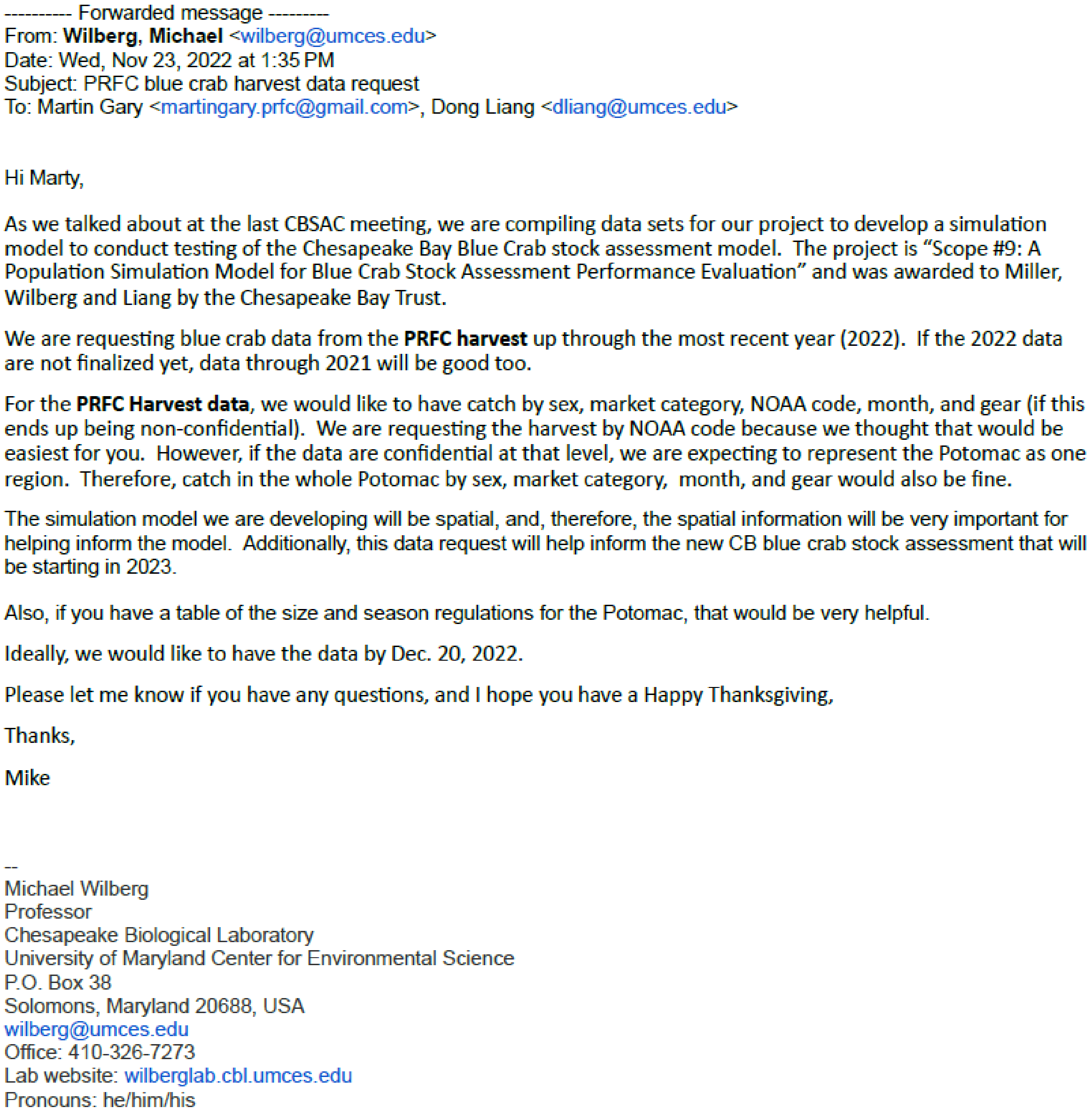
4. I am fully aware of the civil and criminal penalties for unauthorized disclosure, misuse or other violation of the confidentiality of such data.

5. I will not knowingly disclose any statistics identified as confidential under this agreement to any person or persons, except as authorized by the VMRC Data Supervisor, or the Supervisor's designee, in accordance with the law, as authorized by the Commonwealth of Virginia Attorney General.

Michael Wilberg		1/10/2023	1/9/2024
Name of User	Signature	Begin Date	End Date

VMRC Data Supervisor	Signature	Expiration Date

Appendix 1.7 Potomac River Fisheries Commission Harvest Data Request



---------- Forwarded message ---------
From: **Wilberg, Michael** <wilberg@umces.edu>
Date: Wed, Nov 23, 2022 at 1:35 PM
Subject: PRFC blue crab harvest data request
To: Martin Gary <martingary.prfc@gmail.com>, Dong Liang <dliang@umces.edu>

Hi Marty,

As we talked about at the last CBSAC meeting, we are compiling data sets for our project to develop a simulation model to conduct testing of the Chesapeake Bay Blue Crab stock assessment model. The project is “Scope #9: A Population Simulation Model for Blue Crab Stock Assessment Performance Evaluation” and was awarded to Miller, Wilberg and Liang by the Chesapeake Bay Trust.

We are requesting blue crab data from the **PRFC harvest** up through the most recent year (2022). If the 2022 data are not finalized yet, data through 2021 will be good too.

For the **PRFC Harvest data**, we would like to have catch by sex, market category, NOAA code, month, and gear (if this ends up being non-confidential). We are requesting the harvest by NOAA code because we thought that would be easiest for you. However, if the data are confidential at that level, we are expecting to represent the Potomac as one region. Therefore, catch in the whole Potomac by sex, market category, month, and gear would also be fine.

The simulation model we are developing will be spatial, and, therefore, the spatial information will be very important for helping inform the model. Additionally, this data request will help inform the new CB blue crab stock assessment that will be starting in 2023.

Also, if you have a table of the size and season regulations for the Potomac, that would be very helpful.

Ideally, we would like to have the data by Dec. 20, 2022.

Please let me know if you have any questions, and I hope you have a Happy Thanksgiving,

Thanks,

Mike

--
Michael Wilberg
Professor
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University of Maryland Center for Environmental Science
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Pronouns: he/him/his

Appendix 2. General Blue Crab Operating Model

This is the full model code, written in the R programming language, for the operating model and the observation model.

```
#Basic Length-based data simulation model
#To Do:

#------------------------------------------------------------------------------
# Load Libraries
#------------------------------------------------------------------------------
library(TMB)
library(ggplot2)
library(tidyverse)
#------------------------------------------------------------------------------
# Load Functions
#------------------------------------------------------------------------------
setwd("C:\\Users\\wilbe\\OneDrive\\Desktop\\GitHub\\CB_blue_crab_sim")
#setwd("C:\\Users\\Mike\\Documents\\GitHub\\CB_blue_crab_sim")
#------------------------------------------------------------------------------

#Load Rdata file for survey data
load("sslam_data_2b_share.rData")


#Set values we need for the model
nyr<-30 #number of years
nmo<-10 #months per year (jan-mar is one month)
t_initialize<-20*nmo #run model for 10 years to get the starting length composition
#fdyr<-10 #first data year
nmo<-10 #months/year Dec-Feb considered one "month"
maxl<-220 #lower limit of maximum length bin

tsteps<-nyr*nmo #number of time steps
months<-seq(1,nmo,1)  #define months

bin_width<-10 #10 mm length bins

bins<-(seq(0,maxl,bin_width))
#names(bins)<-c("L_CW")
bin_mids<-bins+0.5*bin_width
#names(bin_mids)<-c("CW")
#nb<-length(bin_mids) #count number of bins
nlbins=length(bins)
#linc<-data.frame(matrix(NA, nrow = nlbins, ncol = 1))
#names(linc)<- c("length")
#calculate number of length bins
```

```
#Size distribution of recruits
L0<- 30 #initial mean length of recruits, mm
L0_CV<-0.55 #CV for length distribution of recruits

#--------------------------------------------------
#Parameters for normal growth increment
Linf<-220  #Linf same for males & females mm
Linf_CV <-0.2 #CV for Linf
kp<-0.0003 #proportionality constant to convert GDD to K
K_CV <- 0.2 #CV for K
Linf_SD<-Linf*Linf_CV  #SD of Linf
#K_SD<-K*K_CV  #SD of K
Linf_V<-Linf_SD^2  #variance of Linf
#K_V<-K_SD^2 #variance of K
Linf_K_Cor<--0.0
#--------------------------------------------------
#Maturity parameters
fmat_params<-c(0.1,150) #slope and 50% maturity length for female maturity
m_l_mat=107 #knife edge function for male maturity

#Stock recruitment parameters
R_pm=0.48 #percent male recruits
R_sd=0.45 #log-scale SD of recruitment errors
R_mo<-c(1,0,0,0,0,0,0,0,0,0) #proportion of recruitment in each month
SR_alpha<-exp(3.28) #2011 assessment log_alpha=3.28...  Need to change if we use length-specific M
SR_beta<-exp(-7) #from 2011 assessment

#Natural mortality
#Calculate sex-specific natural mortality per month (same as previous assessment)
Mref<-0.9/nmo
M<-matrix(Mref,nrow=nlbins,ncol=3)

#calculate fishing mortality rate for hard-shell male and female crabs
fh<-matrix(rep(1.05/nmo,2*tsteps),ncol=2)
#fh<-matrix(rep(.5/nmo,2*tsteps),ncol=2)
#fh<-matrix(rep(0/nmo,2*tsteps),ncol=2)
#calculate fishing mortality rate for peelers SET TO ZERO FOR NOW
fp<-matrix(rep(0.0/nmo,2*tsteps),ncol=2)

# for(x in 1:3)
# {
#   M[,x]<-Mref*(bin_mids$CW/(Linf[1]))^-.5 #MADE UP M matrix for Now.  M same for all sexes/stages
# }


#Process error sd
```

```
proc_err_sd=0.0001 #process error sd for abundance

{
 #--------------------------------------------------
 #Function to calculate proportion in a bin using a normal distribution
 init_size_dist<-function(lower_l_bins,mean,sd)
 {
  nbins<-length(lower_l_bins)
  init_size<-as.vector(mode="numeric",rep(0,nbins)) #set up init size vector (proportions at length for recruits)
  init_size[1]<-pnorm(lower_l_bins[2],mean=mean,sd=sd) #fill in first length bin as proportion less than the upper limit of the first length bin
  p<-init_size[1]
  for(l in 2:(nbins-1))  #loop over length bins
  {
   q<-pnorm(lower_l_bins[l+1],mean=L0,sd=L0_CV*L0)
   init_size[l]<-q-p  #use cumulative density function to calculate proportion in each bin
   p<-q
  }
  init_size[l]<-1-p
  #init_size[l]<-1-pnorm(lower_l_bins[nlbins],mean=L0,sd=L0_CV*L0) #fill in last length bin as the rest of the distribution
  return(init_size)
 }
 #--------------------------------------------------

 #Generate monthly temperature and cumulative growing degree days (GDD)
 tempa<-4+10*(1+sin((months/nmo)*2*pi+1.2*pi)) #Average monthly Temperature follows a sine wave
 tempc<-rep(tempa,nyr) #expand for the number of years
 #temp<-rep(20,nmo) #constant temp for testing
 #Generate AR1 random numbers
 temp_err_cor<-0.8 #correlation of errors of temperature over time MADE UP CURRENTLY
 temp_err_sd<-1 #SD of independent random errors MADE UP CURRENTLY
 temp_err<-rnorm(tsteps,0,temp_err_sd) #start by generating independent normal errors
 temp_err[1]=(temp_err[1]/temp_err_sd)*sqrt(temp_err_sd^2/(1-temp_err_cor^2)) #deviation for the first time step
 for(t in 2:tsteps)
 {
  temp_err[t]<-temp_err[t-1]*temp_err_cor+temp_err[t]  #AR1 process to allow for correlated errors
 }
 temp=tempc+temp_err #add error to mean temperature time series
 GDD<-ifelse(temp>8.9,(temp-8.9)*30,0) #Growing degree days (simplified here)

 #Use actual mean GDD for model
 GDD<-rep(sslam.tvg.data$GDD,nyr)
```

```
  K<-GDD*kp #calculate von Bertalanffy K
  K_SD<-K*K_CV
  K_V<-K_SD^2

  #ggplot(data=as.data.frame(cbind(1:(nmo*nyr),GDD)),aes(x=V1,y=GDD))+
   # geom_line()+
   # labs(x="Time", y = "Growing degree days")

  #Function to calculate m from number of months and t
  get_m<-function(t,nmo){
    x<-t%%nmo
    if(x==0){x=nmo}
    return(x)
  }

  #Function to pull time step ts from a list of time steps and the annual routine of sampling
  get_sample_t<-function(tsteps,samplet){
    #  tsteps=1:dtsteps
    # samplet<-I1_mo
    ntpy<-length(samplet)
    nt<-length(tsteps)
    #tout<-tsteps
    ny<-nt/ntpy
    index_t<-rep(samplet,ny)
    answer<-vector(mode="numeric",length=length(tsteps)*sum(samplet)/ntpy)
    ct<-1
    for(t in 1:length(tsteps)){
      if(index_t[t]==1){
        answer[ct]<-t
        ct<-ct+1
      }
    }
    return(answer)
  }

#-------------------------------------------------------------------
#Calculate growth
  #Initial size distribution of recruits
  init_size<-init_size_dist(bins,L0,L0_CV*L0)

#Normal distribution method
  #Function for normal distribution growth increment
  growth_matrix<-function(Linf,K,Linf_Var,K_Var,Linf_K_Cor,bin_mids)
  {

#Linf=Linf[1],K=K[m],Linf_Var=Linf_V[1],K_Var=K_V[m],Linf_K_Cor=Linf_K_Cor,bin_mids=bin_mids$CW
```

```
  nb<-length(bin_mids)
  bw<-bin_mids[2]-bin_mids[1] #calculate width of bins
  mat<-matrix(0,nrow=nb, ncol=nb) #set up empty matrix
  mean_g<-(Linf-bin_mids)*(1-exp(-K)) #calculate mean growth as a function of starting length
  L_diff<-(Linf-bin_mids)  #Calculate difference between Linf and the midpoints of the length bins
  Linf_SD<-sqrt(Linf_Var)  #SD for Linf
  K_SD<-sqrt(K_Var)  #SD for K

  #calculate variance for starting length bin i
  #SD CALCULATIONS CORRECT
  L_SD<-Linf_Var*(1-exp(-K))^2
  L_SD<-L_SD+K_Var*(L_diff*exp(-K))^2
  L_SD<-L_SD+2.0*Linf_K_Cor*Linf_SD*K_SD*(1-exp(-K))*L_diff*exp(-K);
  L_SD<-sqrt(L_SD) #convert from var to SD

  for(i in 1:(nb-1))  #loop over starting length bins
  {
    up_lim=bw/2
    mat[i,i]=pnorm(up_lim,mean_g[i],sd=L_SD[i])
    #p<-mat[i,i]
    for(j in (i+1):(nb-1)) #loop over ending length bins
    {
      if((i+1)>(nb-1)) {
        break
      }
      #calculate increment
      inc=bin_mids[j]-bin_mids[i]
      #calculate lower bound of growth increment
      lo_lim=up_lim
      #calculate upper bound of growth increment
      up_lim=lo_lim+bw
      #Calculate proportion that grow to bin j
      mat[j,i]=pnorm(up_lim,mean_g[i],sd=L_SD[i])-pnorm(lo_lim,mean_g[i],sd=L_SD[i])
      #print(c(i,j))
    }#close j
    #last length bin a plus group
    lo_lim=up_lim
    mat[nb,i]=1-pnorm(lo_lim,mean_g[i],sd=L_SD[i])
  }#close i
  #mat[nb,nb]=1 #Animals in the highest length bin stop growing and stay in that length bin
  return(mat)
}
#Generate transition matrices for immature female maturation and egg stage
growth_matrix_im_fem<-function(G,matl){
  nb<-length(matl)
  mat=matrix(0,nrow=nb,ncol=nb)
  for(i in 1:(nb-1))  #Starting length
```

```
  {
   for(j in i:nb) #ending length
   {
    if(i==j)
    {
     mat[j,i]=G[j,i]  #crabs don't grow, so just use the diagonal element
    } else
    {
     mat[j,i]=G[j,i]*(1-matl[j]) #crabs grow, so some will mature
    }
   }
  }
  mat[nb,nb]=0 #any immature females in the largest size bin become mature
  return(mat)
 }
 #generate matrix for females that mature
 growth_matrix_mat_fem<-function(G,matl){
  nb<-length(matl)
  mat=matrix(0,nrow=nb,ncol=nb)
  for(i in 1:(nb-1)) #starting length
  {
   for(j in (i+1):nb) #ending length
   {
    mat[j,i]=G[j,i]*matl[j]
   }
  }
  mat[nb,nb]=1 #any immature females in the largest size bin become mature
  return(mat)
 }

 #All orange eggs and black eggs are spawned before the next month (it's more complicated, though -
eggs take about 14 days to go from orange to hatch)
 #https://www.bluecrab.info/spongers.html
 #Gofm=diag(nlbins)
 #Gbfm=diag(nlbins)

 #Gfmo=diag(nlbins)
 #Gfmb=diag(nlbins)


 #function for exponential mortality
 exp_mort<-function(N,Z){N*exp(-Z)}

 #function for catch  equation
 catch<-function(F,Z,N){F/Z*(1-exp(-Z))*N}

 #Function for logistic selectivity
```

```
  logistic_sel<-function(sl,p50){
   sel<-1/(1+exp(-sl*(bin_mids-p50)))
   return(sel/sel[length(bin_mids)])}

  #Function for double logistic selectivity
  doub_logistic_sel<-function(sl,p150,s2,p250){1/(1+exp(-sl*(bin_mids-p150)))*1/(1+exp(-s2*(p250-
bin_mids)))}

  #Function for increasing threshold using the midpoints of the bins and a value for the threshold
  #used for male maturity
  inc_threshold<-function(bin_mids,cutoff){
   i=1
   v<-vector(mode="numeric",length=length(bin_mids))
   for(l in bin_mids)
   {
    if(l < cutoff)
    {
     v[i]=0
    } else
    {
     v[i]=1
    }#Close else
    i=i+1
   }#close l loop
   return(v)
  } #end inc_threshold function


  #calculate female maturity
  fmat<-logistic_sel(fmat_params[1],fmat_params[2]) #logistic function for female maturation

  #calculate male maturity
  mmat<-inc_threshold(bin_mids,m_l_mat)

#-------------------------------------------------------------------
  #Calculate growth matrices
#-------------------------------------------------------------------
 G<-array(0,dim=c(nlbins,nlbins,3,tsteps)) #G for three sexes, each time step, number of length bins,
number of length bins
 #t=6 #variable for testing
 #x=1 #variable for testing
 for(t in 1:tsteps)
 {
  for(x in 1:3)
  { #m=2
   if(GDD[t]<=0 && x<=2){
    G[,,x,t]<-diag(nlbins)
```

```
    } else{
      if(x==1) #males
      {
        G[,,x,t]<-
growth_matrix(Linf=Linf,K=K[t],Linf_Var=Linf_V,K_Var=K_V[t],Linf_K_Cor=Linf_K_Cor,bin_mids=bin_mid
s)
      }
      if(x==2) #immature females
      {
        g<-
growth_matrix(Linf=Linf,K=K[t],Linf_Var=Linf_V,K_Var=K_V[t],Linf_K_Cor=Linf_K_Cor,bin_mids=bin_mid
s)
        G[,,x,t]<-growth_matrix_im_fem(g,fmat) #Immature females
      }
      if(x==3) #mature females
      {
        if(GDD[t]<=0) #need to account for periods of no growth for females
        { #This represents the fraction of immature females that grow to become mature females
          #If GDD is zero, then there is no growth and therefore no maturation
          G[,,x,t]=0
        } else
        {
          g<-
growth_matrix(Linf=Linf,K=K[t],Linf_Var=Linf_V,K_Var=K_V[t],Linf_K_Cor=Linf_K_Cor,bin_mids=bin_mid
s)
          G[,,x,t]<-growth_matrix_mat_fem(g,fmat) #Mature females
        }#close if
      } #close if for x=3
    }#close else
  } #close x loop
 } #close t loop

  #-----------------------------------------------------------------------------------------------------------------------
  ##POPULATION DYNAMICS
  #-----------------------------------------------------------------------------------------------------------------------
  #Set up arrays
  N<-array(0,c(tsteps,nlbins,3)) #abundance at size by sex (1 = male, 2=immature female, 3=mature
female:no eggs, 4=mature female orange eggs, 5=mature female black eggs)
  F<-array(0,c(tsteps,nlbins,3)) #fishing mortality rate
  Z<-array(0,c(tsteps,nlbins,3)) #total mortality rate
  C<-array(0,c(tsteps,nlbins,3)) #catch of by size and sex/maturity stage
  R<-vector(mode="numeric",length=tsteps) #recruitment

  #Calculate male selectivity
  selh<-logistic_sel(0.1,85)

  #Peeler selectivity
```

```
  selp<-doub_logistic_sel(0.1,50,0.1,80)
  #selp<-selp/max(selp) #Standardize to have a maximum of 1



SR<-function(sd){return(200*exp(rnorm(1,0,sd)))}

Ricker_SR<-function(alpha,beta,Nf,Nm,sd){
  R<-alpha*Nf*exp(-beta*(Nf+Nm))*exp(rnorm(1,0,sd))
  return(as.numeric(R))
  }

calc_F<-function(x,t)
{
  #Calculate F
  if(x==1) #males
  {
    F<-fh[t,1]*selh #hardshell fishing mortality at length for males is a function of the minimum size limit
  } else
  {  # females
    if(x==2)  #immature females
    {
      F=0.0 #Currently no release mortality
    }
    if(x==3) #mature females
    {
      F<-fh[t,2] #hard-shell fishing mortality at length for females is only a function of maturity
    }
  } #end else
  # if(GDD[t]>0 && x<=2)  #only peeler fishery if crabs are growing and for males and immature females
  # {
  #   F<-F+fp[x,t]*t(selp[,1]) #peeler fishing mortality only happens of crabs are growing
  # } #end if
  return(F)
} #end function



#Calculate F and Z
#calc_F_Z<-function(){
for(t in 1:tsteps)
{
  for(x in 1:3)
  {
    #Calculate F and Z
    F[t,,x]<-calc_F(x,t) #fishing mortality

    Z[t,,x]<-F[t,,x]+M[,x]  #total mortality at length
```

```
 }
}
 #print("done")
#}
#calc_F_Z()

R_temp=0
p_uni_init<-rep(1/nlbins,nlbins) #Uniform distribution for starting size composition for males and immature females
for(t in 1:(tsteps-1))
{
 #calculate month
 m=get_m(t,nmo)
 #apportion among males and females
 if(t==1)
 {
  init_R=SR(R_sd) #Specify starting recruitment to get initial conditions started
  N[t,,1]=R_pm*init_R*p_uni_init #start with uniform size distribution
  N[t,,2]=(1-R_pm)*init_R*p_uni_init
  #init_R2<-0
  for(t2 in 2:t_initialize){ #loop over initialization time steps
   m2<-get_m(t2,nmo)
   for(x in 1:3)
   {
    #calculate abundance
    if(x==1) #males
    {
     N[t,,x]=G[,,x,m2]%*%(N[t,,x]*exp(-Z[m2,,x]))+R_pm*R_temp*R_mo[m2]*init_size
    }
    if(x==2) #immature females
    {
     N[t,,x]=G[,,x,m2]%*%(N[t,,x]*exp(-Z[m2,,x]))+(1-R_pm)*R_temp*R_mo[m2]*init_size
    }
    if(x==3) #mature females
    {  #first part is that mature females don't grow, second is immature females that become mature
     N[t,,x]=N[t,,x]*exp(-Z[m2,,x])+G[,,x,m2]%*%(N[t,,2]*exp(-Z[m2,,2]))
    }
   }#close x loop
   if(m2==5) #Calculate spawning abundance and recruitment assuming that crabs spawn on July 1
   {
    #calculate mature females
    Nf<-sum(N[t,,3])
    #calculate abundance of mature males using dot product of male abundance and male maturity
    Nm<-N[t,,1]%*%mmat
    #recruitment= propostion of recruits that return during a month * total recruitment for the year
    R_temp<-Ricker_SR(SR_alpha, SR_beta,Nf,Nm,sd=0)
    #print(c(Nf,Nm,R_temp))
```

```
  } #end if(t%%nmo==5)
  #apportion recruitment among months
  #init_R2=R_temp
 }#close t2 loop for initialization period
 N[t,,1]=N[t,,1]+R_pm*R_temp*R_mo[m]*init_size
 N[t,,2]=N[t,,2]+(1-R_pm)*R_temp*R_mo[m]*init_size
#}#close if(t==1)
} else{
 #Calculate recruitment using Ricker S-R function
 if(t%%nmo==5) #Calculate spawning abundance and recruitment assuming that crabs spawn on July 1
 {
  #calculate mature females
  Nf<-sum(N[t,,3])
  #calculate abundance of mature males using dot product of male abundance and male maturity
  Nm<-N[t,,1]%*%mmat
  #recruitment= propostion of recruits that return during a month * total recruitment for the year
  R_temp<-Ricker_SR(SR_alpha, SR_beta,Nf,Nm,R_sd)
  #print(c(t,Nf,Nm,R_temp))
  R[(t+5):(t+5+nmo-1)]=R_mo*R_temp
 } #end if(t%%nmo==5)
 #apportion recruitment among months

} #end else

#generate process error for abundance-at-length
N_proc_err=rnorm(nlbins,0,sd=proc_err_sd)

for(x in 1:3)
{
 #Calculate F and Z
 #F[t,,x]<-calc_F(x,t)
 #Z[t,,x]<-F[t,,x]+M[,x]  #total mortality at length

 #calculate abundance
 if(x==1) #males
 {
  N[t+1,,x]=(G[,,x,t]%*%(N[t,,x]*exp(-Z[t,,x])))*exp(N_proc_err)+R_pm*R[t]*init_size
 }
 if(x==2) #immature females
 {
  N[t+1,,x]=(G[,,x,t]%*%(N[t,,x]*exp(-Z[t,,x])))*exp(N_proc_err)+(1-R_pm)*R[t]*init_size
 }
 if(x==3) #mature females without eggs
 {  #first part is that mature females don't grow, second is immature females that become mature
  N[t+1,,x]=(N[t,,x]*exp(-Z[t,,x])+G[,,x,t]%*%(N[t,,2]*exp(-Z[t,,2])))*exp(N_proc_err)
 }
 #Calculate catch
```

```
  C[t,,x]=catch(F[t,,x],Z[t,,x],N[t,,x])
 }
}#end t loop
#do catch calcs for last year
t=tsteps
for(x in 1:3)
{
 F[t,,x]<-calc_F(x,t) #fishing mortality at length
 Z[t,,x]<-F[t,,x]+M[,x]  #total mortality at length
 C[t,,x]=catch(F[t,,x],Z[t,,x],N[t,,x])
}


 #Calculate total catch in numbers wihtout observation error
 TC<-matrix(0,nrow=tsteps,ncol=3)
 for(x in 1:3)
 {
  for(t in 1:tsteps)
  {
   TC[t,x]=sum(C[t,,x]) #*exp(C_obs_err)

  }
 }

 #surv1_sel<-logistic_sel(0.05,30)
 #surv2_sel<-logistic_sel(0.1,15)

 #data length
 fdyr<-1 #first data year
 dyr<-nyr-fdyr+1 #number of years for data
 dtsteps<-dyr*nmo #number of time steps for data
 fdstep<-(fdyr-1)*nmo+1
}

#Observation Model
{
 #Number of surveys
 nsrv<-4

 #number of fleets
 nflt<-1
 cat_sigma<-0.1 #log-scale SD for observed catch data
 C_effN=100 #effective sample size for length composition of the catch

 #survey CV
 I_sigma<-c(0.1,0.3,0.3,0.3)
```

```
  #effective sample size
  I_effN=c(500,500,500,500)

  #Months for sampling (1=month with sampling, 0 = month with no sampling)
  I1_mo<-c(1,0,0,0,0,0,0,0,0,0) #WDS
  I2_mo<-c(0,0,1,1,1,1,1,1,0,0) #MD Trawl Survey
  I3_mo<-rep(1,nmo) #VIMS trawl survey
  I4_mo<-c(0,0,1,1,0,1,1,0,0,0) #ChesMMAP

  Clen_mo<-rep(1,nmo)

  #vectors of data time step indicator variables
  I_mo<-matrix(0,nrow=dtsteps,ncol=nsrv)
  I_mo[,1]<-rep(I1_mo,dyr)
  I_mo[,2]<-rep(I2_mo,dyr)
  I_mo[,3]<-rep(I3_mo,dyr)
  I_mo[,4]<-rep(I4_mo,dyr)
  C_mo<-rep(Clen_mo,dyr)

  #Survey catchability
  surv_q<-c(1,0.05,0.05,0.05)

  #Survey selectivity
  surv_sel_p<-matrix(0,nrow=3,ncol=nsrv)
  surv_sel_p[,1]<-c(0.05,10,1)
  surv_sel_p[,2]<-c(0.1,15,1)
  surv_sel_p[,3]<-c(0.1,15,1)
  surv_sel_p[,4]<-c(0.05,110,1)
  surv_sel<-matrix(0,nrow=nlbins,ncol=nsrv)
  #calculate selectivity for each survey
  for(s in 1:nsrv){
    if(surv_sel_p[3,s]==1){ #increasing logistic  survey selectivity
      surv_sel[,s]<-logistic_sel(surv_sel_p[1,s],surv_sel_p[2,s])
    }#close if
  }#close s loop

  #Generate survey indices without observation error for all time steps (including burn-in)
  I<-array(0,dim=c(tsteps,nlbins,3,nsrv)) #index of abundance at size
  #t=tsteps
for(s in 1:nsrv)
{
  for(x in 1:3)
  {
    for(t in 1:tsteps)
    {
      I[t,,x,s]<-t(as.vector(N[t,,x])*surv_sel[,s]*surv_q[s])
    } #close t loop
```

```
  } #close x loop
}#close survey loop

  #Generate catch and survey observations with observation error only for years of model fitting
  obs_I<-array(-99,dim=c(dtsteps,nlbins,3,nsrv)) #index of abundance at sex and size
  obs_C<-array(-99,dim=c(dtsteps,nlbins,3)) #catch at sex and size
  #x=1
  #t=(fdyr-1)*nmo+1
  #include observation error
  for(x in 1:3)
  {
    for(t in ((fdyr-1)*nmo+1):tsteps)
    {
      t2=t-(fdyr-1)*nmo
      for(s in 1:nsrv)
      {
      if(I_mo[t2,s]==1)
        if(sum(I[t,,x,s])>0) obs_I[t2,,x,s]<-
sum(I[t,,x,s])*exp(rnorm(1,0,I_sigma[s]))*rmultinom(1,I_effN[s],I[t,,x,s]/sum(I[t,,x,s]))/I_effN[s]
      }
      if(C_mo[t2]==1){
        if(sum(C[t,,x])>0) obs_C[t2,,x]<-
sum(C[t,,x])*exp(rnorm(1,0,cat_sigma))*rmultinom(1,C_effN,C[t,,x]/sum(C[t,,x]))/C_effN
      }
    #print(c(t,t2))
    } #close t
  } #close x loop
  #Make arrays to get rid of immature female catch
  obs_C_mod<-array(NA,dim=c(dtsteps,nlbins,2))
  obs_C_mod[,,1]<-obs_C[,,1]
  obs_C_mod[,,2]<-obs_C[,,3]

  #Check results
  # for(x in 3:3)
  # {
  #   for(t in 1:tsteps)
  #   {
  #     write.table(G[,,x,t],sep=",",file="G.csv",append=TRUE)
  #     #write.table(t(N[t,,x]),sep=",",file="N.csv",append=TRUE)
  #
  #   }
  # }
}

  #------------------------------------------------------------------------------
  #Plot WDS
{
```

```
#plot simulated length composition with observed
Nfmo<-seq(251,291,nmo)
dat<-I[Nfmo,,1,1]
pdat<-colSums(dat)
pdat<-as.data.frame(pdat/sum(pdat))
names(pdat)<-"P"
pdat$CW<-bins
pdat$OE<-"est"

obs_plot_data<-rowSums(sslam.tvg.data$obs_p_I[1,,])
obs_plot_data<-obs_plot_data/sum(obs_plot_data)
obs_plot_data<-as.data.frame(obs_plot_data)
names(obs_plot_data)<-"P"
obs_plot_data$CW<-sslam.tvg.data$low_l_bins
obs_plot_data$OE<-"obs"

plot_data_4m<-rbind(pdat,obs_plot_data)
plot_data_4m$sex<-"Male"

# p<-ggplot(data=plot_data_4, aes(x=CW,y=P,fill=OE)) +
#   geom_bar(stat="identity", position=position_dodge())+
#   ggtitle("Winter Dredge Survey Males") +
#   xlab("Carapace width (mm)") + ylab("Proportion")
#
# p

#WDS immature female
dat<-I[Nfmo,,2,1]
pdat<-colSums(dat)
pdat<-as.data.frame(pdat/sum(pdat))
names(pdat)<-"P"
pdat$CW<-bins
pdat$OE<-"est"

obs_plot_data<-rowSums(sslam.tvg.data$obs_p_I[2,,])
obs_plot_data<-obs_plot_data/sum(obs_plot_data)
obs_plot_data<-as.data.frame(obs_plot_data)
names(obs_plot_data)<-"P"
obs_plot_data$CW<-sslam.tvg.data$low_l_bins
obs_plot_data$OE<-"obs"

plot_data_4if<-rbind(pdat,obs_plot_data)
plot_data_4if$sex<-"Im. female"

# p<-ggplot(data=plot_data_4, aes(x=CW,y=P,fill=OE)) +
#   geom_bar(stat="identity", position=position_dodge())+
#   ggtitle("Winter Dredge Survey Immature females") +
```

```
  #   xlab("Carapace width (mm)") + ylab("Proportion")
  #
  # p

  #plot simulated WDS length composition with observed mature female
  dat<-I[Nfmo,,3,1]
  pdat<-colSums(dat)
  pdat<-as.data.frame(pdat/sum(pdat))
  names(pdat)<-"P"
  pdat$CW<-bins
  pdat$OE<-"est"

  obs_plot_data<-rowSums(sslam.tvg.data$obs_p_I[3,,])
  obs_plot_data<-obs_plot_data/sum(obs_plot_data)
  obs_plot_data<-as.data.frame(obs_plot_data)
  names(obs_plot_data)<-"P"
  obs_plot_data$CW<-sslam.tvg.data$low_l_bins
  obs_plot_data$OE<-"obs"

  plot_data_4mf<-rbind(pdat,obs_plot_data)
  plot_data_4mf$sex<-"Mat. female"

  #Combine all sexes for WDS plot
  plot_data_4<-rbind(plot_data_4m,plot_data_4if,plot_data_4mf)

  p<-ggplot(data=plot_data_4, aes(x=CW,y=P,fill=OE)) +
    geom_bar(stat="identity", position=position_dodge())+
    ggtitle("Winter Dredge Survey") +
    xlab("Carapace width (mm)") + ylab("Proportion")+
    facet_wrap(~sex)
  p
}
#---------------------------------------------------------------------------
#MD trawl survey
{
#Males
  Nfmo<-251:300
  dat<-I[Nfmo,,1,2]

  plot_data<-as.data.frame(dat)
  plot_data$mo<-rep(1:nmo,5)

  nt<-5*(8-3+1)

  plot_data2 <- dplyr::filter(plot_data, mo>=3 & mo<=8)  %>%
    pivot_longer(cols=!mo,
             names_to = c("Value"),
```

```
              values_drop_na = TRUE)

plot_data2$CW<-rep(bins,nt)
plot_data_2a<-plot_data2 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))

plot_data_2a$OE<-"est"

#Observed
obs_plot_data<-as.data.frame(sslam.tvg.data$obs2_p_I[1,,])
MTS_mo<-sslam.tvg.data$obs2_t
MTS_mo2<-MTS_mo
for(i in 1:length(MTS_mo)){
  MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
}
obs_plot_data$CW<-bins
plot_data3 <- obs_plot_data %>%
pivot_longer(cols=!CW,
              names_to = c("Value"))
plot_data3$mo<-rep(MTS_mo2,nlbins)

plot_data_3a<-plot_data3 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))
plot_data_3a$OE<-"obs"

plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
plot_data_4m$sex<-"Male"

p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
  geom_bar(stat="identity", position=position_dodge())+
   ggtitle("MD Trawl Survey Males") +
   xlab("Carapace width (mm)") + ylab("Proportion")+
  facet_wrap(~mo)

print(p)

#Immature females
Nfmo<-251:300
dat<-I[Nfmo,,2,2]

plot_data<-as.data.frame(dat)
plot_data$mo<-rep(1:nmo,5)
```

```
nt<-5*(8-3+1)

plot_data2 <- dplyr::filter(plot_data, mo>=3 & mo<=8)  %>%
  pivot_longer(cols=!mo,
               names_to = c("Value"),
               values_drop_na = TRUE)

plot_data2$CW<-rep(bins,nt)
plot_data_2a<-plot_data2 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))

plot_data_2a$OE<-"est"

#Observed
obs_plot_data<-as.data.frame(sslam.tvg.data$obs2_p_I[2,,])
MTS_mo<-sslam.tvg.data$obs2_t
MTS_mo2<-MTS_mo
for(i in 1:length(MTS_mo)){
  MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
}
obs_plot_data$CW<-bins
plot_data3 <- obs_plot_data %>%
  pivot_longer(cols=!CW,
               names_to = c("Value"))
plot_data3$mo<-rep(MTS_mo2,nlbins)

plot_data_3a<-plot_data3 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))
plot_data_3a$OE<-"obs"

plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
plot_data_4m$sex<-"Im. female"

p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
  geom_bar(stat="identity", position=position_dodge())+
  ggtitle("MD Trawl Survey Immature Females") +
  xlab("Carapace width (mm)") + ylab("Proportion")+
  facet_wrap(~mo)

print(p)
#Immature females
Nfmo<-251:300
dat<-I[Nfmo,,3,2]
```

```
plot_data<-as.data.frame(dat)
plot_data$mo<-rep(1:nmo,5)

nt<-5*(8-3+1)

plot_data2 <- dplyr::filter(plot_data, mo>=3 & mo<=8)  %>%
  pivot_longer(cols=!mo,
              names_to = c("Value"),
              values_drop_na = TRUE)

plot_data2$CW<-rep(bins,nt)
plot_data_2a<-plot_data2 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))

plot_data_2a$OE<-"est"

#Observed
obs_plot_data<-as.data.frame(sslam.tvg.data$obs2_p_l[3,,])
MTS_mo<-sslam.tvg.data$obs2_t
MTS_mo2<-MTS_mo
for(i in 1:length(MTS_mo)){
  MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
}
obs_plot_data$CW<-bins
plot_data3 <- obs_plot_data %>%
  pivot_longer(cols=!CW,
              names_to = c("Value"))
plot_data3$mo<-rep(MTS_mo2,nlbins)

plot_data_3a<-plot_data3 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))
plot_data_3a$OE<-"obs"

plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
plot_data_4m$sex<-"Mat. Female"

p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
  geom_bar(stat="identity", position=position_dodge())+
  ggtitle("MD Trawl Survey Mature Females") +
  xlab("Carapace width (mm)") + ylab("Proportion")+
  facet_wrap(~mo)
```

```
  print(p)
}
#-------------------------------------------------------------------------------
#VIMS Trawl Survey
{
  #Males
  Nfmo<-251:300
  dat<-I[Nfmo,,1,3]

  plot_data<-as.data.frame(dat)
  plot_data$mo<-rep(1:nmo,5)

  nt<-5*nmo

  plot_data2 <- plot_data  %>%
    pivot_longer(cols=!mo,
                 names_to = c("Value"),
                 values_drop_na = TRUE)

  plot_data2$CW<-rep(bins,nt)
  plot_data_2a<-plot_data2 %>%
    group_by(mo, CW) %>%
    summarise(T=sum(value)) %>%
    mutate(P=T/sum(T))

  plot_data_2a$OE<-"est"

  #Observed
  obs_plot_data<-as.data.frame(sslam.tvg.data$obs3_p_I[1,,])
  MTS_mo<-sslam.tvg.data$obs3_t
  MTS_mo2<-MTS_mo
  for(i in 1:length(MTS_mo)){
    MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
  }
  obs_plot_data$CW<-bins
  plot_data3 <- obs_plot_data %>%
    pivot_longer(cols=!CW,
                 names_to = c("Value"))
  plot_data3$mo<-rep(MTS_mo2,nlbins)

  plot_data_3a<-plot_data3 %>%
    group_by(mo, CW) %>%
    summarise(T=sum(value)) %>%
    mutate(P=T/sum(T))
  plot_data_3a$OE<-"obs"

  plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
```

```
plot_data_4m$sex<-"Male"

p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
  geom_bar(stat="identity", position=position_dodge())+
  ggtitle("VIMS Trawl Survey Males") +
  xlab("Carapace width (mm)") + ylab("Proportion")+
  facet_wrap(~mo)

print(p)

#Immature females
dat<-I[Nfmo,,2,3]

plot_data<-as.data.frame(dat)
plot_data$mo<-rep(1:nmo,5)

nt<-5*nmo

plot_data2 <- plot_data  %>%
  pivot_longer(cols=!mo,
             names_to = c("Value"),
             values_drop_na = TRUE)

plot_data2$CW<-rep(bins,nt)
plot_data_2a<-plot_data2 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))

plot_data_2a$OE<-"est"

#Observed
obs_plot_data<-as.data.frame(sslam.tvg.data$obs3_p_I[2,,])
MTS_mo<-sslam.tvg.data$obs3_t
MTS_mo2<-MTS_mo
for(i in 1:length(MTS_mo)){
  MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
}
obs_plot_data$CW<-bins
plot_data3 <- obs_plot_data %>%
  pivot_longer(cols=!CW,
             names_to = c("Value"))
plot_data3$mo<-rep(MTS_mo2,nlbins)

plot_data_3a<-plot_data3 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
```

```
  mutate(P=T/sum(T))
plot_data_3a$OE<-"obs"

plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
plot_data_4m$sex<-"Im. female"

p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
  geom_bar(stat="identity", position=position_dodge())+
  ggtitle("VIMS Trawl Survey Immature Females") +
  xlab("Carapace width (mm)") + ylab("Proportion")+
  facet_wrap(~mo)

print(p)
#Mature females
Nfmo<-251:300
dat<-I[Nfmo,,3,3]

plot_data<-as.data.frame(dat)
plot_data$mo<-rep(1:nmo,5)

nt<-5*nmo

plot_data2 <- plot_data  %>%
  pivot_longer(cols=!mo,
             names_to = c("Value"),
             values_drop_na = TRUE)

plot_data2$CW<-rep(bins,nt)
plot_data_2a<-plot_data2 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))

plot_data_2a$OE<-"est"

#Observed
obs_plot_data<-as.data.frame(sslam.tvg.data$obs3_p_I[3,,])
MTS_mo<-sslam.tvg.data$obs3_t
MTS_mo2<-MTS_mo
for(i in 1:length(MTS_mo)){
  MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
}
obs_plot_data$CW<-bins
plot_data3 <- obs_plot_data %>%
  pivot_longer(cols=!CW,
             names_to = c("Value"))
plot_data3$mo<-rep(MTS_mo2,nlbins)
```

```
  plot_data_3a<-plot_data3 %>%
    group_by(mo, CW) %>%
    summarise(T=sum(value)) %>%
    mutate(P=T/sum(T))
  plot_data_3a$OE<-"obs"

  plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
  plot_data_4m$sex<-"Mat. female"

  p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
    geom_bar(stat="identity", position=position_dodge())+
    ggtitle("VIMS Trawl Survey Mature Females") +
    xlab("Carapace width (mm)") + ylab("Proportion")+
    facet_wrap(~mo)

  print(p)
}
#-----------------------------------------------------------------------------
#ChesMMAP
{
  #Males
  Nfmo<-251:300
  dat<-I[Nfmo,,1,4]

  plot_data<-as.data.frame(dat)
  plot_data$mo<-rep(1:nmo,5)

  chesmo<-c(1,3,5,7,9)

  nt<-5*length(chesmo)

  plot_data2 <- dplyr::filter(plot_data, mo %in% chesmo)  %>%
    pivot_longer(cols=!mo,
                 names_to = c("Value"),
                 values_drop_na = TRUE)

  plot_data2$CW<-rep(bins,nt)
  plot_data_2a<-plot_data2 %>%
    group_by(mo, CW) %>%
    summarise(T=sum(value)) %>%
    mutate(P=T/sum(T))

  plot_data_2a$OE<-"est"

  #Observed
  obs_plot_data<-as.data.frame(sslam.tvg.data$obs4_p_I[1,,])
```

```
MTS_mo<-sslam.tvg.data$obs4_t
MTS_mo2<-MTS_mo
for(i in 1:length(MTS_mo)){
  MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
}
obs_plot_data$CW<-bins
plot_data3 <- obs_plot_data %>%
  pivot_longer(cols=!CW,
             names_to = c("Value"))
plot_data3$mo<-rep(MTS_mo2,nlbins)

plot_data_3a<-plot_data3 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))
plot_data_3a$OE<-"obs"

plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
plot_data_4m$sex<-"Male"

p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
  geom_bar(stat="identity", position=position_dodge())+
  ggtitle("ChesMMAP Trawl Survey Males") +
  xlab("Carapace width (mm)") + ylab("Proportion")+
  facet_wrap(~mo)

print(p)

#Immature females
Nfmo<-251:300
dat<-I[Nfmo,,2,4]

plot_data<-as.data.frame(dat)
plot_data$mo<-rep(1:nmo,5)


plot_data2 <- dplyr::filter(plot_data, mo %in% chesmo)  %>%
  pivot_longer(cols=!mo,
             names_to = c("Value"),
             values_drop_na = TRUE)

plot_data2$CW<-rep(bins,nt)
plot_data_2a<-plot_data2 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))
```

```
plot_data_2a$OE<-"est"

#Observed
obs_plot_data<-as.data.frame(sslam.tvg.data$obs4_p_I[2,,])
MTS_mo<-sslam.tvg.data$obs4_t
MTS_mo2<-MTS_mo
for(i in 1:length(MTS_mo)){
  MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
}
obs_plot_data$CW<-bins
plot_data3 <- obs_plot_data %>%
  pivot_longer(cols=!CW,
               names_to = c("Value"))
plot_data3$mo<-rep(MTS_mo2,nlbins)

plot_data_3a<-plot_data3 %>%
  group_by(mo, CW) %>%
  summarise(T=sum(value)) %>%
  mutate(P=T/sum(T))
plot_data_3a$OE<-"obs"

plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
plot_data_4m$sex<-"Im. female"

p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
  geom_bar(stat="identity", position=position_dodge())+
  ggtitle("ChesMMAP Trawl Survey Immature Females") +
  xlab("Carapace width (mm)") + ylab("Proportion")+
  facet_wrap(~mo)

print(p)

#Mature females
Nfmo<-251:300
dat<-I[Nfmo,,3,4]

plot_data<-as.data.frame(dat)
plot_data$mo<-rep(1:nmo,5)

plot_data2 <- dplyr::filter(plot_data, mo %in% chesmo)  %>%
  pivot_longer(cols=!mo,
               names_to = c("Value"),
               values_drop_na = TRUE)

plot_data2$CW<-rep(bins,nt)
plot_data_2a<-plot_data2 %>%
  group_by(mo, CW) %>%
```

```
    summarise(T=sum(value)) %>%
    mutate(P=T/sum(T))

  plot_data_2a$OE<-"est"

  #Observed
  obs_plot_data<-as.data.frame(sslam.tvg.data$obs4_p_I[3,,])
  MTS_mo<-sslam.tvg.data$obs4_t
  MTS_mo2<-MTS_mo
  for(i in 1:length(MTS_mo)){
    MTS_mo2[i]<-get_m(MTS_mo[i],nmo)
  }
  obs_plot_data$CW<-bins
  plot_data3 <- obs_plot_data %>%
    pivot_longer(cols=!CW,
               names_to = c("Value"))
  plot_data3$mo<-rep(MTS_mo2,nlbins)

  plot_data_3a<-plot_data3 %>%
    group_by(mo, CW) %>%
    summarise(T=sum(value)) %>%
    mutate(P=T/sum(T))
  plot_data_3a$OE<-"obs"

  plot_data_4m<-rbind(plot_data_2a,plot_data_3a)
  plot_data_4m$sex<-"Mat. Female"

  p<-ggplot(data=plot_data_4m, aes(x=CW,y=P,fill=OE)) +
    geom_bar(stat="identity", position=position_dodge())+
    ggtitle("ChesMMAP Trawl Survey Mature Females") +
    xlab("Carapace width (mm)") + ylab("Proportion")+
    facet_wrap(~mo)

  print(p)
}
#----------------------------------------------------------------------------------------------------
#END SIMULATION MODEL
#---------------------------------------------------------------------------------------------------

#----------------------------------------------------------------------------------------------------
#BEGIN ASSESSMENT MODEL
#----------------------------------------------------------------------------------------------------
SSLAM_BC<-function(parms){
  #RTMB function to use "local" variable names
  getAll(parms,alldat)

  #Define needed arrays
```

```
  G<-array(0,dim=c(nlbins,nlbins,3,tsteps)) #G for three sexes, each time step, number of length bins, number of length bins

  N<-array(0,c(tsteps,nlbins,3)) #abundance at size by sex (1 = male, 2=immature female, 3=mature female:no eggs, 4=mature female orange eggs, 5=mature female black eggs)
  F<-array(0,c(tsteps,nlbins,3)) #fishing mortality rate
  Z<-array(0,c(tsteps,nlbins,3)) #total mortality rate
  C<-array(0,c(tsteps,nlbins,3)) #catch of by size and sex/maturity stage
  R<-vector(mode="numeric",length=tsteps) #recruitment
  est_I<-array(-99,dim=c(dtsteps,nlbins,3,nsrv)) #index of abundance at sex and size
  est_C<-array(-99,dim=c(dtsteps,nlbins,3)) #catch at sex and size

  #Calculate male selectivity
  selh<-logistic_sel(0.1,85)

  #Backtransform parameters

  #Calculate growth

  #Calculate population dynamics


  nll=0 #Testing - set nll equal to zero
  return(nll) #return the negative log likelihood value
}

alldat <- list(fyear=fdyr,
            lyear=nyr,
            nmo=nmo,
            years=seq(fdyr,nyr,1),
            months=seq(1,nmo,1),
            low_l_bins=bins,
            binw=bin_width,
            lbins=1:nlbins,
            fmat=fmat, #probability of a female maturing at length
            mmat=mmat, #male maturity at length
            GDD=GDD, #growing degree days during each month
            M=M[,1], #natural mortality rate

            #Harvest=obs_C_mod,
            #Index=obs_I,
            #in_C_sd=cat_sigma,
            #in_effN_C=C_effN,
            #in_I_sd=I_sigma,
            #in_effN_I=I_effN,
            #mat_params=fmat_params,
```

```
            #Gest=ifelse(rep(GDD,(nyr-fdyr+1))>0,1,0)
            )

#initial parameter values
param_init_vals<-list(log_Linf=log(Linf),
                 log_kp=log(kp),
                 log_L0=log(L0),
                 log_L0_sd=log(L0*L0_CV),
                 #log_Linf_cv=log(Linf_CV),
                 #log_K_cv=log(K_CV),
                 #tan_Linf_K_cov=tan(Linf_K_Cor*3.1416/2),
                 #log_q=log(1),
                 #log_R0=log(2000),
                 #log_F0=log(f[1]),
                 #log_N0=log(N[(fdyr-1)*nmo+1,]),
                 #log_R=log(R[((fdyr-1)*nmo+1):(tsteps-1)]),
                 #log_f=log(f[((fdyr-1)*nmo+1):(tsteps)]),
                 #log_fish_sel_params=c(log(0.1),log(85)),
                 #log_surv_sel_params=c(log(0.05),log(15)),
                 #nu_C=0,
                 #phi_C=1,
                 #nu_I=0,
                 #phi_I=1,
                 #proc_err=array(0,dim=c(3,nlbins,(dtsteps-1))),
                 #log_proc_err_sd=log(0.1)
                 )

params_to_estimate<-list(log_Linf=factor(1),
                   log_kp=factor(1),
                   log_L0=factor(1),
                   log_L0_sd=factor(1),
                   #log_Linf_var=factor(1),
                   #log_K_var=factor(1),
                   #Linf_K_cov=factor(1),
                   #log_q=factor(1),
                   #log_R0=factor(1),
                   #log_F0=factor(1),
                   #log_R=factor(rep(NA,length(R[((fdyr-1)*nmo+1):(tsteps-1)]))),
                   #log_R=factor((1:length(R[((fdyr-1)*nmo+1):(tsteps-1)]))),
                   #log_f=factor(rep(NA,length(f[((fdyr-1)*nmo+1):(tsteps)]))),
                   #log_f=factor((1:length(f[((fdyr-1)*nmo+1):(tsteps)]))),
                   #log_fish_sel_params=factor(1:2),
                   #log_surv_sel_params=as.factor(matrix(1:4),nrow=2,ncol=nsrv),

                   #nu_C=factor(NA),
                   #phi_C=factor(NA),
```

```
                  #nu_I=factor(NA),
                  #phi_I=factor(NA),
                  #proc_err=factor(matrix(NA,nrow=nlbins,ncol=(dtsteps-1))),
                  #proc_err=factor(matrix(1:((dtsteps-1)*nlbins),nrow=nlbins,ncol=(dtsteps-1))),
                  #log_proc_err_sd=factor(1)
                  )

obj <- MakeADFun(alldat, param_init_vals, random="proc_err", DLL=model,map=params_to_estimate)
#obj <- MakeADFun(alldat, param_init_vals, DLL=model,map=params_to_estimate)

# Minimize log likelihood using nlminb.
opt <- nlminb(obj$par,obj$fn,obj$gr,
         control = list(eval.max = 100000, iter.max = 100000),
         lower = -50, upper = 50)

#-----------------------------------------------------------------------------------------------------------------------
#Model fitting stuff below here
#------------------------------------------------------------------------------------------------------------------------

  #set up data for model

  alldat <- list(fyear=fdyr, lyear=nyr, nmo=nmo,
years=seq(fdyr,nyr,1),months=seq(1,nmo,1),low_l_bins=bins,binw=bin_width,
            Harvest=obs_C_mod, Index=obs_I, M=M[1:2,],in_C_sd=cat_sigma, in_effN_C=C_effN,
in_I_sd=I_sigma,in_effN_I=I_effN,
            mat_params=fmat_params, lbins=1:nlbins,GDD=rep(GDD,(nyr-
fdyr+1)),Gest=ifelse(rep(GDD,(nyr-fdyr+1))>0,1,0))
  #initial parameter values
  param_init_vals<-list(log_Linf=log(Linf),log_kp=log(kp),log_L0=log(L0),
                 log_L0_sd=log(L0*L0_CV),log_Linf_cv=log(Linf_CV), log_K_cv=log(K_CV),
                 tan_Linf_K_cov=tan(Linf_K_Cor*3.1416/2),log_q=log(1),log_R0=log(2000),log_F0=log(f[1]),
                 #log_N0=log(N[(fdyr-1)*nmo+1,]),
                 log_R=log(R[((fdyr-1)*nmo+1):(tsteps-1)]),
                 log_f=log(f[((fdyr-1)*nmo+1):(tsteps)]),log_fish_sel_params=c(log(0.1),log(85)),
                 log_surv_sel_params=c(log(0.05),log(15)),nu_C=0,phi_C=1,nu_I=0,phi_I=1,
                 proc_err=array(0,dim=c(3,nlbins,(dtsteps-1))),log_proc_err_sd=log(0.1))

  params_to_estimate<-list(log_Linf=factor(1),
                   log_kp=factor(1),
                   log_L0=factor(1),
                   log_L0_sd=factor(1),
                   log_Linf_var=factor(1),
                   log_K_var=factor(1),
                   Linf_K_cov=factor(1),
                   log_q=factor(1),
                   log_R0=factor(1),
                   log_F0=factor(1),
```

```
                        #log_R=factor(rep(NA,length(R[((fdyr-1)*nmo+1):(tsteps-1)]))),
                        log_R=factor((1:length(R[((fdyr-1)*nmo+1):(tsteps-1)]))),
                        #log_f=factor(rep(NA,length(f[((fdyr-1)*nmo+1):(tsteps)]))),
                        log_f=factor((1:length(f[((fdyr-1)*nmo+1):(tsteps)]))),
                        log_fish_sel_params=factor(1:2),
                        #log_fish_sel_params=factor(rep(NA,2)),
                        #log_surv_sel_params=factor(rep(NA,2)),
                        log_surv_sel_params=factor(1:2),
                        nu_C=factor(NA),
                        phi_C=factor(NA),
                        nu_I=factor(NA),
                        phi_I=factor(NA),
                        #proc_err=factor(matrix(NA,nrow=nlbins,ncol=(dtsteps-1))),
                        proc_err=factor(matrix(1:((dtsteps-1)*nlbins),nrow=nlbins,ncol=(dtsteps-1))),
                        log_proc_err_sd=factor(1))

  model="BC_SSLAM_tvG"
  # Compile c++ file with objective function
  compile(paste0("src/", model,".cpp"))  #dyn.unload(dynlib(paste0("src/", model)))

  # Add dynlib extension
  # From TMB documentation: Add the platform dependent dynlib extension. In order
  # for examples to work across platforms DLLs should be loaded by dyn.load(dynlib("name")).
  dyn.load(dynlib(paste0("src/", model)))
  # MakeADFun constructs an objective function with derivatives based on the c++ template
  obj <- MakeADFun(alldat, param_init_vals, random="proc_err", DLL=model,map=params_to_estimate)
  #obj <- MakeADFun(alldat, param_init_vals, DLL=model,map=params_to_estimate)

  # Minimize log likelihood using nlminb.
  opt <- nlminb(obj$par,obj$fn,obj$gr,
              control = list(eval.max = 100000, iter.max = 100000),
              lower = -50, upper = 50)



#------------------------------------------------------------------------------------------------------------------------------
#Simulation Model Plots for documentation
#---------------------------------------------------------------------------------------------------------------------------------




#female maturity
  pdat<-cbind(fmat,bins)
ggplot(pdat, aes(x=bins,y=fmat))+
  geom_line()+
  labs(x="Carapace width", y = "Maturity")
```

```
#Growing degree days
pdat<-as.data.frame(cbind(GDD[1:nmo],1:nmo))

ggplot(pdat, aes(x=V2,y=V1))+
  geom_line()+
  labs(x="Month", y = "Cumulative growing degree days")

#mean growth
pdat<-as.data.frame(cbind(kp*GDD,rep(Linf[1],length(GDD)),seq(1:length(GDD))))
pdat<-as.data.frame(cbind(bin_mids,(pdat$V2[6]-bin_mids)*(1-exp(-pdat$V1[6]))))

ggplot(pdat, aes(x=bin_mids,y=V2))+
  geom_line()+
  labs(x="Carapace width", y = "Mean growth increment (mm)")

#length-based Natural mortality per month
pdat<-as.data.frame(cbind(bin_mids,M[,1]))

ggplot(pdat, aes(x=bin_mids,y=V2))+
  geom_line()+
  labs(x="Carapace width", y = "Natural mortality rate (per mo)")

#fishery and survey selectivity
pdat<-as.data.frame(cbind(bin_mids,selh,surv_sel))
names(pdat)<-c("CW","selh","sels1","sels2","sels3","sels4")

ggplot(pdat, aes(x=CW))+
  geom_line(aes(y=selh),color="red")+
  geom_line(aes(y=sels1),color="blue")+
  geom_line(aes(y=sels2),color="black")+
  geom_line(aes(y=sels3),color="black")+
  geom_line(aes(y=sels4),color="purple")+
  labs(x="Carapace width", y = "Selectivity")

#function to plot length composition
plot_length_comp<-function(ft,lt,dat,ylabel){
  pdat<-as.data.frame(cbind(ft:lt,dat))
  pdat<-gather(pdat,key="V1",value="N",2:(nlbins+1))
  pdat$CW<-sort(rep(bins,lt-ft+1))
  pdat$mo<-rep(1:nmo,nlbins)
  pdat$t<-rep(1:(lt-ft+1),nlbins)

pp<-ggplot(data=pdat, aes(x=CW, y=N)) +
    geom_bar(stat="identity")+
    facet_wrap(~t)+
    labs(x="Carapace width", y = ylabel)
  return(pp)
```

```
}

ft=291
lt=300
#Male population
plot_length_comp(ft,lt,dat=N[ft:lt,,1],"Abundance")

#Immature female population
plot_length_comp(ft,lt,dat=N[ft:lt,,2],"Abundance")

#Mature female population
plot_length_comp(ft,lt,dat=N[ft:lt,,3],"Abundance")

#Male Catches
plot_length_comp(ft,lt,dat=C[ft:lt,,1],"Catch")

#mature female catches
plot_length_comp(ft,lt,dat=C[ft:lt,,3],"Catch")

#Survey male catch at length
plot_length_comp(ft,lt,dat=I[ft:lt,,1,1],"Index")

#Survey immature female catch at length
plot_length_comp(ft,lt,dat=I[ft:lt,,2,1],"Index")

#Survey mature female catch at length
plot_length_comp(ft,lt,dat=I[ft:lt,,3,1],"Index")




ggsave("surv2_length_dist.pdf",plot=p,width=24,height=36,units="in")









pdat<-as.data.frame(cbind(1:10,obs_I_mod[1,31:40,]))
pdat<-gather(pdat,key="V1",value="I",2:28)
j=1
for(i in 1:length(pdat$I))
{
  j=as.integer(trunc(1+(i-1)/10))
  pdat$CW[i]<-bins$L_CW[j]
```

```
  mo<-i%%10
  if(mo==0) mo=10
  pdat$t[i]<-mo
}
ggplot(data=pdat, aes(x=CW, y=I)) +
  geom_bar(stat="identity")+
  facet_wrap(~t)+
  labs(x="Carapace width", y = "Index")

#total male abundance
NT<-rowSums(N[,,1])
pdat<-as.data.frame(cbind(NT,1:300))

ggplot(pdat, aes(x=V2,y=NT))+
  geom_line()+
  labs(x="Month", y = "Male abundance")

#Total Recruitment
Rdat<-seq(10,300,10)
pdat<-as.data.frame(cbind(R[Rdat],Rdat))
pdat$y<-seq(1:30)

ggplot(pdat, aes(x=y,y=V1))+
  geom_line()+
  labs(x="Year", y = "Recruitment")


  #-----------------------------------------------------------------------------
  #report out values to check code
  #obj$adreport()
  res<-obj$report() #get results into an R list
  rep <- sdreport(obj, bias.correct = TRUE)
  summary(rep, "random")                      ## Only random effects
  summary(rep, "fixed", p.value = TRUE)       ## Only non-random effects
  summary(rep, "report")                      ## Only report

  #unload DLL
  dyn.unload(dynlib(paste0("src/", model)))


#-----------------------------------------------------------------------------
#Diagnostics
#-----------------------------------------------------------------------------
#Linf
Linf-res$Linf
#K
K-res$K
```

```
#L0
L0-res$L0
#L0_sd
L0_CV*L0-res$L0_sd
#fishery selectivity
res$fsel-sel
#abundance
Nd<-res$N-t(N[((fdyr-1)*nmo+1):tsteps,])
Nt<-t(N[((fdyr-1)*nmo+1):tsteps,])
Nt[,1]-res$N[,1]
res$Ntest
t(N[1:10*nmo,])
res$Ntest-t(N[1:(10*nmo),])
#Total abundance
(colSums(res$N)-rowSums(N[((fdyr-1)*nmo+1):tsteps,]))/rowSums(N[((fdyr-1)*nmo+1):tsteps,])
#growth
res$G-G[1,,]
#R
(res$R-R[((fdyr-1)*nmo+1):(tsteps-1)])/R[((fdyr-1)*nmo+1):(tsteps-1)]
log(res$R)-log(R[((fdyr-1)*nmo+1):(tsteps-1)])
#Recruitment proportions at length
res$init_pL-init_size
#survey selectivity
res$ssel-surv_sel

#Graph catch
pdata<-
data.frame(est_C=res$TC,obs_C=res$obs_C,obs_C_u=exp(log(res$obs_C)+2*cat_sigma),obs_C_l=exp(lo
g(res$obs_C)-2*cat_sigma),time=1:length(res$obs_C))

p<-ggplot(data=pdata,aes(x=time,y=obs_C))+
   geom_point()+
   geom_errorbar(aes(ymin=obs_C_l, ymax=obs_C_u), width=.1,
             position=position_dodge(0.05))+
   geom_line(aes(x=time,y=est_C))+
  labs(title="Total Catch",x="Time", y = "Catch (numbers)")
p
#plot index
pdata<-
data.frame(est_C=res$TI,obs_C=res$obs_I,obs_C_u=exp(log(res$obs_I)+2*surv_sigma),obs_C_l=exp(log
(res$obs_I)-2*surv_sigma),time=1:length(res$obs_I))

p<-ggplot(data=pdata,aes(x=time,y=obs_C))+
  geom_point()+
  geom_errorbar(aes(ymin=obs_C_l, ymax=obs_C_u), width=.1,
             position=position_dodge(0.05))+
  geom_line(aes(x=time,y=est_C))+
```

```
  labs(title="Total Index",x="Time", y = "Index (numbers)")
p
#plot catch composition
#calculate catch proportion residuals
est<-as.data.frame((res$p_C-res$obs_p_C)/sqrt(res$p_C*(1-res$p_C)/res$in_effN_C))
colnames(est)<-c(as.factor(1:ncol(est)))
nt<-length(colnames(est))
est$L<-as.factor(bins$L_CW)

pdata<-gather(est,"t","est_p",1:36)
pdata$posneg<-ifelse(pdata$est_p>0,"pos","neg")
p<-ggplot(data=pdata,aes(x=L,y=as.numeric(t),size=abs(est_p),color=as.factor(posneg)))+
 geom_point()+
  labs(title="Catch composition",x="Length",y="Time",color="Sign
of\nresidual",size="Residual\nmagnitude")
p

x<-gather(as.data.frame(res$p_C),"t","est_p",1:36)
y<-gather(as.data.frame(res$obs_p_C),"t","est_p",1:36)
qqplot(x$est_p,y$est_p,xlab = "estimated", ylab = "observed", main = "Catch Q-Q Plot")

#plot index composition
est<-as.data.frame((res$p_I-res$obs_p_I)/sqrt(res$p_I*(1-res$p_I)/res$in_effN_I))
colnames(est)<-c(as.factor(1:ncol(est)))
nt<-length(colnames(est))
est$L<-as.factor(bins$L_CW)

pdata<-gather(est,"t","est_p",1:36)
pdata$posneg<-ifelse(pdata$est_p>0,"pos","neg")
p<-ggplot(data=pdata,aes(x=L,y=as.numeric(t),size=abs(est_p),color=as.factor(posneg)))+
  geom_point()+
  labs(title="Index composition",x="Length",y="Time",color="Sign
of\nresidual",size="Residual\nmagnitude")
p

x<-gather(as.data.frame(res$p_I),"t","est_p",1:36)
y<-gather(as.data.frame(res$obs_p_I),"t","est_p",1:36)
qqplot(x$est_p,y$est_p,xlab = "estimated", ylab = "observed", main = "Index Q-Q Plot")

#-----------------------------------------------------------------------------------------------
#test  if model is running
diff<-res$C-t(C[((fdyr-1)*nmo+1):tsteps,])
diff/t(C[((fdyr-1)*nmo+1):tsteps,])

Idiff<-res$I-t(I[((fdyr-1)*nmo+1):tsteps,])

#fishing intensity
```

```
res$f
f
#selectivity
res$fsel-sel
#abundance
Nd<-res$N-t(N[((fdyr-1)*nmo+1):tsteps,])
Nd/t(N[((fdyr-1)*nmo+1):tsteps,])
#Z
res$Z-t(Z[((fdyr-1)*nmo+1):tsteps,])
#growth
res$G-G[1,,]
#R
res$R-R[((fdyr-1)*nmo+1):(tsteps-1)]
#Recruitment proportions at length
res$init_pL-init_size

colSums(res$C)
res$TC
colSums(t(obs_I))
(res$TC-res$obs_C)/res$obs_C
(res$TI-res$obs_I)/res$obs_I
colSums(res$obs_p_I)
colSums(res$obs_p_C)
Idiff<-res$I-t(obs_I)
Idiff/t(obs_I)
res$ssel-surv_sel
res$q


ogc=res$TC_nll
ogil=res$nll_I_lcomp
ogi=res$TI_nll
ogcl=res$nll_C_lcomp

#Old code below here

all_mod_fit <- summary(sdreport(obj))
all_mod_fitRowNames <- row.names(all_mod_fit)
row.names(all_mod_fit) <- 1:nrow(all_mod_fit)


all_mod_fit_df <- as.data.frame(all_mod_fit)
names(all_mod_fit_df) <- c("Estimate", "StError")
all_mod_fit_df$Name <- all_mod_fitRowNames
#all_mod_fit_df$NOAACode <- rep(dat$NOAANumber, times = nrow(all_mod_fit_df))
TMBresults <- data.frame()
TMBresults <- rbind(all_mod_fit_df, TMBresults)
```

```
# make a text file with the likelihood results
ModelResultsText(obj = obj, opt = opt, modelname = "LAM", plot_title = plot_title)



#Call estimation model
#end simulation loop
p<-as.vector(c(0.2,0.5,0.3))
n<-rmultinom(1,15,p)

dmultinom(x=n,size=NULL,prob=p,T)


N_plot<-cbind(seq(1,tsteps),N)
colnames(N_plot)<-c("t",seq(5,maxl,bin_width))

ndata<- gather(as.data.frame(N_plot),key="Length",value="N",2:(nlbins+1))

tmin=37
tmax=48
pdat<-subset(ndata,t>=tmin)
pdat<-subset(pdat,t<=tmax)

p<-ggplot(data=pdat, aes(x=as.numeric(Length), y=N)) +
  geom_bar(stat="identity")+
  facet_wrap(~t,ncol=1)

p

I_plot<-cbind(seq(1,tsteps),I)
colnames(I_plot)<-c("t",seq(5,maxl,bin_width))

Idata<- gather(as.data.frame(I_plot),key="Length",value="I",2:(nlbins+1))

tmin=37
tmax=48
pdat<-subset(Idata,t>=tmin)
pdat<-subset(pdat,t<=tmax)

p<-ggplot(data=pdat, aes(x=as.numeric(Length), y=I)) +
  geom_bar(stat="identity")+
  facet_wrap(~t,ncol=1)
```

Appendix 3. Spatially Explicit Length-Based Assessment Model (SSLAM)

```
// Length-based assessment model that uses a normal distribution for the
transition probabilities conditional on current length
// Basic model to allow testing of code and state-space estimation
// Authors: Mike Wilberg
// Date Started: 22 May 2023

// Comments:
// Rec constraint to zero for certain months
// Fmult constrant to zero for certain months
// time series of GDD to allow growth to show annual variability
//Include statements to get the right libraries
#include <iostream>
#include <TMB.hpp>
#include "age_comp_osa.hpp"
#include "SSLAM_helper.hpp"
#include <fenv.h>
#include "SSLAM_tvG_DLStudy_index2.hpp"


//template<class Type>
//Type multinom

template <class Type>
Type objective_function<Type>::operator()()
{
  //feenableexcept(FE_INVALID | FE_OVERFLOW | FE_DIVBYZERO |
FE_UNDERFLOW);

  //--------------------------------------------------------------------------
-----
  //DATA
  //--------------------------------------------------------------------------
-----
  DATA_INTEGER(dtsteps); // number of time steps
  DATA_INTEGER(fyear); //first year
  //DATA_INTEGER(lyear); //last year
  DATA_INTEGER(nmo);  //number of months per year
  //DATA_IVECTOR(years);  // years per time step
  DATA_IVECTOR(months); // months per time step
  DATA_VECTOR(low_l_bins); //lower bound of length bins
  DATA_SCALAR(binw);  //width of length bins
  DATA_VECTOR(Harvest); //number harvested per fishing  month
  DATA_IVECTOR(Harvest_t);// zero-based indices of non-zero hearvest month
  DATA_IVECTOR(Rec_t); // zero-based indices of non-zero recruit month
  DATA_IVECTOR(Rec_sea); // monthly boolean variable of non-zero recruit
season
  DATA_IVECTOR(obs_t); // observed time indices
  DATA_VECTOR(obs_I);// observed indices by month
```

```
  DATA_MATRIX(obs_p_I);// observed proportion at length in index
  // the second index is subject to catch-ability constraint
  DATA_IVECTOR(obs2_t);// observed time second index
  DATA_VECTOR(obs2_I); // observed indices by month
  DATA_MATRIX(obs2_p_I);// observed proportion at length in index 2
  DATA_VECTOR(M); // constant M (only include if can't estimate in the
model)
  DATA_SCALAR(in_C_sd); //constant log-scale SD for catch
  DATA_SCALAR(in_I_sd); //log-scale SD for the index of abundance
  DATA_SCALAR(in_effN_I); //effective sample size for the index of
abundance
  //DATA_IVECTOR(lbins); //numbers for lbins to use in composition
likelihood functions
  DATA_VECTOR(GDD); //Growing degree days each seasonal step
  DATA_IVECTOR(Gest); //vector of ones and zeros to determine if growth
should be estimated for that season step
  DATA_VECTOR(GDD_ts); // Growing degree days each time step
  DATA_IVECTOR(Gest_ts);// binary whether growth should be estimated for
that time step
  DATA_SCALAR(debug__);// debug flag;

  //----------------------------------------------------------------------
------
  //ESTIMATED PARAMETERS
  //----------------------------------------------------------------------
-----
  PARAMETER(log_Linf); // log scale Linfinity for von Bertalanffy  growth
model
  PARAMETER(log_kp); // log scale proportionality constant for GDD->K
  PARAMETER(log_L0); //log scale mean length of recruits
  PARAMETER(log_L0_sd); //log scale SD of length at recruitment
  PARAMETER(log_Linf_cv);//log of the coefficient of variation of Linf
  PARAMETER(log_K_cv); //log of the coefficient of variation of K
  PARAMETER(tan_Linf_K_cor); //tangent of the correlation of Linf and K
  PARAMETER(log_R0); //log initial recruitment
  PARAMETER(log_F0); //log initial fishing intensity
  PARAMETER_VECTOR(log_R); //log_recruitment
  PARAMETER_VECTOR(log_f);  //log scale fishing intensity (F when
selectivity is 1)
  PARAMETER_VECTOR(log_fish_sel_params); //log-scale logistic fishery
selectivity parameters
  PARAMETER_VECTOR(log_surv_sel_params);  //log-scale logistic survey
selectivity parameters
  PARAMETER(nu_C); //offset for catch sd
  PARAMETER(phi_C); //offset for catch effective sample size
  PARAMETER(nu_I); //offset for index sd
  PARAMETER(phi_I); //offset for index effective sample size
  PARAMETER_MATRIX(proc_err); //process error for population dynamics
  PARAMETER(log_proc_err_sd); //Process error SD (on the log scale)
  // parameters for lognormal priors for the von Bertalanffy parameters
  PARAMETER(mean_log_Linf);
  PARAMETER(sd_log_Linf);
  PARAMETER(mean_log_Linf_cv);
  PARAMETER(sd_log_Linf_cv);
```

```
  PARAMETER(mean_log_kp);
  PARAMETER(sd_log_kp);
  PARAMETER(mean_log_kp_cv);
  PARAMETER(sd_log_kp_cv);

  // prior for the von Bertalanffy parameters
  Type var_log_Linf = square(sd_log_Linf);
  Type Linf_pen = Type(-1.0)*dnorm(log_Linf,mean_log_Linf-
0.5*var_log_Linf,sd_log_Linf,true);
  Type var_log_Linf_cv = square(sd_log_Linf_cv);
  Type Linf_cv_pen = Type(-1.0)*dnorm(log_Linf_cv,mean_log_Linf_cv-
0.5*var_log_Linf_cv,sd_log_Linf_cv,true);
  Type var_log_kp = square(sd_log_kp);
  Type kp_pen = Type(-1.0)*dnorm(log_kp,mean_log_kp-
0.5*var_log_kp,sd_log_kp,true);
  Type var_log_kp_cv = square(sd_log_kp_cv);
  Type kp_cv_pen = Type(-1.0)*dnorm(log_K_cv,mean_log_kp_cv-
0.5*var_log_kp_cv,sd_log_kp_cv,true);

  //INTERMEDIATE PARAMETERS
  //Local variables for indexing.
  int nt = dtsteps;
  int nh = Harvest.size();
  int nr = Rec_t.size();

  vector<Type> binmids = low_l_bins+0.5*binw;  //Calculate the midpoint of
each bin

  //int debug__ = 2;

  //----------------------------------------------------------------------
-----
  // PROCEDURE SECTION
  //----------------------------------------------------------------------
------
  Type Linf = exp(log_Linf);  //Backtransform Linf
  Type kp = exp(log_kp);
  vector<Type> K = exp(log_kp)*GDD;  //calculate K as a function of GDD
  Type L0 = exp(log_L0); //Backtransform L0
  Type L0_sd = exp(log_L0_sd);  //Backtransform the SD of L0
  Type Linf_sd = exp(log_Linf_cv)*Linf;  //Backtransform sd of Linf
  Type Linf_var = square(Linf_sd);
  Type K_cv = exp(log_K_cv); //Backtransform variance of K
  vector<Type> K_sd = K_cv*K; //calculate SD of K for each timestep
  Type Linf_K_cor = atan(tan_Linf_K_cor)/Type(3.1416/2.); //backtransform
Linf-K correlation
  int nb=binmids.size(); //get length of mean_g vector
  vector<Type> mean_g(nb);
  REPORT(Linf_K_cor);
  REPORT(kp);

  // 1. Proportions at length  for recruits

  vector<Type> init_pL(nb);
```

```
  int ulb=nb-1; //Upper index for length bins
  init_pL(0)=pnorm(low_l_bins(1),L0,L0_sd);  //first length bin represents
that range and all smaller
  for(int l=1;l<ulb;l++)  //loop over length bins
  {
    init_pL(l)=pnorm(low_l_bins(l+1),L0,L0_sd)-
pnorm(low_l_bins(l),L0,L0_sd);  //calculate proportion in each length bin
assuming normal distribution for length of recruits
  }
  init_pL(ulb)=Type(1.0)-pnorm(low_l_bins(ulb),L0,L0_sd);  //Last length
bin is a plus group representing individuals in that bin and larger.

  // 2. Calculate growth matrix
  //Calculate growth Transition matrix
   matrix<Type> G(nb,nb);  //Specify size of Growth transition matrix
   G.setZero();  //fill with zeros

   //Calculate mortality rates
   //Calculate selectivity as column vector
   vector<Type> fsel(nb);
   vector<Type> ssel(nb);

   //backtransform selectivity parameters
   vector<Type> fsel_params(2);
   vector<Type> ssel_params(2);
   //Fishery Selectivity
   fsel_params=exp(log_fish_sel_params);  //backtransform fishery
selectivity parameters
   fsel=Type(1.)/(Type(1.0)+exp(-fsel_params(0)*(binmids-
fsel_params(1))));  //logistic function
   //Survey selectivity
   ssel_params=exp(log_surv_sel_params);  //backtransform survey
selectivity parameters
   ssel=Type(1.)/(Type(1.0)+exp(-ssel_params(0)*(binmids-
ssel_params(1))));  //Logistic function

   //backtransform fishing intensity for each time step
   vector<Type> f(nh);
   f=exp(log_f);

   //Fishing (F) and total (Z) mortality
   matrix<Type> F(nb,nt);  //Fishing mortality (rows=lengths, cols=time)
   //F.setZero();
   F.setZero();

   matrix<Type> Z(nb,nt);  //Total instantaneous mortality rate
   Z.setZero();

   int t2=0;
   for(int t=0;t<nh;t++){ // for each month harvest allowed
     t2 = Harvest_t(t);
     F.col(t2)=fsel*f(t); // Calculate F as the product of selectivity and
fishing intensity
   }
```

```
   for(int t=0;t<nt;t++)
   {
       Z.col(t)=M; //Calculate Z as the sum of F and M (total
instantaneous mortality)
       Z.col(t)+=F.col(t);
   }

   if(debug__>0){
     std::cout <<"\nSSLAM_tvG ver. 3f\n";
     std::cout <<"nt="<<nt<<",nb="<<nb<<",nh="<<nh<<",nr="<<nr<<"\n";
   }

   if(debug__>0){
     std::cout <<"Growth parameters.\n";
     std::cout <<"Linf="<<Linf<<","<<"kp="<<kp<<","<<"L0="<<L0<<"\n";
     std::cout
<<"Linf_sd="<<Linf_sd<<",K_cv="<<K_cv<<",L0_sd="<<L0_sd<<"\n";
     std::cout <<"K=";
     for(int t=0;t<nmo-1;t++){
       std::cout<<K(t)<<"\t";
     }
     std::cout<<K(nmo-1)<<"\n";
     std::cout <<"K_sd=";
     for(int t=0;t<nmo-1;t++){
       std::cout<<K_sd(t)<<"\t";
     }
     std::cout<<K_sd(nmo-1)<<"\n";
    }

   if(debug__>1){
     std::cout <<"Mortality rates.\n";
     std::cout <<"log_f(0):"<<log_F0<<"\n";
     std::cout <<"log_f:";
     for(int t=0;t<nh;t++){
       std::cout << log_f(t) <<"\t";
     }
     std::cout <<"\n";
     std::cout <<"fsel:"<<std::endl;
     for(int b=0;b<nb;b++){
       std::cout << fsel(b) <<"\t";
     }
     std::cout <<"\n";
   }

   //Calculate abundance at length
   matrix<Type> N(nb,nt);  //Abundance at length matrix
   N.setZero(); //fill with zeros

   matrix<Type> S(nb,nb); //survival at length

   //Fill in first column of the N matrix
   //N.col(0)=exp(log_N0);
   int t_initialize=fyear*nmo+months(0)-1;
```

```
   vector<Type> N_init(nb);
   Type R0=exp(log_R0);

   if(debug__>1){
     std::cout <<"Initial abundance at length.\n";
     std::cout <<"R(0):"<<R0<<"\n";
   }

   vector<Type> Z_init(nb);
   Type F0=exp(log_F0);
   Z_init=M+F0*fsel;
   matrix<Type> S0(nb,nb);
   S0.setZero();
   S0.diagonal()=exp(-Z_init.array());
   matrix<Type> Ntest(nb,t_initialize);
   Ntest.setZero();
   //calculate initial abundance at length in the first model year by
calculating the approximate equilibrium by
   //running the model out with constant R and Z
   vector<Type> Ntemp(nb);
   vector<Type> K_calc(t_initialize);
   int m; // index for month

   for(int t=1;t<=t_initialize;t++)
   {
     m=get_mo(t,nmo);
     if(t==1)
     {
       N_init=R0*init_pL;  //start off with just recruits
     }
     else
     {
       G=G_matrix(binmids, Linf, K(m), Linf_var, square(K_sd(m)),
Linf_K_cor*Linf_sd*K_sd(m), Gest(m));
       //Build up the initial numbers at length over the t_initialize
period
       Ntemp=G*(S0*N_init);  //growth and survival
       N_init=Ntemp+R0*Rec_sea(m)*init_pL;  //add in recruitment
     }
     K_calc(t-1)=K(m);
     Ntest.col(t-1)=N_init;
     //std::cout << t << " " << t-1 << std::endl;
     //std::cout << m << std::endl;
     if(debug__>2){
       std::cout <<"t="<<t<<",m="<<m;
       std::cout <<",R="<<R0*Rec_sea(m)<<"\n";
       std::cout <<"Growth and Z:\n";
       for(int b=0;b<nb-1;b++){
         std::cout <<Ntemp(b)<<"\t";
       }
       std::cout <<Ntemp(nb-1)<<"\n";
       std::cout <<" N_init:";
       for(int b=0;b<nb-1;b++){
         std::cout <<N_init(b)<<"\t";
```

```
       }
       std::cout <<N_init(nb-1)<<"\n";
     }
   }
   REPORT(N_init);
   REPORT(Z_init);
   REPORT(R0);
   REPORT(F0);
   REPORT(Ntest);
   REPORT(K_calc);

   //calculate recruitment for each time step
   vector<Type> R(nt-1);
   vector<Type> Rtemp = exp(log_R.array());
   R.setZero();
   for(int t=0;t<nr;t++){
     t2 = Rec_t(t);
     R(t2) = Rtemp(t);
   }
   //vector<Type> R=exp(log_R.array());
   N.col(0)=N_init;

   vector<Type> K_ts(nt);
   vector<Type> K_sd_ts(nt);
   K_ts = exp(log_kp) * GDD_ts;
   K_sd_ts = K_ts * K_cv;

   if(debug__>0){
     std::cout <<"Abundance at length.\n";
   }
   for(int t=1;t<nt;t++)
   {
      //Calculate growth
      //Calculate survival
      S.setZero();
      S.diagonal()=exp(-Z.col(t-1).array());
      //Growth occurs before mortality
      //N.col(t)=G*N.col(t-1);
      //N.col(t)=N.col(t).array()*exp(-Z.col(t-1).array());

      //calculate growth for each time step
      G=G_matrix(binmids, Linf, K_ts(t-1), Linf_var, square(K_sd_ts(t-1)),
Linf_K_cor*Linf_sd*K_sd_ts(t-1), Gest_ts(t-1));
      //Growth occurs after mortality
      Ntemp=G*S*N.col(t-1);
      N.col(t)=Ntemp.array()*exp(proc_err.col(t-1).array())+R(t-
1)*init_pL.array();
      /*
      for(int l=0;l<=ulb;l++)
      {
        N(l,t)+=R(t-1)*init_pL(l); //add in recruitment.  Need to use
previous t because R has one fewer t than N
      } // end l loop
      */
```

```
      if(debug__>2){
        std::cout << t <<std::endl;
        std::cout << "R("<< t-1<< "):"<<R(t-1) <<std::endl;
        std::cout <<"proc_error("<<t-1<<"):"<<std::endl;
        for(int b=0; b<nb; b++){
          std::cout << proc_err(b,t-1) <<"\t";
        }
        std::cout <<std::endl;
        std::cout <<"Growth and mortality("<<t<<"):"<<std::endl;
        for(int b=0; b<nb; b++){
          std::cout <<Ntemp(b)<<"\t";
        }
        std::cout << "\n";
        std::cout <<"N("<<t<<"):\n"<<std::endl;
        for(int b=0; b<nb;b++){
          std::cout << N(b,t)<<"\t";
        }
        std::cout << "\n";
      }
   }  //end t loop

   //Calculate catch-at-length and total catch
   matrix<Type> C=(F.array()/Z.array())*(Type(1.0)-exp(-
Z.array()))*N.array();
   vector<Type> TC(nh);
   for(int t=0; t<nh; t++){
     t2 = Harvest_t(t);
     TC(t) = C.col(t2).sum();
   }

   //Calculate catchability of second indices of abundance
   Type q;
   q = calculate_catchability_indices(obs2_I,obs2_p_I,N,ssel,
                                      obs2_t,nb,nt,debug__);

   if(debug__>0){
     std::cout <<"q="<<q<<"\n";
   }

   //Calculate indices of abundance - index 1
   matrix<Type> I(nb,nt);    //Index of abundance at length
   I.fill(0.0); //fill with zeros
   I = calculate_predicted_indices(Type(1.0),N,ssel,nb,nt);
   vector<Type> TI=I.colwise().sum();
   //Calculate indices of abundance - index 2
   matrix<Type> I2(nb,nt);
   I2.fill(0.0); //fill with zeros
   I2 = calculate_predicted_indices(q,N,ssel,nb,nt);
   vector<Type> TI2=I2.colwise().sum();

  // 6. Calculate likelihood
  //Total catch
  Type TC_nll;
  Type sig_C;
```

```
  sig_C=in_C_sd*exp(nu_C);
  Type var_C=square(sig_C);
  vector<Type> obs_C=Harvest;//C3: Total catch by timestep

  TC_nll=-sum(dnorm(log(obs_C),log(TC)-0.5*var_C,sig_C,true)); //true
means give the log density
  REPORT(obs_C);
  REPORT(TC);

  if(debug__>0){
    //std::cout <<"obs_C="<<obc_C<<"\n";
    std::cout <<"TC=[";
    for(int i_=0;i_<TC.size();i_++)
      std::cout <<obs_C(i_)<<"~"<< TC(i_)<<" ";
    std::cout <<"]\n";
    std::cout <<"TC_nll="<<TC_nll<<"\n";
  }

  //Total index objective
  //Total index of abundance - index 1
  Type TI_nll;
  TI_nll = calculate_objective_total_indices(obs_I,TI,in_I_sd,nu_I,obs_t);
  // index 2;
  Type TI2_nll;
  TI2_nll =
calculate_objective_total_indices(obs2_I,TI2,in_I_sd,nu_I,obs2_t);

  if(debug__>0){
    //std::cout <<"TI="<<TI<<"\n";
    std::cout <<"TI=[";
    for(int i_=0;i_<obs_t.size();i_++)
      std::cout <<obs_I(i_)<<"~"<<TI(obs_t(i_))<<" ";
    std::cout <<"]\n";

    std::cout <<"TI_nll="<<TI_nll<<"\n";
    //std::cout <<"TI2="<<TI2<<"\n";
    std::cout <<"TI2=[";
    for(int i_=0;i_<obs2_t.size();i_++)
      std::cout <<obs2_I(i_)<<"~"<<TI2(obs2_t(i_))<<" ";
    std::cout <<"]\n";

    std::cout <<"TI2_nll="<<TI2_nll<<"\n";
  }


  //Calculate proportions at length for catch
  matrix<Type> p_C(nb,nh); //estimated proportions at length in the catch
  //C3 matrix<Type> obs_p_C(nb,nt); //observed proportions at length in
the catch

  for(int t=0;t<nh;t++)
  {
    t2 = Harvest_t(t);
```

```
    p_C.col(t)=C.col(t2)/TC(t);  //Calculate estimated proportions at
length in the catch
    //C3 obs_p_C.col(t)=Harvest.col(t)/obs_C(t);  //Calculate observed
proportions at length in the catch
  }

  //Calculate proportions at length for index - index 1
  matrix<Type> p_I(nb,nt); //estimated proportions at length in the index
  //matrix<Type> obs_p_I(nb,nt); //observed proportions at length in the
index

  for(int t=0;t<nt;t++)
  {
    p_I.col(t)=I.col(t)/TI(t);  //calculate estimated proportions at
length in the index
    //obs_p_I.col(t)=Index.col(t)/obs_I(t);  //calculate observed
proportions at length in the index
  }
  // index 2
  matrix<Type> p_I2(nb,nt);
  for(int t=0;t<nt;t++)
  {
    p_I2.col(t)=I2.col(t)/TI2(t);
  }

  REPORT(p_C);
  REPORT(p_I);
  REPORT(p_I2);
  //REPORT(obs_p_C);
  //REPORT(obs_p_I);

  //Likelihood for proportions at length for catch

  //Likelihood for proportions at length for index - index 1
  vector<Type> nll_I_lcomp(nt);
  nll_I_lcomp.setZero();

  nll_I_lcomp = calculate_objective_prop_length_indices(
    obs_p_I, p_I, in_effN_I,nb,nt, obs_t, debug__
  );
  // index 2
  vector<Type> nll_I2_lcomp(nt);
  nll_I2_lcomp.setZero();

  nll_I2_lcomp = calculate_objective_prop_length_indices(
    obs2_p_I, p_I2, in_effN_I, nb,nt,obs2_t, debug__
  );

  //Process error likelihood
  Type nll_proc_err;
  Type proc_err_sd=exp(log_proc_err_sd);
  nll_proc_err=Type(0.0);
  //v2.setZero();
  vector<Type> v1(nb);
```

```
for(int t=0;t<nt-1;t++)
{
  v1=proc_err.col(t);
  nll_proc_err+=-sum(dnorm(v1,Type(0.0),proc_err_sd,true));
}
//REPORT(obs_I);
Type sig_I;
sig_I=in_I_sd*exp(nu_I);
Type var_I=square(sig_I);
REPORT(TI);
REPORT(TI2);
REPORT(var_I);
REPORT(sig_I);
REPORT(TI_nll);
REPORT(TI2_nll);
REPORT(nll_I_lcomp);
REPORT(nll_I2_lcomp);
//C3: REPORT(nll_C_lcomp);
REPORT(proc_err);
REPORT(proc_err_sd);
REPORT(tan_Linf_K_cor);
//Index length composition


//Total negative log likelihood
//----------




REPORT(in_C_sd); //input log-scale sd of catch
//C3: REPORT(in_effN_C); //input effective sample size of catch
REPORT(in_I_sd); //input log-scale sd of index
REPORT(in_effN_I); //input effective sample size of index


// Any parameters in a call to REPORT() will show point estimates in R

REPORT(log_Linf);
REPORT(log_kp);
REPORT(Linf);
REPORT(K);
REPORT(L0);
REPORT(L0_sd);
REPORT(Linf_var);
REPORT(K_sd);
REPORT(Linf_K_cor);
REPORT(binmids);
REPORT(mean_g);
//REPORT(L_SD);
REPORT(nb);
REPORT(G);
REPORT(N);
REPORT(fsel_params);
REPORT(fsel);
```

```
  REPORT(F);
  REPORT(f);
  REPORT(Z);
  REPORT(init_pL);
  REPORT(R);
  REPORT(C);
  vector<Type> TN=N.colwise().sum();
  vector<Type> logTN=log(TN);
  //DL edits start
  //REPORT(TN);
  REPORT(N);
  //DL edits stop

  REPORT(I);
  REPORT(I2);
  REPORT(ssel);
  REPORT(ssel_params);
  REPORT(sig_C);
  REPORT(nu_C);
  REPORT(nu_I);
  REPORT(phi_C);
  REPORT(phi_I);
  REPORT(TC_nll);
  //Type q=exp(log_q);
  REPORT(q);
  //REPORT(log_q);


  Type nll = 0.0;  //Don't run the optimization version of the model- just
do the calculations

  nll+=TC_nll;
  nll+=TI_nll;
  nll+=TI2_nll;
  //C3: nll+=sum(nll_C_lcomp);
  nll+=sum(nll_I_lcomp);
  nll+=sum(nll_I2_lcomp);
  nll+=nll_proc_err;

  // prior
  nll+= Linf_pen;
  nll+= Linf_cv_pen;
  nll+= kp_pen;
  nll+= kp_cv_pen;


  if(debug__>0){
    //std::cout <<"TC_nll="<<TC_nll<<", TI_nll="<<TI_nll<<",
TI2_nll="<<TI2_nll;
    //std::cout <<",nll_I_lcomp="<<nll_I_lcomp << "
,nll_I2_lcomp="<<nll_I2_lcomp;

    std::cout <<"nll_I_lcomp=[";
    for(int i_=0;i_<nll_I_lcomp.size();i_++)
```

```
      std::cout <<nll_I_lcomp(i_)<<" ";
    std::cout <<"]\n";


    std::cout <<"nll_I2_lcomp=[";
    for(int i_=0;i_<nll_I2_lcomp.size();i_++)
      std::cout <<nll_I2_lcomp(i_)<<" ";
    std::cout <<"]\n";

    std::cout <<",nll_proc_err="<<nll_proc_err<<"\n";
    std::cout <<",nll="<<nll<<"\n";

  }
  //nll = 0.0;  //uncomment for testing
  return nll;
  //return nll; //need this in tmb.  Returns the negative log likelihood
to the R optimization program
}
```