Design and Parameterization of the Chesapeake Bay Atlantis Model: A Spatially Explicit End-to-End Ecosystem Model

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U.S. Department of Commerce
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Executive Summary

This document presents the basic formulations and parameterization for the biology and physics of the Chesapeake Atlantis Model (CAM). Our goal is to develop a robust simulation of the Chesapeake Bay ecosystem that will allow us to explore potential effects of natural and human-induced changes over a range of spatial and temporal scales. The model is designed to explore the ecological and socioeconomic trade-offs of alternative management strategies, and to understand better how the system responds to climate change and habitat loss.

Model extent and design

The CAM domain (8,896 sq. km/3,434 sq. mi.) includes the brackish waters and sediments of the Chesapeake Bay and seven of its largest tributaries: in Virginia, the James, York (including large portions of the Mattaponi and Pamunkey), Rappahannock, and Potomac Rivers; and in Maryland, the Patuxent, Choptank (on the eastern shore of Maryland), and Nanticoke Rivers. The model area is divided into 97 irregular polygons or "boxes," which are aggregated areas defined by salinity, depth, and in the main trunk of the system, by bottom type.

Physical model

CAM includes physical inputs for temperature, salinity, water movement, dissolved inorganic nitrogen, dissolved organic nitrogen, labile and refractory particulate matter, and silica. Water movements are driven by the Navy Coastal Ocean Model (NCOM) Relocatable Model. NCOM has a horizontal resolution of 1/30 degrees, which is roughly 3 km in the CAM domain (http://ecowatch.ncddc.noaa.gov/amseas/). The Hybrid Coordinate Ocean Model (HYCOM) provides boundary conditions, and atmospheric forcing is from the Coupled Ocean-Atmosphere Mesoscale Prediction System (COAMPS). Tidal forcing is included. Because our main goal was to capture the strong seasonal patterns of this shallow estuary, rather than interannual variability, we repeated the oceanographic conditions from 2012 for each year simulated in the CAM.

Nutrient and sediment inputs

Nutrient and sediment loads to the model were derived from the Chesapeake Bay Phase 5.3 Community Watershed Model (http://www.chesapeakebay.net/about/programs/modeling/53/). This model predicts nitrogen, phosphorous, and sediment transport to the Bay system and how these substances respond to changes in watershed management. The model includes non-point nutrient inputs such as atmospheric deposition, fertilizer, and manure. We use two simulations of the Watershed Model, the first being a calibration scenario. The second simulation is a scenario that assumes reduced loads under restrictions associated with a Total Maximum Daily Load (TMDL). The TMDL scenario includes a 25% reduction in nitrogen and 20% reduction in sediment inputs as required under the federal Clean Water Act (http://www.epa.gov/reg3wapd/tmdl/ChesapeakeBay/tmdlexec.html). For our application, the limits associated with the TMDL scenario are assumed to apply to the period from 1991 through 2000.

Biological model

CAM includes 55 functional groups to model biological processes; of these groups, 26 are invertebrates (including the primary producers) and 29 are vertebrates. Most invertebrates are modeled as single biomass pools (mgN/m^3), but two invertebrate groups (blue crab and brief squid) are modeled as linked juvenile and adult biomass pools. All vertebrate groups are divided into 10 age classes, each tracked by abundance and weight-at-age. Weights are measured through both structural and reserve nitrogen, with structural nitrogen representing bones and other hard parts and reserve nitrogen representing muscle, fat, reproductive parts, and other soft tissue. The separation of age classes for vertebrates allows for ontogenetic shifts in the parameterization. CAM uses nitrogen as the currency for nutrient exchange for all groups.

Habitat associations

Habitat types in CAM include both physical and biogenic habitats. We defined four physical habitats: mud; sand (only the portion of sand substrate that can support oyster recruitment); rock (or man-made structures such as artificial reefs, hardened shoreline, etc.); and woody debris. Biogenic habitat types are marsh, submerged aquatic vegetation (SAV), and oyster reef. The proportion of these seven types sums to 1 for each CAM box. Fish and other animal groups were assigned a “dependence” to one or more of the seven habitat types. At least one of those habitats must be available in a CAM box to allow a group to move into that box.

Model application

As an example application of the CAM, we estimated the biological effects of fully achieving the goals of the EPA TMDL requirements for the jurisdictions of the Chesapeake Bay watershed. To accomplish this goal, we by compared base model production to that of a model revised with TMDL-level reductions in nutrient and sediment loads. Nutrient and sediment inputs for the TMDL and base simulations varied and are described earlier under “Nutrient and sediment inputs”; all other aspects of the scenarios were identical. Though the majority of groups (72%) were predicted to have increased production under the TMDL, the changes were generally small. Realized change for most groups was less than 1%. Small differences (1–5 %) were relatively common as well; only four fish groups (alosines, catfish, panfish, and other flatfish) had slightly larger increases (5–6%) in production, and only one group had an increase in production greater than 10% (dinoflagellates, 12%). Similarly, few groups realized moderate or large decreases in productivity in the TMDL simulation compared with the base case.

TMDL with expected temperature increase

Significant effects of climate change are expected for the Chesapeake Bay region during the next 70 years (reviewed by Pyke et al., 2008). Pyke and colleagues report that, though the direction of precipitation trends (and consequent salinity trends) remains unclear, temperature increase is more certain. In addition, an increase of more than 1.5 ºC should be expected for the Chesapeake Bay. Consequently, we modeled TMDL-specified improvements in nitrogen and sediment loads together with the anticipated temperature increase for the system.

When TMDL conditions were modeled along with the anticipated temperature increase, changes in group productivity were more pronounced; the magnitude of both positive and negative changes were relatively large compared with the TMDL simulation; and modeled benefits of the TMDL appear likely to be lost. Positive change no longer dominates when temperature increase effects were modeled along with TMDL effects, and groups with predicted productivity gains were evenly split with losses. Of those groups that benefited with more than a 5% increase in productivity (panfish, Atlantic croaker, weakfish, blue crab, menhaden, alosines, terrapins, catfish, and gizzard shad), only gizzard shad increased more than 15% over the base model. Most productivity increases were very small to moderate (0.2% to 15%). However, all primary producer groups were either negatively impacted by the increase in temperature or remained at extremely low levels of productivity (microphytobenthos) in this scenario. Consequently, the overall effect of the expected temperature increase appears to negate largely the moderate benefits modeled in the TMDL scenario for the Chesapeake Bay.

Discussion

Our work with CAM is driven by a need for more sophisticated modeling approaches to help characterize the efficacy of management actions within the Chesapeake ecosystem, and to predict cumulative effects from a large number of simultaneous stressors in this complex system.

The most pressing management questions for the Chesapeake are nutrient concerns, which resource managers believe to be equal to, or exceed concerns about, fishing pressure. Other critical issues include the potential effects of climate change on the Chesapeake system, and related management questions that concern the effects of: sea level rise; habitat loss (for both marsh and SAV); latitudinal shifts in migratory populations; changes to the timing of migrations; and of the increasing frequency of major storm events. Simultaneously, managers can apply CAM to improve their understanding of the effects of restoration efforts for Oyster populations, changing disease rates for Oysters and Striped bass, and the cumulative effects of rapidly spreading invading populations of blue and flathead catfish—both of which eat most other groups, are long-lived, and can reach sizes in excess of 100 lb (45 kg). All of these issues could be equally important to managers as fishing mortality in this system. The current biogeophysical model documented here is a flexible, valuable tool to provide managers with insights concerning all of these critical issues and the potential trade-offs of alternative management actions.

Acknowledgments

Many decisions about the model were based on individual contributions of a large group of Chesapeake Bay scientists and managers too numerous to list here; thank you, to all. Especially critical input was provided by Donna Marie Bilkovic, Chris Bonzek, Linda Schaffner, Walt Boynton, Michael Kemp, Elizabeth Metheratta, Roberto Llanso, Jodi Dew-Baxter, Denise Brietburg, and Rich Fulford. Cameron Ainsworth, Jason Link, and Robert Gamble provided valuable insights for the creation of the model. The generous time donated, and innovative programming, by Charles Carleton and Scott Cross of the National Centers for Environmental Information made our use of the NCOM model possible.

Bec Gorton was invaluable for modifying the Atlantis code to accommodate the extreme nature of the Chesapeake system. Nutrient and sediment loads were provided by Guido Yactayo, Jing Wu, and Gary Shenk. Initial concentrations of nutrients and chlorophyll a were provided by Mike Mallonee, and much guidance was provided by Mary Ellen Ley. Landings data was provided by Michael T. Lewis (commercial) and Lauren Dolinger-Few (recreational).

This work was funded by the NOAA/NMFS Office of Habitat Conservation and the NMFS Office of Science and Technology through the NOAA Chesapeake Bay Office.

Introduction

Concerns over declining benefits of the Nation's shared aquatic resources have resulted in a variety of recommendations[1] and ultimately, current U.S. policy (National Ocean Council, 2013) to implement ecosystem-based management (EBM) of these various resources. Because EBM defines management strategies for entire systems, the approach accounts for interactions among ecosystem components and sectors, seeks to identify cumulative impacts of multiple sectors, and includes human responses as an integral part of the system (Levin et al., 2009).

Integrating scientific information at a variety of scales to provide decision-makers with information concerning societal trade-offs requires computationally intensive, end-to-end modeling techniques. Of such techniques, Atlantis (Fulton et al., 2003; Fulton et al., 2004a) was identified by the U.N. Food and Agriculture Organization (Plagányi, 2007) as one of the best ecosystem models, particularly for evaluating management strategies. The approach has been a cornerstone in the development of the National Marine Fisheries Service (NOAA/NMFS) Integrated Ecosystem Assessment (IEA) approach for fisheries management (Levin et al., 2009; Levin and Schwing, 2011). Atlantis has been used to advise decision-making for nearly a decade in Australia and has been applied in multiple applications in the U.S. as well (Brand et al., 2007; Horne et al., 2010; Link et al., 2010; Fulton et al. 2011).

Atlantis is a whole-ecosystem model that integrates a wide variety of information, including biophysical (nutrient input and dynamics, physical characteristics and movement of water), and a full suite of biological characteristics (predator–prey interactions, age, growth, reproduction, movement, and mortality) for the full range of groups needed to capture the essential dynamics of the ecosystem. These groups include phytoplankton, zooplankton, macroscopic benthic invertebrates, fishes, reptiles, birds, marine mammals, detritus (labile, refractory, and carrion), and biogenic habitats (in the Chesapeake, these include submerged aquatic vegetation (SAV), oyster reef, and marsh).

The Atlantis approach is a deterministic model that projects differential equations forward in time. It is designed to simulate the ecosystem, with multiple spatially explicit submodels operating simultaneously and interacting to capture ecosystem dynamics. These submodels represent the physical and biogeochemical processes that drive primary production, the subsequent production of higher trophic levels all the way to human harvests, and the human responses to changes in the system. Calculations for all submodel estimates feed back to dynamically modify the input parameters for other submodels. This approach allows Atlantis to predict cumulative changes in the system as well as unforeseen and unintended consequences of policy change that could undermine management decisions (Link et al., 2010) that are also unlikely to be predicted by simpler approaches.

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[1] Christensen et al., 1996; Larkin, 1996; Murawski, 2000; National Research Council, 2002; Garcia et al., 2003; Pikitch et al., 2004; U.S. Ocean Policy Task Force, 2010; and Seagraves and Collins, 2012.

The Chesapeake Bay is the largest estuary in the U.S. with a very large watershed (> 165,760 sq. km/64,000 sq. mi.). The watershed encompasses portions of six states, the entire District of Columbia, and numerous metropolitan areas, the largest of which include Norfolk, Richmond, and Charlottesville, VA; Washington, DC; Harrisburg, PA; Baltimore, MD; and Cooperstown, NY. The nature of the Chesapeake Bay system is extreme in several respects, including size, jurisdictional complexity, human population, shallow depth, seasonal hypoxia, freshwater flushing, complexity of life histories of its flora and fauna, seasonal temperatures, extensive areas of habitat, and high exploitation rates The system bridges multiple jurisdictions and is therefore subject to a complex mix of regulations as well. There is a growing population of more than 17 million people, as well as a relatively large agricultural sector, all of which contribute to exceptionally high nutrient loads to the system. Residence time for nutrients and particulate matter is relatively high (90–180 days (d)) due to high levels of freshwater flow from river inputs and consequent lower-layer counterflow (Kemp et al., 2005). The Chesapeake is extremely shallow with a mean depth of only 6.5 m (Kemp et al., 2005); consequently, benthic dynamics are critical. Turbidity is high enough to limit plant growth, even in relatively shallow areas of the Bay. Deeper areas of the system are subject to seasonal hypoxic and anoxic events. There is a relatively strong freshwater influence, with multiple large river inputs in the system as well as numerous small tributaries (> 100,000 streams, creeks and rivers; www.chesapeakebay.net/faq/category/C44#inline, accessed May 2013).

The Chesapeake Bay is just north of a major biogeographic break (Briggs and Bowen, 2012). As a result, there is seasonal variation in animal populations, with southern populations present during summer and more northerly populations predominating from fall through spring. Most Bay populations migrate out of the system at some point during the year (Murdy et al., 1997); consequently, their populations are subject to mortality outside the system, and the parameterization and simulation of such groups can be problematic. The Chesapeake has some of the most extreme ranges of water temperature for any coastal system, with winter extremes as low as 1 ºC (Murdy et al., 1997). Because of the lack of deepwater refuge from such temperature extremes, the relatively few species that remain throughout the year become mostly inactive or enter torpor during this portion of the year. Marsh, SAV, and oysters all provide habitat important to the functionality of the Chesapeake system. However, over the last three decades, marsh and SAV have been declining steadily due to high nutrient loads, development, shoreline hardening, and coastal inundation associated with climate change. Once, abundant oysters were responsible for large reef tracks that dominated Bay habitat and affected circulation patterns, but oysters are now nearly extirpated from the system. Wilberg et al. (2011) estimates the current population is less than 1% of the original population in Maryland. Humans have a long history of exploitation in the Chesapeake, and the current system is highly modified compared to that of the early 1800's due to heavy oyster harvests by dredging. Harvest rates from both the commercial and recreational sectors remain high for a variety of species including fish, shellfish, and birds.

The Chesapeake Atlantis Model (CAM) is one of the most complex Atlantis models built to date, largely due to the need to capture the essential dynamics of a shallow system characterized by extremes. The first application of Atlantis was in the Port Phillip Bay estuary (Fulton and Smith, 2004; Fulton et al., 2004b; Fulton et al., 2004c), another relatively shallow, eutrophic embayment. However, that application did not have to accommodate many of the extreme features of the Chesapeake Bay. Most recent applications of Atlantis have been to offshore, coral, or shelf systems (Fulton et al., 2011) where the benthic influences that are so important to the Chesapeake have been of minimal importance.

In this document, we present the basic formulations and parameterization for the biology and physics of the Chesapeake Atlantis Model (CAM). Our goal is to develop a robust simulation of the Chesapeake Bay ecosystem that will allow us to explore potential effects of natural and human-induced changes over a range of spatial and temporal scales. We intend to apply the model to explore ecological and socioeconomic trade-offs of alternative management strategies; understand how management scenarios impact the system's response to variations in climate and habitat loss; and identify indicator metrics that are most effective for measuring ecosystem attributes and informing management decisions.

Model Extent and Design

The Chesapeake Atlantis Model (CAM) domain (8,896 sq. km/3,434 sq. mi.) includes the brackish waters and sediments of the Chesapeake Bay and seven of its largest tributaries: in Virginia, the James, York (including large portions of the Mattaponi and Pamunkey), Rappahannock, and Potomac Rivers; and in Maryland, the Patuxent, Choptank (on the eastern shore of Maryland), and Nanticoke Rivers. The brackish extent of the Bay varies throughout the year. Therefore, to define the model domain, we assumed that salinity zones (and subsequently, the model domain) follow those shown in Lippson and Lippson (1997; Appendix A).

The model area is divided into 97 irregular polygons or "boxes" (Figure 1). Boxes are aggregated areas defined by salinity and depth throughout the model, and also by bottom type in the main trunk or "mainstem" of the Bay. A 98th box (number "0") is included as a boundary box. This box is non-dynamic and necessary to allow for the exchange of water nutrients and migratory groups to and from the dynamic model domain, but other processes are not explicitly modeled for this box. The Bay outline and bathymetry were derived from a 10 m x 10 m bathymetry grid that was precise to 0.1 m (see Appendix A for details).

The model roughly characterizes the geography of the Chesapeake Bay, but with a simplified, less sinuous geometry. Each CAM polygon is geo-representative of an equivalent physical volume of the Bay that shares the polygon characteristics in that general locality of the Bay (Table 1). In addition, though many critical boundaries (e.g., the state line between Virginia and Maryland) and specific features are georeferenced, all vertices represented in each polygon are not. Our goal is to capture the essential dynamics of the system while minimizing the number of sides for each polygon. We used this approach because the model must calculate a flux across each "side" of each polygon, for each factor modeled, on every time step. Thus, three-, four-, and five-sided polygons are preferred box shapes because they minimize the computational overhead required for each time step. The resulting map (Figures 1a, 1b) is a simplified, geometric representation of the Bay's geography.

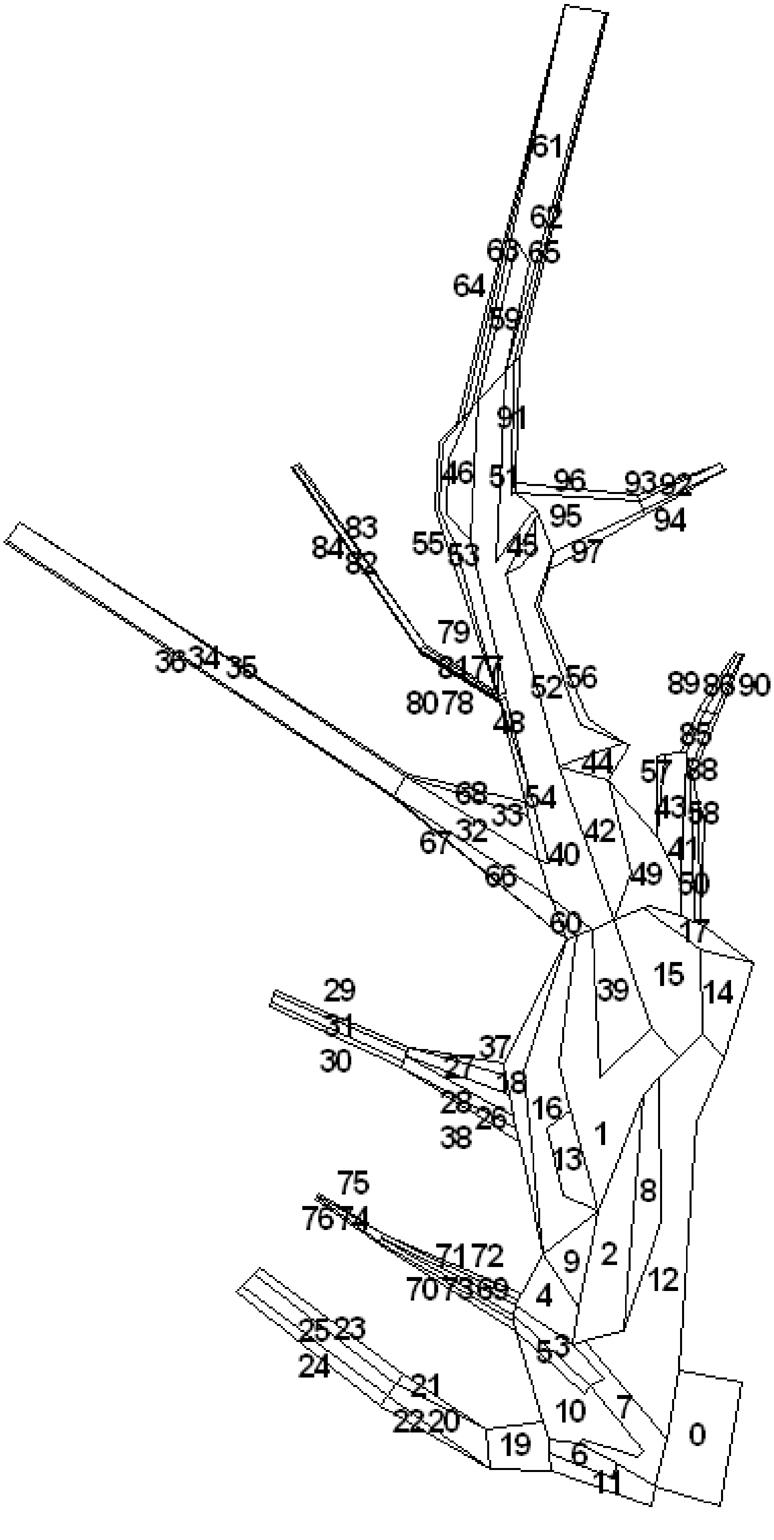

Figure 1a. Spatial structure of CAM. The model consists of 97 irregular polygons determined by salinity, depth, bottom type (mainstem only), and management boundaries.

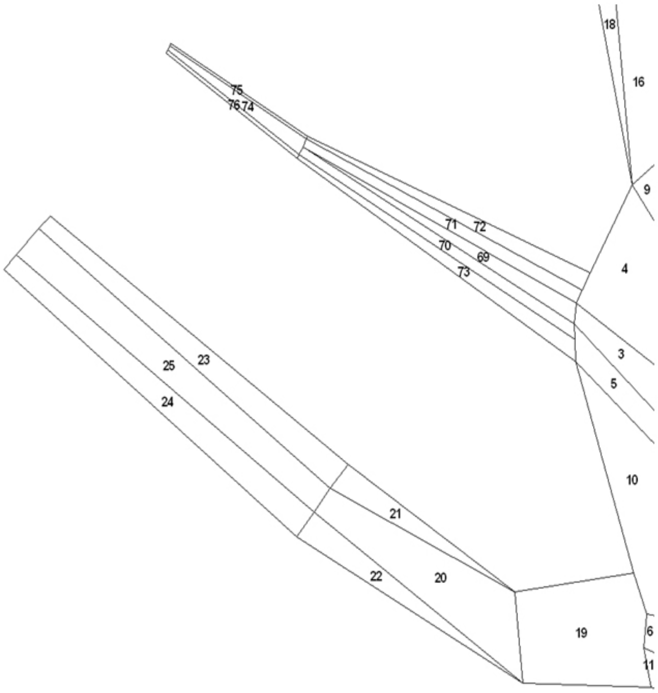

Figure 1b. Detailed river structure of CAM.

Wherever practical, the shallowest boxes were defined to follow two depth contours throughout the model. Areas less than 2 m deep were important to distinguish from deeper waters because these are the areas where SAV can be restored (Batiuk et al., 1992). Due to turbidity, deeper areas are not useful for restoration and will not support SAV growth. Similarly, areas less than 10 m deep were important to separate from deeper areas because this is the historically preferred habitat for oysters in the Chesapeake (U.S. Army Corps of Engineers, 2012).

The vertical design of the model also attempts to capture the most important functions of the system by depth (Figure 2). Throughout CAM, the first vertical layer extends to the first meter of the water column (0–1 m), both because this layer is generally well mixed and because it is characterized by adequate light to support phytoplankton growth (W. Boynton, University of Maryland Center for Environmental Science (UMCES, personal communication).

Below the surface mixed layer, the pycnocline forms an important barrier to vertical water mixing. Seasonal hypoxia occurs below the pycnocline, resulting from normal consumption but greatly augmented by the decomposition of large phytoplankton blooms that grow in the nutrient-rich and well-lit surface mixed layer, only to sink below the pycnocline after the bloom dies out. The dissolved oxygen is depleted below the pycnocline and the strong density gradient prevents mixing and replenishment (Kemp and Boynton, 1992). The resulting hypoxic conditions are an important stressor to Bay animal groups, causing large-scale movements away from these waters for swimmers and die-offs for sedentary groups. Hypoxic waters may also have a short-term benefit for some populations, functioning either as a refuge from predators for groups that have relatively low oxygen demands, or as a "habitat squeeze" that concentrates a predator's prey in the smaller water volume of well-oxygenated water (Costantini et al., 2008). Accordingly, the second vertical layer extends from depths deeper than 1 m to the top of the pycnocline (5 m).

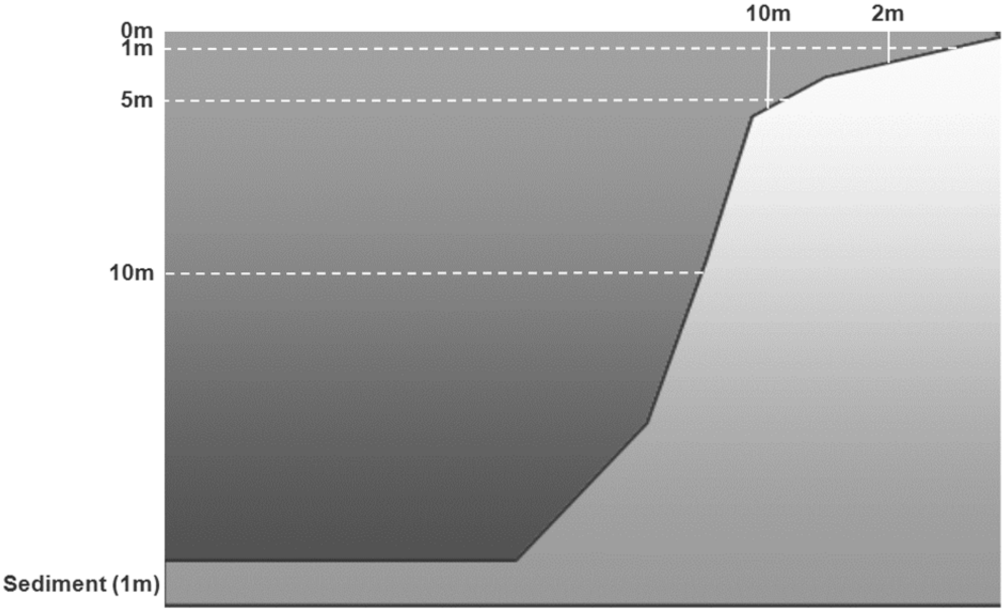

Figure 2. Vertical structure of CAM.

The third vertical layer is the pycnocline itself. In reality, the depth of the pycnocline varies with depth of the water column. CAM, however, assumes a common depth of the pycnocline throughout the model (> 5 m –10 m), a simplifying compromise between the deep mainstem and relatively shallow tributaries. The fourth vertical layer consists of depths greater than 10 m. The fifth vertical layer simulated in CAM represents the first meter of sediment, important to include for groups that bury themselves in the substrate, as well as for benthic bacteria, nutrient cycling, bioturbation, and resuspension of sediments. CAM boxes vary in the number of water column levels present (Table 2), following the depth of the Bay areas represented by those boxes. All boxes include at least two water column layers and the sediment layer.

Projection Years

The Atlantis model was initialized to represent January 1, 2002, and is projected forward for 70 years from these conditions on a 12-hour time step. Biological, physical, and biogeochemical initial conditions were taken from 2002 or recent years for which data were available, as described in the following sections.

Physical Model

The Atlantis hydrographic submodel is based on the physical transport model (Port Phillip Bay Integrated Model, PPBIM) developed by Murray and Parslow (1999) and Walker (1999). Details of modifications and enhancements of the PPBIM developed for Atlantis are found in Link et al. (2011).

CAM includes physical inputs for temperature, salinity, water movement, dissolved inorganic nitrogen (DIN; includes ammonia [NH] and nitrite-nitrate [NO_2 and NO_3 are combined in CBP data, from now on abbreviated "NO"], dissolved organic nitrogen (DON), labile and refractory particulate matter, and silica.

Water Flux, Temperature, and Salinity

In the first version of the model, temperature, salinity, and water movements (or fluxes) are driven by the Navy Coastal Ocean Model (NCOM) Relocatable Model. NCOM has a horizontal resolution of 1/30 degrees, roughly 3 km in the CAM domain (http://ecowatch.ncddc.noaa.gov/amseas/). The Hybrid Coordinate Ocean Model (HYCOM) provides boundary conditions, and atmospheric forcing is from the Coupled Ocean–Atmosphere Mesoscale Prediction System (COAMPS; http://www.nrlmry.navy.mil/coamps-web/web/home). Tidal forcing is included.

This NCOM includes Chesapeake Bay but was not designed specifically for this application or for such a small spatial scale. A more realistic Regional Ocean Modeling System (ROMS) that captures realistic water movements for each time step is currently in development. The NCOM appears to predict very low salinities for much of Chesapeake Bay, except the mouth of the Bay south and east of the York River. Nonetheless, here we use NCOM to force Atlantis temperatures and water flux. Salinities are imported to Atlantis but do not currently drive biological processes in the model.

NCOM output for 2012 was downloaded and re-gridded onto the Atlantis model domain (Charles Carleton, NOAA National Coastal Data Development Center [NCDDC]). In cases where the Atlantis polygons did not overlap with bathymetry (Figure 3), net flux was assumed 0 and temperature and salinity were assumed to be equal to values in an adjacent polygon and similar depth layer. Of the 98 Atlantis polygons, 27 polygons in the upper reaches of tributaries required this extrapolation. To simulate mixing and diffusion, we added small amounts of horizontal and vertical flux to all Atlantis polygons in each time step. Because our main goal was to capture the strong seasonal patterns of this shallow estuary, rather than interannual variability, we repeated the oceanographic conditions from 2012 for each year simulated in CAM.

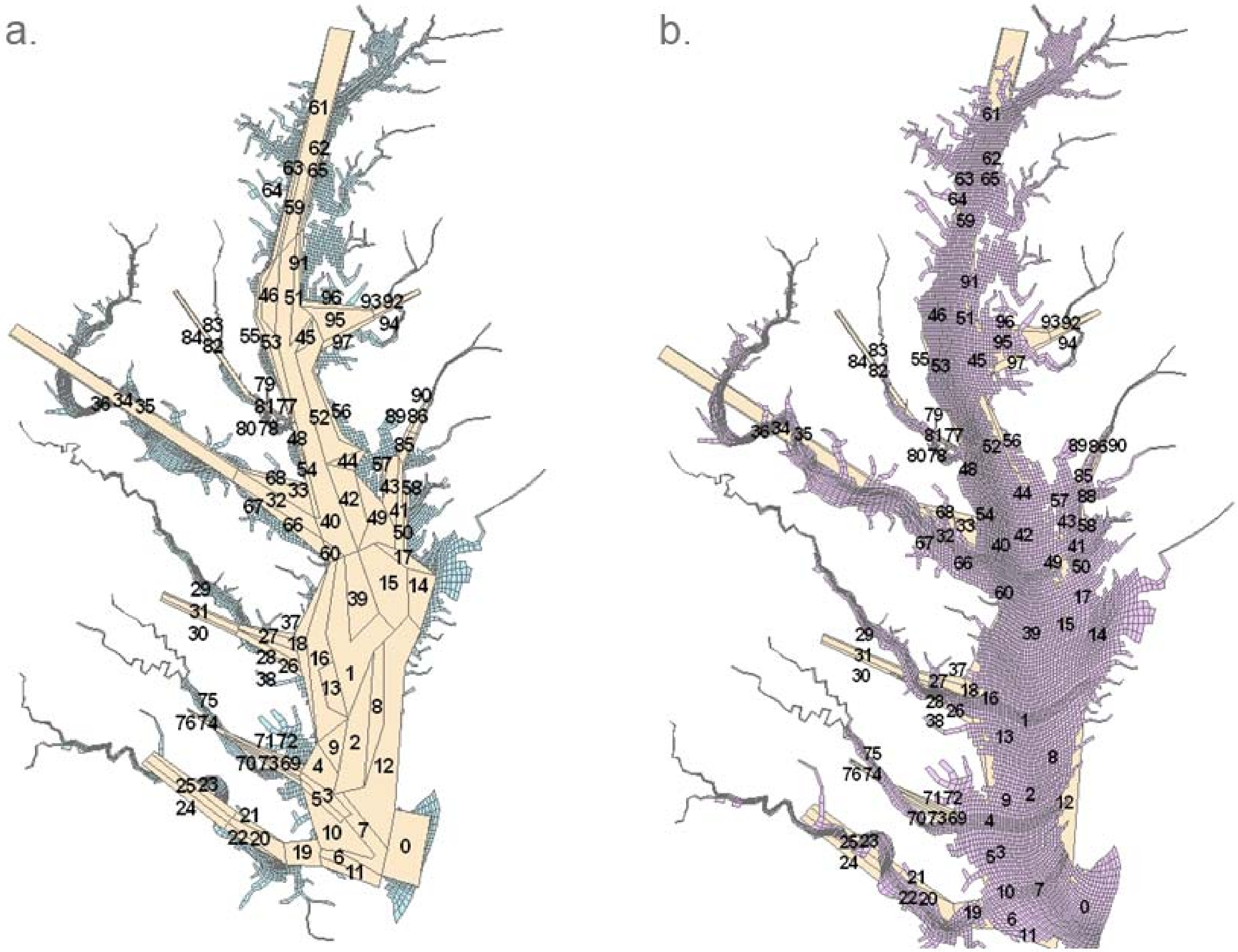

Figure 3. Chesapeake Bay Water Quality Model (fine-scale cells) superimposed on Atlantis model polygons (yellow) (a), and Atlantis model polygons superimposed on Chesapeake Bay Water Quality Model (b).

Nutrient and Sediment Inputs

Initial Concentrations

Initial nutrients and chlorophyll *a* (CHLA) concentrations were from the Chesapeake Bay Program Water Quality Monitoring Database (CBPWQMD; accessed by Mike Mallonee, March 2011). A description of the database, parameter definitions, abbreviations, station descriptions, sampling scheme, collection methodology, detection limits, etc. are detailed in Olson, 2010. The most current version of the document is available at http://www.chesapeakebay.net/documents/3676/wq_data_userguide_10feb12_mod.pdf (accessed August 2013). Note that these data inform the initial conditions of the Atlantis model; after the first day of the model run (January 1 2002) nutrient and chlorophyll concentrations evolve dynamically within Atlantis.

Observations in the Bay Program dataset are segregated according to the Chesapeake Bay 2003 Segmentation (CBSEG) scheme (http://www.chesapeakebay.net/maps/map/chesapeake_bay_2003_segmentation_scheme_codes, accessed August 2013; Figure 4). However, freshwater stations were removed from the dataset. In addition, individual observations recorded with problem codes were removed with guidance from Mary Ellen Ley (U.S Geological Survey, Chesapeake Bay Program [CBP]) and per the "Database Design and Data Dictionary" (U.S. Environmental Protection Agency [EPA], 2004; p. 39). Bay Program observations recorded in the database during December and January from 2000 to 2004 were summarized by Segment using PROC MEANS in SAS/STAT® 9.2[1] (SAS Institute, Cary, NC). It was assumed that mean values from this time period represented initial concentrations for a January 1, 2002, start date for the model (Table 3). Individual areas represented in the CBSEG scheme differ from those of CAM boxes, so we identified which CBSEGs should inform each CAM box (Table 4). If more than one CBSEG informed any particular CAM box, a mean concentration was used to populate that CAM box (by depth). The statistical program R (R Development Core Team, 2011) was used to populate the matrix of CAM boxes by depth for each water quality parameter.

Chlorophyll *a*, dissolved inorganic nitrogen (DIN), dissolved organic nitrogen (DON), and particulate nitrogen observations informed multiple initial inputs for CAM, while silica was used directly. Chlorophyll *a* observations (CHLA; n= 2955) were used to estimate initial concentrations of picophytoplankton (PS), large phytoplankton (PL), and dinoflagellates (DF), based on the findings of Adolf et al. (2006), where PS (cyanobacteria) make up12%, DF make up 13%, and cryptophytes and diatoms (together, the CAM group PL) make up the remaining 76% of CHLA. DIN observations (DIN; n=3023) were used to estimate NH3, NO2, and NO3 concentrations; we assume each nitrogen species makes up 33% of the total DIN. Particulate nitrogen (PN; n= 2567) and DON (n=3016) observations were used to estimate refractory and labile detritus (CAM groups DR and DL, respectively). Although all DON is assumed to be labile, we followed the assumption of the CBP as to the lability of PN; i.e., 30% is labile and 70% is refractory nitrogen (Carl Cerco, U.S. Army Corps of Engineers [ACE], personal communication). Silica observations (SIF; n=2483) were used directly to estimate initial silica concentrations for the model.

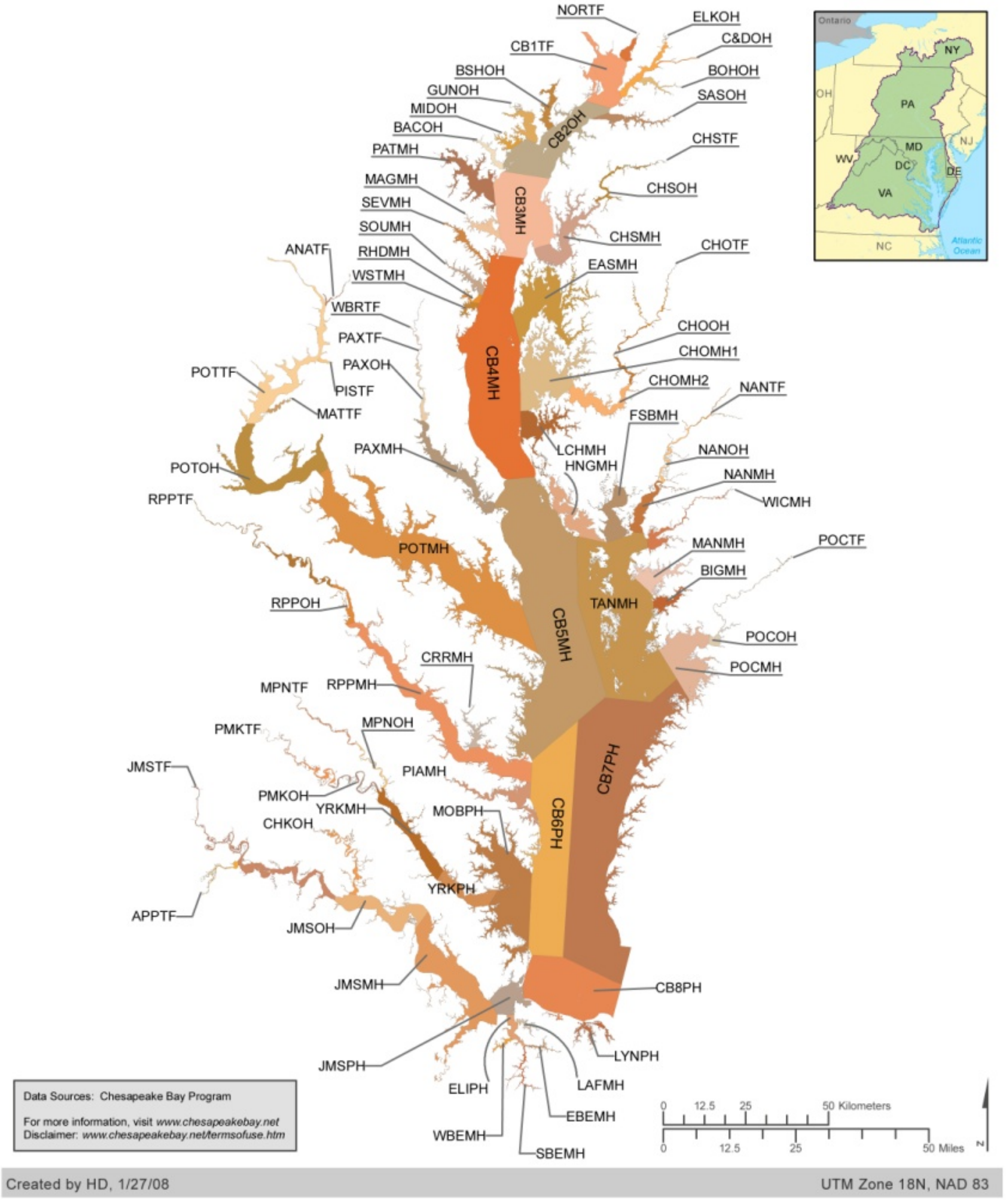

Figure 4. Chesapeake Bay 2003 segmentation scheme (78 segments).

Nutrient and Sediment Loadings

Nutrient and sediment loads that are inputs to Atlantis derive from the Chesapeake Bay Phase 5.3 Community Watershed Model (from now on abbreiviated as "Watershed Model"; U.S. EPA, 2010). This watershed model is an application of a Fortran code base and Hydrologic Simulation Program, which is a deterministic, watershed simulation model (http://water.usgs.gov/software/HSPF/). The model predicts nitrogen, phosphorous, and sediment transport to the Bay system and how these substances respond to changes in watershed management. The model also includes non-point nutrient inputs, such as atmospheric deposition, fertilizer, and manure (U.S. EPA, 2010).

For this application to Atlantis, we use two simulations of the Watershed Model. One is a calibration scenario (1991 to 2000; U.S. EPA, 2010); the other scenario assumes reduced loads under restrictions associated with a Total Maximum Daily Load (TMDL). The TMDL scenario includes a 25% reduction in nitrogen and 20% reduction in sediment inputs required under the Federal Clean Water Act (http://www.epa.gov/reg3wapd/tmdl/ChesapeakeBay/tmdlexec.html). In actuality, the TMDL sets Bay watershed limits of 85 million kg of nitrogen, 5.7 million kg of phosphorus, and 2.9 billion kg of sediment per year. For our application, these limits associated with the TMDL scenario are assumed to apply to the period from 1991 to 2000.

TMDL with expected temperature increase

In addition to the base and TMDL scenarios, we performed a third scenario that simulates TMDL nutrient and sediment loads in the context of expected increased temperature due to climate change. Expected temperature increase is based on Pyke et al. (2008), who projected temperature change for the system based on both downscaled climatic and hydrological forcing factors, and estimated that Chesapeake waters would realize a 1.5 ºC increase in temperature over a 50-year time span. Ding and Elmore (2015) predict an even more extreme increase of 1.2 ºC per decade for the Maryland (northern) portion of the Bay, based on an analysis of 30 years of water surface temperatures from Landsat thermal images. We chose to be relatively conservative in the scenario and applied the 1.5 ºC increase predicted by Pyke et al. (2008) in combination with nutrient and sediment loadings specified in the TMDL. The temperature increase was simulated by adding 1.5 ºC to the physical forcing file outputs of NCOM. No biological parameters were altered for this scenario.

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[1] SAS and all other SAS Institute Inc. product or service names are registered trademarks or trademarks of SAS Institute Inc. in the USA and other countries. ® indicates USA registration.

For both the TMDL scenarios and the calibration scenario, we import NH4, NO23, and total suspended solids from the Watershed Model into Atlantis for both point source and non-point source loads (Figures 5 and 6). Because the start date of the Atlantis model is January 1, 2002, the most recent nutrient loads (from 2000) were used to force all Atlantis projection years, both for the base scenario and for the TMDL scenario.

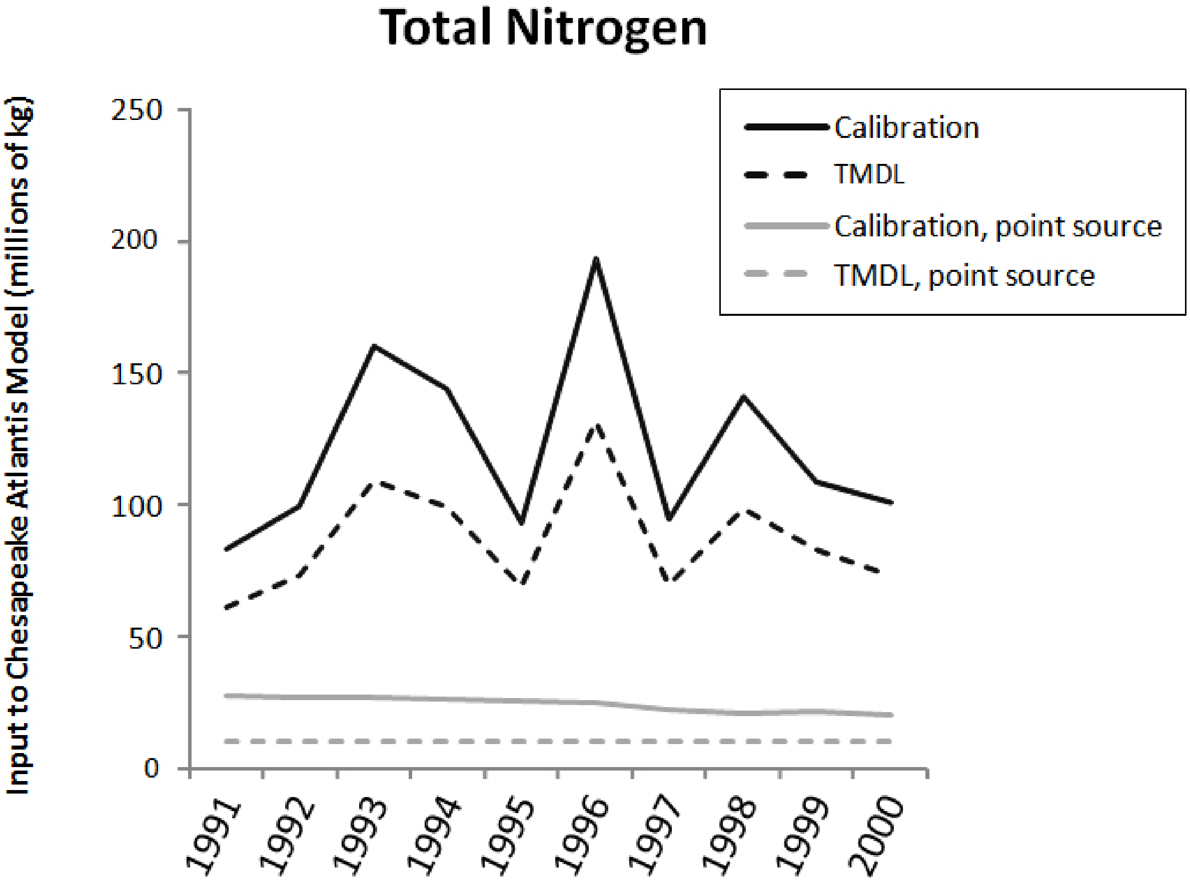

Figure 5. Nitrogen inputs for years 1991–2000, as specified by Chesapeake Bay Phase 5.3 Community Watershed model. For the Atlantis simulations presented here, values from 2000 were applied for all projection years, since Atlantis simulations began January 1, 2002.

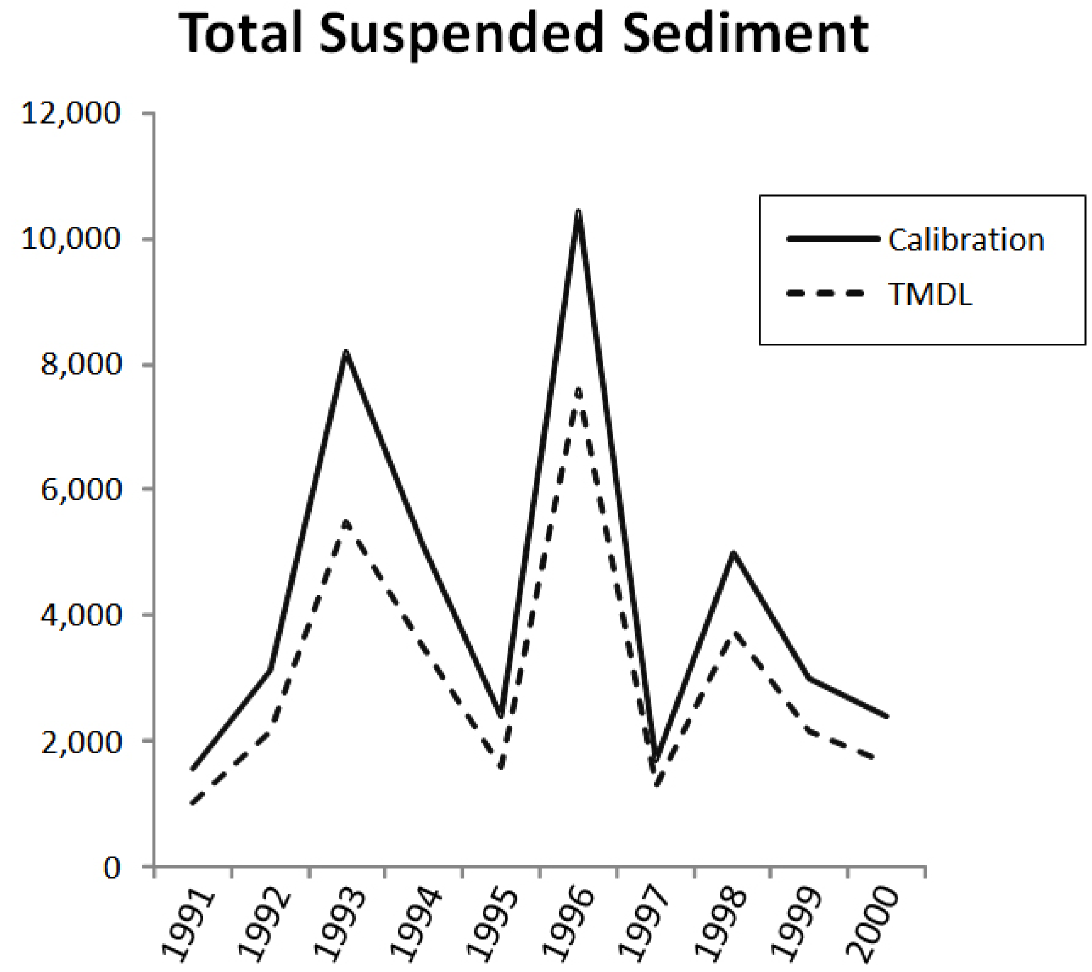

Figure 6. Sediment inputs for years 1991–-2000, as specified by Chesapeake Bay Phase 5.3 Community Watershed model. For the Atlantis simulations presented here, values from 2000 were applied for all projection years, since Atlantis simulations began January 1, 2002.

Loads of nutrients and sediment from the Watershed Model must be assigned to spatial cells (polygons) within the Bay. Through previous efforts at the EPA, output (nutrient and sediment loads) from the Watershed Model had been mapped as spatial inputs into a Bay model, the Chesapeake Bay Water Quality Model (WQM). We identified the overlap of Atlantis cells with the finer-scale WQM cells (Figure 3) and then used this correspondence to assign nutrient and sediment loads to the Atlantis Bay model. Specifically, an overlap analysis in ArcGIS was used to match EPA WQM cells to corresponding Atlantis cells. In instances where EPA cells do not overlap with Atlantis cells, nutrients were assigned to the closest Atlantis cell along the shoreline. The exceptions to this were cases where the simpler Atlantis geography did not capture the sinuosity of main channels of the bay (e.g., upper mainstem of the Chesapeake, Atlantis cell 61, Figure 3). In these cases, WQM were assigned to Atlantis mainstem cells rather than to cells along the shoreline.

Biological Model

CAM includes 55 functional groups to model biological processes; of these groups, 26 are invertebrate and 29 are vertebrate. Invertebrates include the following groups: 2 bacteria (pelagic and sediment); 6 detritus (labile, refractory, and carrion, each with a pelagic and sediment component); 4 algae (including 1 dinoflagellate); 4 zooplankton; 8 invertebrate (including 3 biogenic habitats that provide refuge from predators); and 2 age-structured invertebrate groups. Vertebrate groups include the following: 18 finfish, 4 elasmobranch, 4 bird, 2 reptile, and one mammal. Most invertebrates are modeled as single biomass pools (mgN/m^3), but 2 invertebrate groups (blue crab and brief squid) are modeled as linked juvenile and adult biomass pools. All vertebrate groups are divided into 10 age classes, each tracked by abundance and weight-at-age. Weights are measured through both structural and reserve nitrogen (measured in mg N), with structural nitrogen representing bones and other hard parts and reserve nitrogen representing muscle, fat, reproductive parts, and other soft tissue. The separation of age classes for vertebrates allows for ontogenetic shifts in the parameterization.

The processes modeled by Atlantis are summarized in Appendix B. Additional details on the dynamics of bacteria, detritus, and sediment chemistry, as well as specific parameterizations for dinoflagellates and macrophytes, are found in Fulton et al. (2004a).

Nutrients

CAM uses nitrogen as the currency for nutrient exchange. Initial concentrations and initial loadings of all nutrients for the model are based on EPA data as described earlier for the physical model. Dissolved inorganic nitrogen is composed of both ammonia (NH) and nitrite–nitrate (NO). Concentrations of these two nitrogen pools are governed by uptake by autotrophs, excretion by consumers, and the bacteria-mediated processes of remineralization (of detritus and DON via respiration), nitrification, and denitrification.

Following Fulton (2004a) and Horne et al. (2010), rates of change for NH (Equation 1) and NO (Equation 2) in the water column (*w*) are:

$$\Delta NH_w = -\sum_{i=PX_w} A_{NH_w,i} - A_{NH_w,DF} - A_{NH_w,MB_w} - A_{NH_w,MA} - A_{NH_w,PFB} + \sum_{i=CX_w,BF} E_i + \sum_{i=FX} E_i + \sum_{\substack{i=pelagic\\ bacteria}} E_i - S_{NIT,PAB} + R_{NET_w} \tag{1}$$

$$\Delta NO_w = -\sum_{i=PX_w} A_{NO_w,i} - A_{NO_w,DF} - A_{NO_w,MB_w} - A_{NO_w,MA} + S_{NIT,PAB} \tag{2}$$

where $A_{\mathrm{Nx,XX}}$ is uptake of NH or NO by autotrophs: phytoplankton (i=PX), dinoflagellates (DF), microphytobenthos (MB; i.e., "benthic microalgae"), marsh grass (MA), and pelagic free-living bacteria (PFB). E_{i} is production of NH by consumers: general invertebrates (CX_{w}), benthic suspension feeders (BF includes BFS, BFD, BFF), fish (i = FX), and pelagic bacteria. $S_{\mathrm{NIT,PAB}}$ is the amount of NH converted to NO by pelagic attached bacteria (nitrification). R_{NET} is the amount of NH that remains available for nitrification and denitrification; i.e., the NH produced by denitrification or remineralization of detritus or DON via respiration, minus local production.

Rates of change for NH (Equation 3) and NO (Equation 4) in the sediment (*sed*) are:

$$\Delta NH_{sed} = R_{\mathrm{NET}\ \mathrm{sed}} - S_{\mathrm{NIT}\ \mathrm{sed}} - A_{\mathrm{NH}\ \mathrm{sed,MB}\ \mathrm{sed}} - A_{\mathrm{NH}\ \mathrm{sed,SG}\ \mathrm{sed}} + \sum_{i \neq \mathrm{BF,CX}_{w}} E_{i} \tag{3}$$

$$\Delta NO_{sed} = S_{\mathrm{NIT}\ \mathrm{sed}} - S_{\mathrm{DENIT}\ \mathrm{sed}} - A_{\mathrm{NO}\ \mathrm{sed,MB}\ \mathrm{sed}} - A_{\mathrm{NO}\ \mathrm{sed,SG}\ \mathrm{sed}} \tag{4}$$

with abbreviations as described earlier and where S_{NIT} and S_{DENIT} are nitrification and denitrification, respectively, carried out by sediment bacteria. Unlike other invertebrate consumers, the BF groups do not contribute to the production of NH in the sediments in Equation 3 because they excrete waste directly into the water column.

Primary Production

CAM contains six primary producer groups: seagrass, marsh grass, dinoflagellates, picophytoplankton and large phytoplankton, and microphytobenthos. Estimates of initial biomass (Table 5) and distribution were taken from a variety of sources.

"Seagrass," from now on referred to as "SAV" (Atlantis code SG), represents an aggregate group that includes both saltwater and freshwater species, mainly the genera *Zostera*, *Ruppia*, *Potamogeton*, and "freshwater mixed" as described by Moore et al. (2000). Seasonal SAV biomass was based on Moore et al. (2000) and Cerco and Moore (2001). Current SAV spatial coverage was based on that reported for the most extensive coverage observed in recent years (Orth et al., 1998) and the authors' assumptions of current SAV proportions for each CAM box (Table 6). Table 6 is based on both physical characteristics that were aggregated into each CAM box (Table 1) and expert opinion. Maximum potential spatial coverage is based on Batiuk et al. (1992). An estimate of standing stock for SAV was based on Orth and Moore (1986) and estimated spatial coverage.

"Marsh grass" (MA) is assumed to be composed mainly of two species, *Spartina alterniflora* (saltmarsh cordgrass) and *Spartina cynosuroides* (giant cordgrass). Chesapeake Bay marsh also contains substantial tracts of *Phragmites australis*, an invasive species; however, bay-wide population estimates of *Phragmites spp.* are not currently known and its effects on the role of marsh for the Bay system are still poorly understood. In contrast, there is a wealth of literature available for *Spartina* of the Atlantic coast. Consequently, we have assumed that the characteristics of the two dominant species of *Spartina* are sufficient to represent the marsh group for modeling purposes of this first Atlantis application to the Chesapeake Bay. Future simulations may want to incorporate an aggregate marsh group that includes characteristics of *Phragmites spp.* as well as those of *Spartina spp*. Initial biomass was based on Schubauer and Hopkinson (1984), author assumptions of current marsh proportions for each CAM box (Table 6), and area estimates based on imagery from the National Wetlands Inventory (U.S. Fish and Wildlife Service, 1988 to1995 for Maryland and 1990 to2000 for Virginia). We also used estimates extracted by D. M. Bilkovic, Virginia Institute of Marine Science (VIMS),March 2013 for wetland categories “salt marsh” and “brackish marsh.” To estimate winter biomass, we assumed that perennial *Spartina* marsh had seasonal losses comparable to that reported for SAV (Moore et al., 2000); i.e., approximately 12% of summer biomass survives winter. Standing stock was based on Schubauer and Hopkinson (1984).

Biomass and distribution of dinoflagellates (DF), picophytoplankton (PS), and large phytoplankton (PL) were estimated jointly as described earlier. Estimates were based on CBPWQMD chlorophyll *a* (CHLA) observations made during December and January from 2000 to 2004 and constituent composition estimates published by Adolf et al. (2006) for the Chesapeake Bay. Growth is driven by Michaelis–Menten dynamics and varies with nutrient, light, and space availability.

To estimate current levels of initial biomass of microphytobenthos (MB), we started with a biomass estimate from a balanced Ecopath model. We then distributed that biomass proportionally (by box area) into CAM boxes that contain depths suitable for MB growth (i.e., boxes that contain areas < 8 m in depth (Kemp, personal communication). However, evidence reviewed by Kemp et al. (2005) suggests an inverse relationship between MB production and light availability. In addition, data presented by Rizzo and Wetzel (1985) suggest that MB biomass varies with sediment type. Consequently, we weighted MB biomass estimates according to the expected values (Kemp, personal communication) for each CAM box (Table 7). Specifically, MB biomass estimates were reduced in boxes with deeper water and those boxes were characterized by sediments other than sand (which favors MB growth from January through March [Rizzo and Wetzel, 1985] when the model is initialized). All biomass estimates were then uniformly adjusted to reflect the range of field observations for January through March reported by Rizzo and Wetzel (1985). Though a portion of MB occurs in the model in the water column, most grows in the sediment layer. For simplicity, we assume that all CHLA observed in the water column is phytoplankton, not MB. Accordingly, we initialized the entire biomass of MB in the sediment layer.

Biomass of primary producers is lost to predation, natural mortality, and lysis. The rate of change for primary producers is:

$$\Delta A = G_A - M_{A,lys} - M_{A,lin} - M_{A,quad} - \sum_{j=1}^{n} M_{A,\mathrm{Pr}ed_j} \tag{5}$$

where G_A is growth of autotroph (A), $M_{A,lys}$ is loss of A due to lysis, $M_{A,lin}$ is linear mortality of A, $M_{A,quad}$ is quadratic mortality of A, $M_{A,\mathrm{Pred}i}$ is mortality of A due to predator j, and n is the number of predators of A. Though in most applications Atlantis will model linear mortality as shown in Equation 5, linear mortality is not used for any autotroph in CAM. Marsh has an additional loss term available for the additional physical stress of scour, or bottom stress; similarly, SAV has an additional loss term for the physical stress of excessive nutrients (DIN).

Growth of an autotroph is:

$$G_{AX} = \mu_{AX} \times \delta_{irr} \times \delta_{N} \times \delta_{space} \times A_{abund} X \tag{6}$$

where μ_A is maximum growth rate of autotroph (X); δ_{irr} is light limitation ; δ_{space} is space limitation; δ_N is nutrient limitation (where N = NH and NO for all autotrophs, but also dissolved silicate [Si] for PL and MB); and A_{abund} is abundance of autotroph (X). See Fulton (2004a) for a full description and formulation of the factors limiting growth, as well as nutrient uptake functions for primary producers.

Invertebrates

CAM includes 12 invertebrate faunal groups that are each modeled as biomass pools (Table 8; note that bacteria are not listed in Table 8 because they are estimated inside the model run and not set at the start of the model). Most invertebrates are three-dimensional (3-D) groups; i.e., they occur in multiple depth layers of the model and their units of density are mgN/m^3. However, five of these groups are epibenthic, living only on the sediment surface of the model (2-D) and their units of density are mgN/m^2. Initial densities were based on a variety of available sources as described next.

Initial densities of ctenophores (*Mnemiopsis leidyi*, ZG), sea nettles (*Chrysaora quinquecirrha*, ZL), mesozooplankton (ZM), microzooplankton (ZS), and oysters (*Crassostrea virginica*, BFF) were provided by Richard Fulford (personal communication, U.S. EPA, Gulf Breeze, FL). Zooplankton data originated from the Chesapeake Bay Monitoring Program and were originally compiled at the Academy of Natural Sciences Estuarine Research Center (ANSERC). Oyster data were compiled by C. Cerco for Cerco and Noel (2005) based on data originally collected by R. Mann (VIMS). Densities were provided as monthly bay-wide averages from1991 to 2001. Initial densities for ctenophores, mesozooplankton, and microzooplankton applied to the model were each based on an average of respective December and January values; we assumed this approach best approximated the densities of each group that was available for a January 1 start of CAM. Only an annual average density was available for sea nettles. Consequently, we assumed that sea nettle availability on April 1 (Table 9) was reduced from the average annual density while encysted over winter. We further assumed the proportion of biomass present in mid-winter was similar to that observed for ctenophores (i.e., 0.36 * annual density). Oyster data were provided as average densities per CBSEG.

Individual areas represented in the CBSEG scheme differ from those of CAM boxes. Therefore, a procedure similar to that described previously to estimate initial concentrations of nutrients per CAM box was applied to determine initial oyster densities in each box. We first identified which CBSEGs should inform each CAM box (Table 4); if more than one CBSEG informed any particular box, a mean concentration was used to populate that box. The statistical program R (R Development Core Team, 2011) was used to populate the vector of CAM boxes for oyster density in the epibenthic layer of each box.

Benthic groups (benthic filter feeders [BFD]; saltwater clams *Macoma spp.* [BFS]; benthic carnivores [BC]; and benthic deposit feeders [BD, composed of both omnivores and detritivores]) are all aggregate groups based on 8 years of data from the Benthic Index of Biological Integrity (B-IBI) of the Chesapeake Bay Program (from 2002 to 2009). Details of the long-term benthic monitoring program can be found at http://www.baybenthos.versar.com/ (accessed November 2013). Initial biomass estimates (ash-free dry weight) for each of these four groups are taken directly from spatially explicit biomass (density) measurements from field collections, expanded specifically to CAM box areas. Expanded biomass of each group was provided by Versar, Inc.[1] The four faunal benthic invertebrate groups were subset from the B-IBI, but the final aggregate groups of CAM were based on the top 90% (abundance and biomass) of the species observed in the B-IBI. This approach excludes a large number of B-IBI species that, though they occur in the system, are rare or inconsistently sampled, contributing little to the survey data and to the benthos of the Bay. Lists of the species that compose each aggregate group are found in Table 10.

Changes in invertebrate biomass are affected by growth, predation, and multiple sources of mortality. The rate of change for invertebrate biomass is given by:

$$\Delta I = G_I - \sum_{j=1}^{n} M_{I,pred_j} - M_{I,lin} - M_{I,quad} - M_{I,F} \tag{7}$$

where G_I is growth of invertebrate consumer (I), $M_{I,pred\,j}$ is mortality of I due to predator j, n is the number of predators of I, $M_{I,lin}$ is linear mortality of I, $M_{I,quad}$ is quadratic mortality of I, and $M_{I,F}$ is fishing mortality on I, and where:

$$G_I = \left(\sum_{i=1}^{n} P_{I,i} \times \varepsilon_{I,i} + \sum_{j=DL,DR} P_{I,j} \times \varepsilon_{I,j} \right) \times \delta_{O_2} \times \delta_{space} \tag{8}$$

where $P_{I,i}$ is predation by I on living prey i, $\varepsilon_{I,i}$ is assimilation efficiency of I feeding on living prey (i), $P_{I,j}$ is predation by I on detrital prey j, $\varepsilon_{I,j}$ is assimilation efficiency of I feeding on detrital prey j, δ_{02} is oxygen limitation, and δ_{space} is space limitation.

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[1] Versar, Inc., Applied Ecosystem Assessment Group, Ecological Science & Application Division, 9200 Rumsey Road, Columbia, MD 21045.

Oxygen and space limitation apply only to benthic invertebrates living on or in the sediment layer. Oxygen limitation is governed by a Michaelis–Menten relationship in which limitation increases with depth. We adopted half saturation constants and the depth of oxygen horizon for this relationship from Fulton et al. (2004a). Similarly, space limitation is driven by Michaelis–Menten dynamics. As the density of an invertebrate group increases beyond a lower threshold, the growth of that group is increasingly inhibited until it reaches a maximum allowed density. Lower thresholds, maximum densities, and half saturation constants for invertebrate space limitation were also adapted from Fulton et al. (2004a).

Vertebrates

CAM represents vertebrate biomass in 29 functional groups: 18 finfish, 4 elasmobranch, 4 bird, 2 reptile, and 1 mammal (Table 11). Each vertebrate group is divided into 10 age classes, with each class representing one-tenth of the overall life span of the group. Estimates for aggregate groups represent summary values weighted by relative abundance of each species in the group in Chesapeake Bay. The initial biomass for most vertebrate groups was ultimately dependent on a preliminary, balanced Ecopath model that was developed to initialize CAM, and values used to parameterize that Ecopath model were specific to the Chesapeake whenever possible. Preliminary biomass estimates used in the Ecopath model were based on a wide variety of sources, including (in descending order of use): landings data (used for all groups except bay anchovy, other flatfish, bird, reptile, and mammal groups); stock assessments (Atlantic menhaden, summer flounder, weakfish, bluefish, Atlantic croaker, reef fish, and spiny dogfish); available literature; unpublished data; and expert opinion (Table 11). Due to a lack of original sources, only bay anchovy and other flatfish were based solely on Ecopath estimates. Ecopath estimates of biomass of birds, reptiles, and mammals differed only slightly from preliminary estimates. Therefore, preliminary estimates were used directly as initial values for these groups.

Parameterization settings for initial age and size structure, reproduction, and mortality are found in Table 12; growth and clearance rates by age class are shown in Tables 13 and 14, respectively. Biological timing (reproduction and migration) are shown in Table 15. References for basic vertebrate life history parameterization are found in Appendix C. We estimated initial abundance at age using instantaneous mortality rates, total abundance, and life span estimates from the literature. Growth of fish and reptiles was assumed to follow von Bertalanffy age–weight relationships, while growth of bird and dolphin groups was assumed to follow Gompertz age–weight curves.

Following Fulton et al. (2004a), abundance (or availability; *a*) of a vertebrate of age group (*i*) in any CAM box is a function of individual movement (*T*), predation ($_{\mathrm{Pred}}$), fishing (*F*) mortality (*M*), and both linear (*lin*) and quadric (*quad*) mortality terms:

$$\Delta V_{i,a} = T_{Im,Vi} - T_{Em,Vi} - \sum_{j=1}^{n} M_{Vi,\mathrm{Pred}_j} - M_{Vi,F} - M_{Vi,lin} - M_{Vi,quad} \tag{9}$$

where $T_{Im,Vi}$ is movement of individuals into a cell, $T_{Em,Vi}$ is movement of individuals out of a cell, $M_{Vi,\mathrm{Pred}j}$ is mortality due to predator j, $M_{Vi,F}$ is mortality due to fishing, $M_{Vi,lin}$ is linear mortality, and $M_{Vi,Quad}$ is quadratic mortality. The base CAM model documented here is limited to biogeophysical dynamics and does not include fishing. Moreover, linear mortality is set at 0 for all vertebrates in this model. Consequently, vertebrate abundance (Equation 9) in this application of Atlantis simplifies to:

$$\Delta V_{i,a} = T_{Im,Vi} - T_{Em,Vi} - \sum_{j=1}^{n} M_{Vi,\mathrm{Pred}_j} - M_{Vi,quad} \tag{10}$$

Vertebrate growth follows the same form as for invertebrates (Equation 8), but following Fulton (2004a) and Horne et al. (2010), includes an extra term to allocate growth between structural and reserve nitrogen pools:

$$dV_{i,s} / dt = \Lambda \times G_{Vi} \tag{11}$$

$$dV_{i,r} / dt = (1 - \Lambda) \times G_{Vi} \tag{12}$$

where Λ describes the relationship between structural (s) and reserve (r) nitrogen for each functional group such that:

$$\Lambda = \frac{(1/X_{RS}) + X_{pR,V} \times (-V_{i,r} /(X_{RS} \times V_{i,x}))}{(1/X_{RS}) + (V_{i,r} /(X_{RS} \times V_{i,x}))} \quad \text{if } > 0 \text{ and } G_{V,i} \text{ is} > 0;\ \text{otherwise, } \Lambda = 0 \tag{13}$$

with X_{RS} the maximum ratio of reserve to structural weight V can have, and $X_{pR,V}$ is the relative degree to which V concentrates on replenishing reserves rather than undergoing structural growth when underweight. Spawning and recruitment also affect vertebrate fluxes, and these processes in CAM are described next.

Predation

We implemented the modified version of the Holling Type II predation response designed by Fulton et al. (2003) to model predation (P) by consumers in CAM:

$$P_{ij} = \frac{B_i \times a_{ij} \times B_j \times C_j}{1 + \dfrac{C_j}{g_j}\left(\sum_{i=1}^{n} B_i \times a_{ij} \times E_{ij}\right)} \tag{14}$$

where P_{ij} is ingestion of prey i by predator j (mgN), B_i is biomass of prey i (mgN/m^3), a_{ij} is availability of prey i to predator j (unitless), B_j is biomass of predator j (mgN/m^3), C_j is clearance rate of predator j (m^3/mgN/day; Table 14), g_j is growth rate of predator j (per day; Table 13), and E_{ij} is growth efficiency of predator j eating prey i (unitless; Table 12).

The availability term *a* in Equation 14 is a combined measure of prey preference (i.e., contribution of prey in a predator's diet) and the relative availability of the prey to the predator. This parameter is designed to reflect that not all prey is available to predators at all times. To derive availability parameters, we began by constructing a diet matrix to define the relative contribution of each functional group to each predator's diet where the terms for each predator group in this matrix sum to 1. Atlantis, however, requires availability values for each predator that are not expressed as proportions and that sum to less than 1 (typically, much less). Consequently, we initialized CAM with a diet matrix populated with availability values that were one-tenth of our preliminary proportions (Table 16). Post-calibration values are shown in Table 17.

Diet relationships were based on published literature, FishBase.org, and unpublished data, in order of usage (see Appendix D for details). When parameterizing Atlantis, it is important to establish all possible predator–prey relationships, because if a predator–prey relationship is designated as a 0 in the matrix, the model will not allow the predator to consume that prey. Consequently, in some cases, where no information is available (a common situation for soft-bodied invertebrates, which are seldom recognized in gut content analyses) and a predator–prey relationship is possible, we added a small arbitrary value so the model would allow predators to consume a potential prey when it is available. See Appendix D for more information and for references used to establish the predator–prey matrix.

Following Horne et al. (2010), the availability parameter *a* (Equation 14) is inversely related to the half saturation point of the functional response. The result for model dynamics is that predation is linearly related to prey availability when prey is scarce or availability is low. Higher values of availabilities or higher prey abundance lead to higher consumption rates, but with a nonlinear (asymptotic) relationship between prey abundance and consumption rates per predator. Availability of prey *i* in Equation 14 is further modified if the prey is associated with one of the biogenic habitat types, which provides some degree of protection from predators if that habitat is available. See "Habitat Associations" (later) for further detail.

The maximum growth rate *g* in Equation 14 represents the upper bound for predator growth when food is abundant (Table 13). Further details for estimating maximum growth and maximum ingestion rate of different predator types (i.e., fish, mammals, birds, etc.) are found in Horne et al., 2010.

Spawning and Recruitment

Reproduction modeling follows Horne et al. (2010) and occurs in two distinct phases in CAM. Spawning occurs in a time window that is specified for each functional group (Table 15). The biomass (nitrogen) required for reproduction is removed from the reserve nitrogen pool for each group (including both gonadal and somatic tissue). There is a corresponding decrease in parental weight-at-age. Immediately after spawning, each age class is incremented by one year, and the oldest age class leaves the model domain. In the second phase of reproduction, individuals are recruited to the population at a user-specified time after spawning. The new recruits are assigned to the first age class. The lag time between spawning and recruitment represents larval settlement time for fish, incubation for birds, and gestation for mammals.

Recruitment for fish groups again follows Horne et al. (2010) and assumes Beverton–Holt dynamics with “alpha” and “beta” parameters taken from stock assessments and published literature (Meyers and Barrowman, 1996) but modified for entry in accordance with the input requirements of Atlantis (see Appendix C and Table 12 for further information). We estimated bird, reptile, elasmobranch, and mammal recruitment using a fixed number of offspring produced per adult. Following the methods described by Horne et al. (2010), recruit per adult for birds, reptiles, and elasmobranchs is the product of hatch success, broods per year, and clutch size; for mammals, it is the product of number of calves per female, pregnancy rate, proportion of females in the population, and pregnancy interval.

Habitat Associations

Habitat types in Atlantis include both physical and biogenic habitats. We defined four physical habitats: mud (which includes “silty” and “clayey” sand types; see Appendix A for more information); sand (only the portion of sand substrate that can support oyster recruitment); rock (or man-made structure such as artificial reefs, hardened shoreline, etc.); and woody debris. Biogenic habitat types are marsh, SAV, and oyster reef (see the earlier sections “Primary Production” and “Invertebrates”). The proportion of these seven types sums to 1 for each CAM box (Table 6).

If a group is assigned a “dependence” (i.e., 1 in Table 18) to one or more of the seven habitat types, at least one of those habitats must be available in a CAM box to allow that group to move into that box. Though dependence on habitat associations for two or three of the habitat groups in CAM may be documented for some of the species in the model, quantitative estimates of habitat importance are not available. Consequently, we subjectively assigned quantitative dependence relationships in Table 18 based on our qualitative understanding.

Biogenic habitat confers refuge for an age-structured prey group from its predatory groups by modifying the availability a of prey i to a predator j (following Equation 14):

$$a'_{ij} = a_{ij} * \rho_i \tag{15}$$

where a' is exposure and ρ is refuge status. The degree of refuge afforded to a prey group if biogenic habitat is present is determined by:

$$\rho = Acov * (e^{(-Kcov*Cover+Bcov)} + \frac{1}{kcov}) \quad , \rho \leq 1 \tag{16}$$

where *Acov* is a scalar for the response of the refuge relationship, *Kcov* determines the curvature of the refuge relationship, *Bcov* is the coefficient of the refuge relationship with biogenic habitat (ensures minimal refuge benefit for prey), and *Cover* is the relative portion of biogenic cover available to prey in a box (possible range of *Cover* is 0 to 1; see Table 6 for *Cover* available by box). For the base model of CAM, we assume *Kcov* = 3 and *Bcov* = 0.6 for all juveniles and adults. *Acov*, however, varies to allow a greater (or lesser) influence of refuge for age-structured groups to be more (or less) dependent on habitat in their juvenile or adult stages (Table 19, Figure 7).

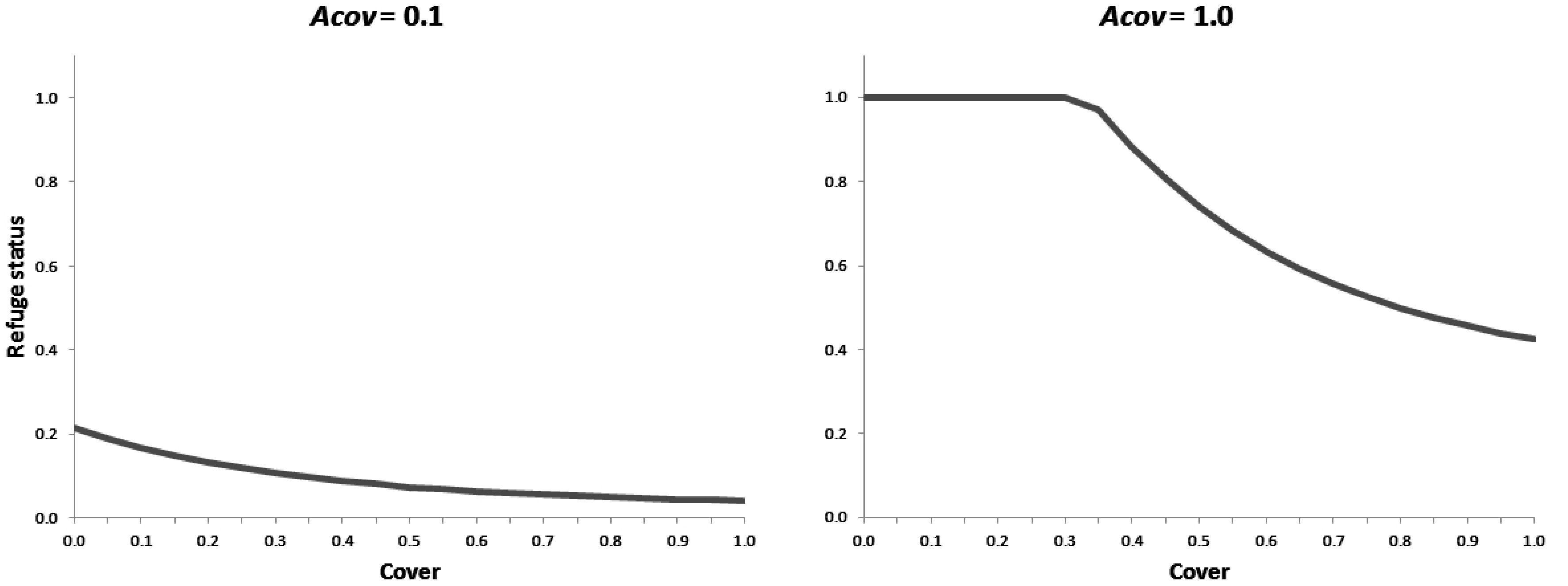

Figure 7. Refuge status (≤ 1) to prey from cover of biogenic habitat group BFF, SG, or MA at differing levels of Acov. Low Acov values are appropriate for groups that benefit little in the presence of biogenic habitat, while high values of Acov (e.g., > 0.5) designate groups that depend on biogenic habitat as refuge from predators.

Model Calibration

Calibration of the CAM largely follows the methods outlined in Horne et al. (2010). To calibrate CAM, we applied an iterative process, adjusting parameters to reproduce more ecologically reasonable dynamics and to fit historical observations. This process typically involved adjusting the most uncertain parameters (growth, clearance, mortality rates, and predator–prey interactions) for each functional group until populations were maintained at recent observed biomass levels. We took a simple approach to the calibration of the base model. We initialized the model with 2002 estimates of biomass and ran the model forward without fishing. Our initial goals in these runs were to keep functional groups from going extinct and to produce steady biomass through time.

The challenges (and solutions) we experienced in calibration were similar to those described by Horne et al. (2010). Extinctions (or population explosions) during calibration often indicated extremely low (or high) productivity of the stock, or inadequate control of density-dependent factors. Following Horne et al. (2010), the primary parameters used to resolve problems in CAM were growth (*g*, see Equation 14) and clearance rates (*C*), and predation pressure (specified by the availability parameter *a*) for all groups. For vertebrates, recruit weight (parameters *KWRR* and *KWSR* for reserve and structural weight, respectively) and assimilation efficiencies (*E*) were modified to tune weight-at-age. Vertebrate numbers at age were tuned with Beverton-Holt recruitment parameters for fish groups (*BHalpha* and *BHbeta*), or constant recruitment numbers for birds, elasmobranchs, reptiles, and mammals (*KDENR*). Numbers were further tuned for all groups using quadratic mortality. As Horne et al. (2010) report, we also found the parameter to be especially useful for tuning top predators and other groups with small levels of predation (e.g., sea nettles, ctenophores). Though Atlantis includes a linear mortality setting for each group as well, we added this only during calibration if it became clear that a source of mortality was not captured by the model. In most cases we expect the explicitly modeled predation and food limitation to restrict population growth.

Model Performance

Initial Calibration: No Fishing

During initial calibration, we aimed to keep vertebrate groups from going extinct and to achieve stable biomass through time (Figures 8a through 8k). In the base model of CAM, true equilibrium behavior is prevented by stochastic shocks from oceanographic forcing and is delayed by the long age span of some vertebrates.

Most groups (both invertebrate and vertebrate) performed well in these simulations, reaching a steady state after only 10 to 15 years (Figures 8a through 8j). Several groups took somewhat longer to stabilize (20 years for oyster, catfish, and reef associated fish; 35 years for sea turtles). Some groups, however, never stabilized (black drum, piscivorous seabirds, and bottlenose dolphin). For the groups that never stabilized, it appears the difficulty is due both to having few (e.g., black drum, piscivorous seabirds) or no (e.g., bottlenose dolphin) predators, and to these groups spending an important portion of their lives outside the system being modeled.

Primary producers were the most difficult groups to calibrate initially, with the various populations either exploding to unreasonable levels or collapsing. Once calibrated, however, their production remained reliable, without being undermined by most calibration adjustments to higher trophic-level groups.

During the initial calibration phase, we also aimed to maintain an age structure that roughly followed an exponential decline in abundance with age as might be expected based on natural mortality rates (Figures 9a through 9e). Most groups again performed well in the base model and demonstrated reasonable age structure at the unfished equilibrium. In several cases (bay anchovy, forage fish, butterfish), we do not see a decline with age because these groups do not live beyond 2 years and only a small portion of their populations age beyond the first age class. Because the current version of Atlantis does not allow age classes to be less than 1 year, in these cases we had to aggregate all biomass (parameters KWRR and KWSR) and numbers of animals into the first two age classes and add high quadratic mortality. The result is that, effectively, all animals die after 2 years in the model. Consequently, the pattern showing large numbers of age class 1 animals and few, if any, animals in age class 2 or older was expected. In other cases (gizzard shad, catfish, spiny dogfish), the very large numbers seen in the progression of the first age class (before the model reaches steady state) obscure the lower (but still sufficient) numbers of animals in the years that follow.

Most vertebrate groups in the base model performed well in simulating weight-at-age (Figures 10a through 10e) after the model “spin-up” (i.e., approximately 15 to 20 years). The primary parameters adjusted to calibrate weight-at-age included maximum growth rates (g, Equation 14), clearance rates (C), and weight of recruits (KWSR and KWRR). We did not force or expect weight-at-age to be constant because Atlantis allows differential growth based on time-varying consumption rates. Some problems with highly migratory groups remain with weights at age by the end of the run greater than five times initial values; this is especially evident in some bird and elasmobranch groups. However, current performance was considered acceptable for the base model run.

Model Application

TMDL Scenario

We estimated the biological effects of fully achieving the goals of the EPA TMDL requirements for the jurisdictions of the Chesapeake Bay watershed by comparing base model production to that of a model modified with TMDL-level reductions in nutrient and sediment loads. Nutrient and sediment inputs for the two simulations are described earlier (see “Initial Loadings” in the “Physical Model” section and Figures 5 and 6). However, all other aspects of the TMDL model were identical to the base model. Though the majority of groups were predicted to have increased production under the TMDL scenario, change for most groups was close to 0 (Table 20): 40 of 52 groups (only one refractory and one labile detrital group are distinguished in this count) had differences of 3% or less compared to the base model, and an additional 10 groups had differences that ranged between 3% and 7% change. Only two groups had relatively large differences between runs; of these, only the increase in dinoflagellates (+12%) appears to be important. In contrast, the relatively large decrease in microphytobenthos between the base and TMDL runs is of little consequence because the biomass of this group predicted for both runs was very small compared to the initial biomass; i.e., the population of microphytobenthos had collapsed in both the base and TMDL runs.

TMDL with expected temperature increase

When TMDL conditions were modeled along with the anticipated temperature increase, both positive and negative changes in group productivity were more pronounced compared to the TMDL simulation, and modeled benefits of the TMDL appear to be lost. Positive change no longer dominates when temperature increase effects were modeled along with TMDL effects, and groups with predicted productivity gains were evenly split with losses. Of those groups that benefited with more than a 5% increase in productivity (panfish, Atlantic croaker, weakfish, blue crab, menhaden, alosines, terrapins, catfish, and gizzard shad), increases ranged from 8% to 57%; only gizzard shad increased more than 15% over the base model. Most productivity increases were very small to moderate (0.2% to 15%). However, all primary producer groups were either negatively impacted by the increase in temperature or remained at extremely low levels of productivity (microphytobenthos) in this scenario. Moreover, the single, relatively large increase of dinoflagellates seen in the TMDL simulation (+12%) was reversed (-41%) when temperature increase was simultaneously accounted for. Consequently, the overall effect of the expected temperature increase appears to largely negate the moderate benefits modeled by the TMDL scenario for the Chesapeake Bay.

Discussion

Our work with CAM is driven by a need for more sophisticated modeling approaches to help characterize the efficacy of management actions within the Chesapeake ecosystem. We also aim to predict cumulative effects from a large number of simultaneous stressors in this complex system. CAM brings together physical, chemical, and biological processes in a 3-D framework that allows for exploration and testing at a variety of spatiotemporal scales. Although no such model will ever perfectly replicate ecosystem processes in nature, we have calibrated CAM under a wide variety of conditions. As a result, we believe the model produces an adequate representation of ecosystem dynamics for the scenarios explored to date.

Upon testing the base model with a simple comparison of its predictions to those of a TMDL scenario, results appeared reasonable. In addition, predicted biological changes were on a comparable scale to results of simpler modeling approaches (H.Townsend, NOAA, unpublished Ecopath with Ecosim (EmE) comparison; S. Newbold, EPA, unpublished production model comparison). Specifically, the various models agreed that most groups would have a small (0 to 3%) increase in production under TMDL conditions, but, the moderately large productivity changes predicted by CAM were not captured by the simpler approaches. Thus, the increased complexity of CAM appears to offer some important benefits in capturing cumulative changes to the system that simpler approaches cannot capture.

Improvement of the physical model driving salt, heat, and water fluxes should facilitate more accurate predictions from the model. The current NCOM model, though fairly well-resolved, was not designed for inshore, estuarine use (as described earlier). We are currently working to incorporate a ROMS-type hydrodynamic model that is specifically designed for the Chesapeake estuary.

Recent work in the Chesapeake has begun to improve our understanding of habitat refuge relationships (oyster reef, H. Townsend and D. Bruce, unpublished data). This work has also called for improved shallow-water sampling within coastal habitats (i.e., monitoring within marsh and SAV habitats; Ihde et al., 2015). Such work could greatly improve the current parameterization of habitat refuge and the accuracy of model predictions.

Further calibration of CAM is planned to follow Horne et al. (2010), where after initial biomass and number at age calibration, the authors further calibrated vertebrate growth and resulting weight-at-age. Subsequently, we also plan to perform secondary and tertiary calibrations as described by Horne et al. (2010), further testing the model under constant fishing pressure and then tuning CAM to historical fishing pressure. We recognize that the development of the fisheries module of CAM is important, and will remain so; however, other management concerns have pushed the growth of CAM to examine stressors other than fishing.

The most pressing management questions for the Chesapeake are not just about fishing pressure. As in Port Phillip Bay, where nutrient concerns for resource managers are on par with or exceed concerns about fishing pressure (Fulton and Smith 2004), resource managers in the Chesapeake are deeply concerned with a wide variety of issues. These issues include eutrophication and the seasonal hypoxic conditions that are closely related to the extreme nutrient loads of this system. Other critical issues include the potential effects of climate change on the Chesapeake system and related management questions. These questions concern the effects of sea level rise, habitat loss (both marsh and SAV), latitudinal shifts in migratory populations, changes to the timing of migrations, and of the increasing frequency of major storm events. Simultaneously, managers could apply CAM to advise them about the effects of restoration efforts for oyster populations, changing disease rates for oysters and striped bass, and the cumulative effects of rapidly spreading invading populations of blue and flathead catfish. Both species eat most other groups, are long-lived, and can reach sizes in excess of 100 pounds (45 kg). All of these issues could potentially be as important to managers as fishing mortality. Moreover, as discussed earlier, we are still able to address simple questions of changing fishing pressure with the current model by carefully applying linear mortality. The current biogeophysical model documented here is a flexible, valuable tool to provide managers with insights concerning all of these critical issues and the potential trade-offs of alternative management actions.

Current and Future Work

CAM is one of a growing number of Atlantis models developed for marine and estuarine ecosystems worldwide (see Fulton et al., 2011, for a recent review). For nearly two decades, Atlantis has been used to understand the dynamics of exploited marine systems; identify cumulative effects of multiple, simultaneous stressors; identify knowledge gaps; and rank the scale of effect of major processes like fishing, eutrophication, and oceanographic effects. The model provides a “flight simulator” to test management strategies before implementing them in the complex reality of an inter-jurisdictional region like the Chesapeake. CAM should assist natural resource managers to make the best informed decisions possible as they work to make Ecosystem-Based Management a reality in the Chesapeake Bay and the mid-Atlantic region.

Figures 8a–10e and Tables

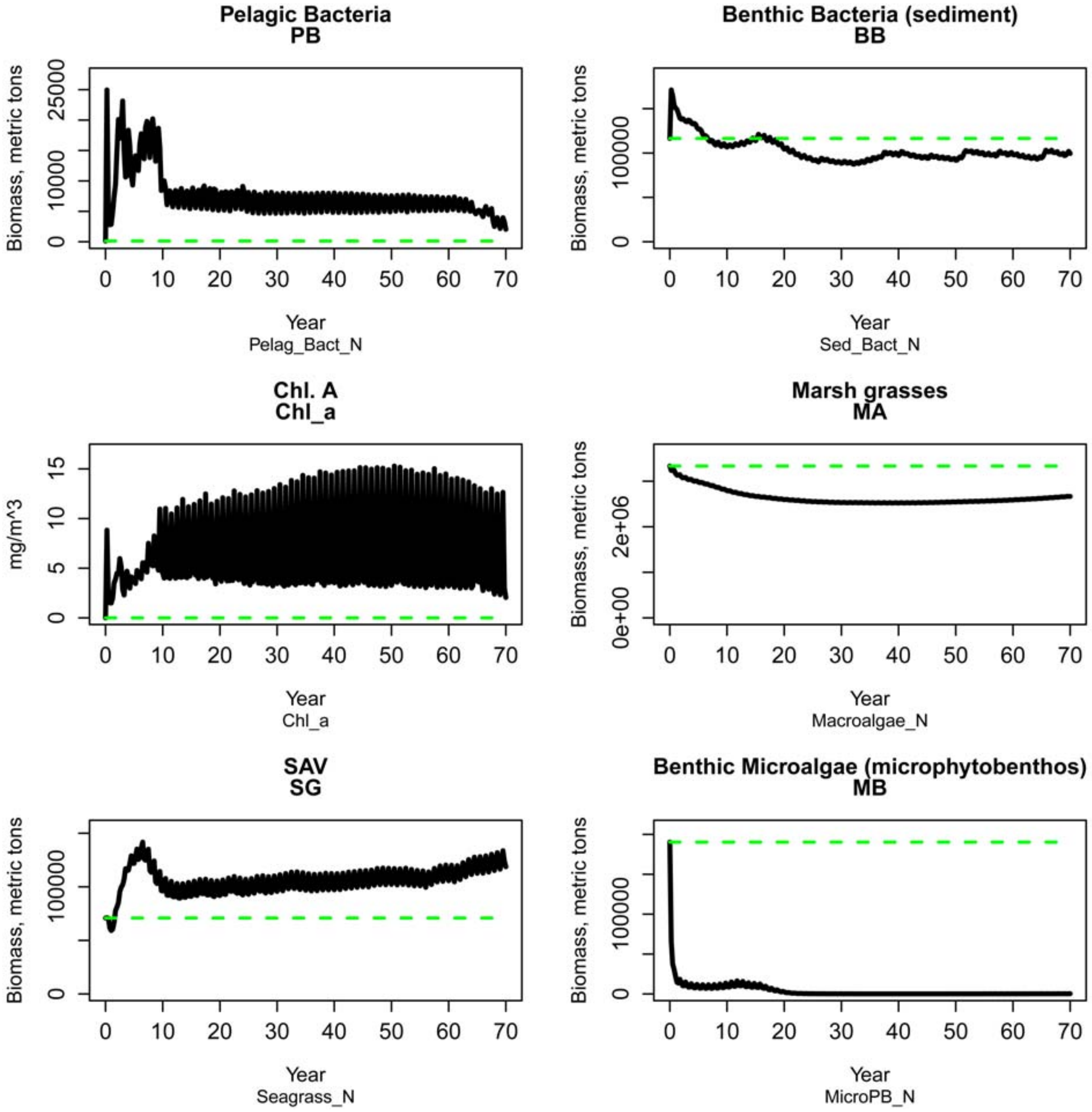

Figure 8a. Biomass results for each functional group after initial tuning phase: bacteria and benthic primary producers. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

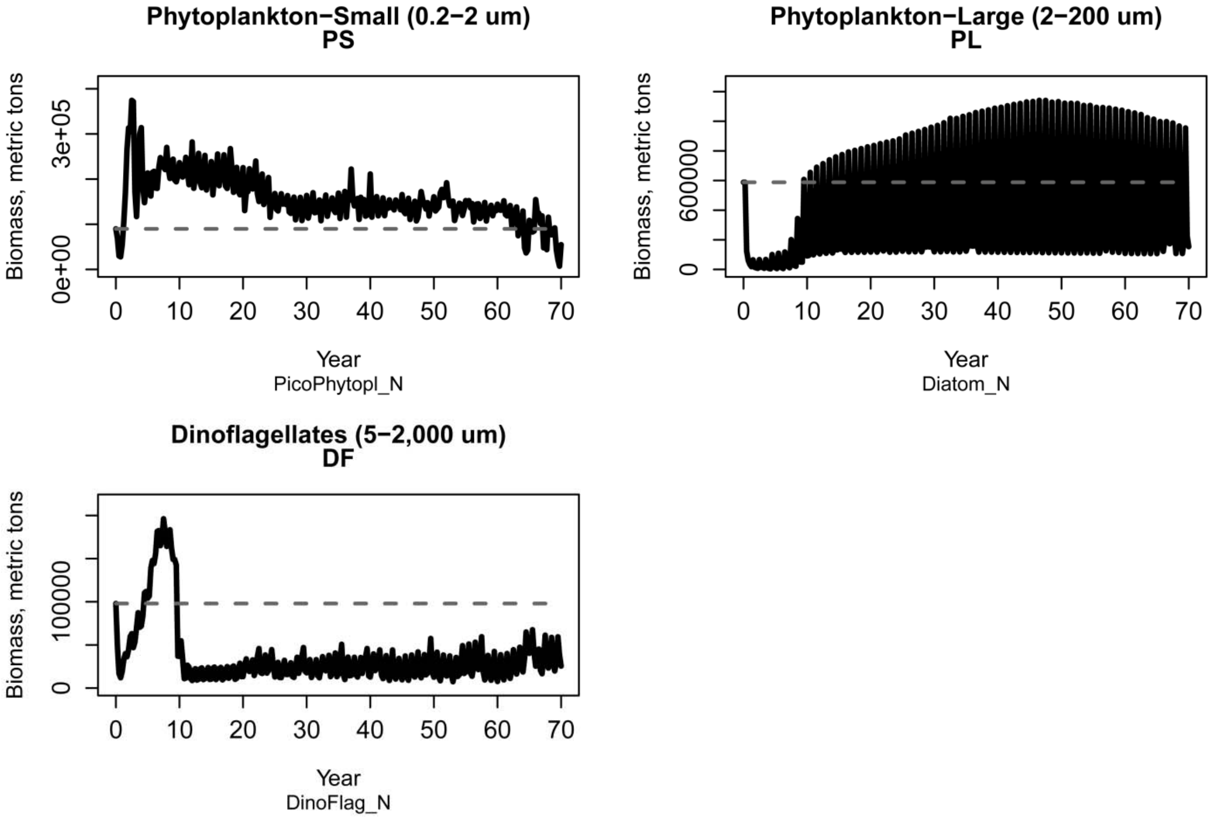

Figure 8b. Biomass results for each functional group after initial tuning phase: planktonic primary producers. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

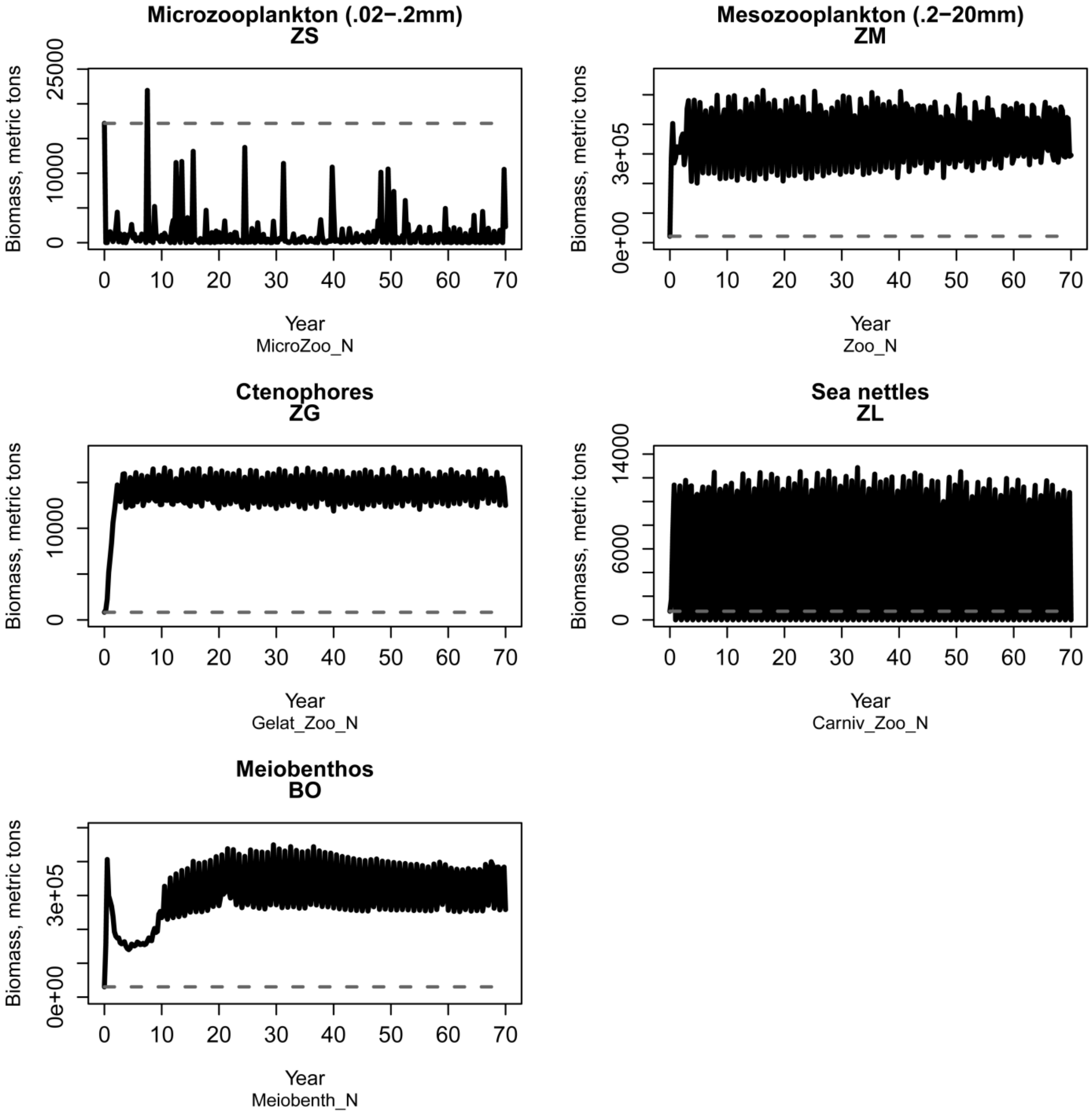

Figure 8c. Biomass results for each functional group after initial tuning phase: zooplankton and meiobenthos. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

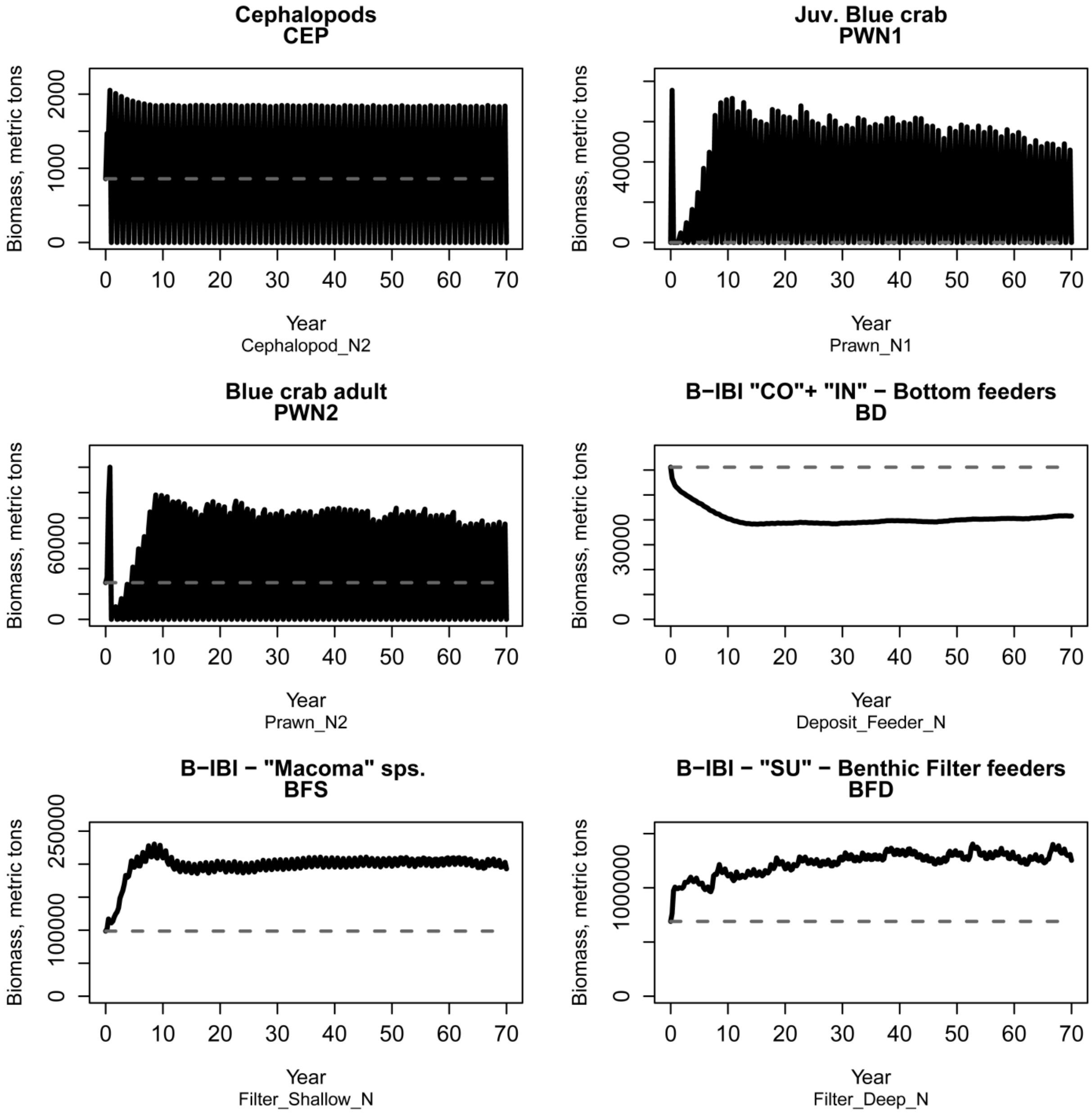

Figure 8d. Biomass results for each functional group after initial tuning phase: brief squid (CEP) and benthic invertebrates (continued on 7e). Dashed line indicates biomass estimate at the start of the simulation. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

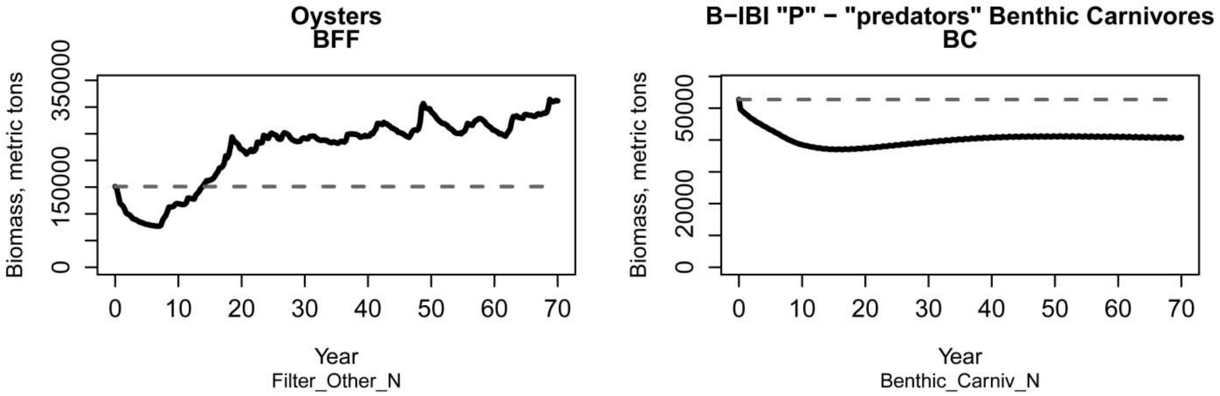

Figure 8e. Biomass results for each functional group after initial tuning phase: benthic invertebrates (continued). Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

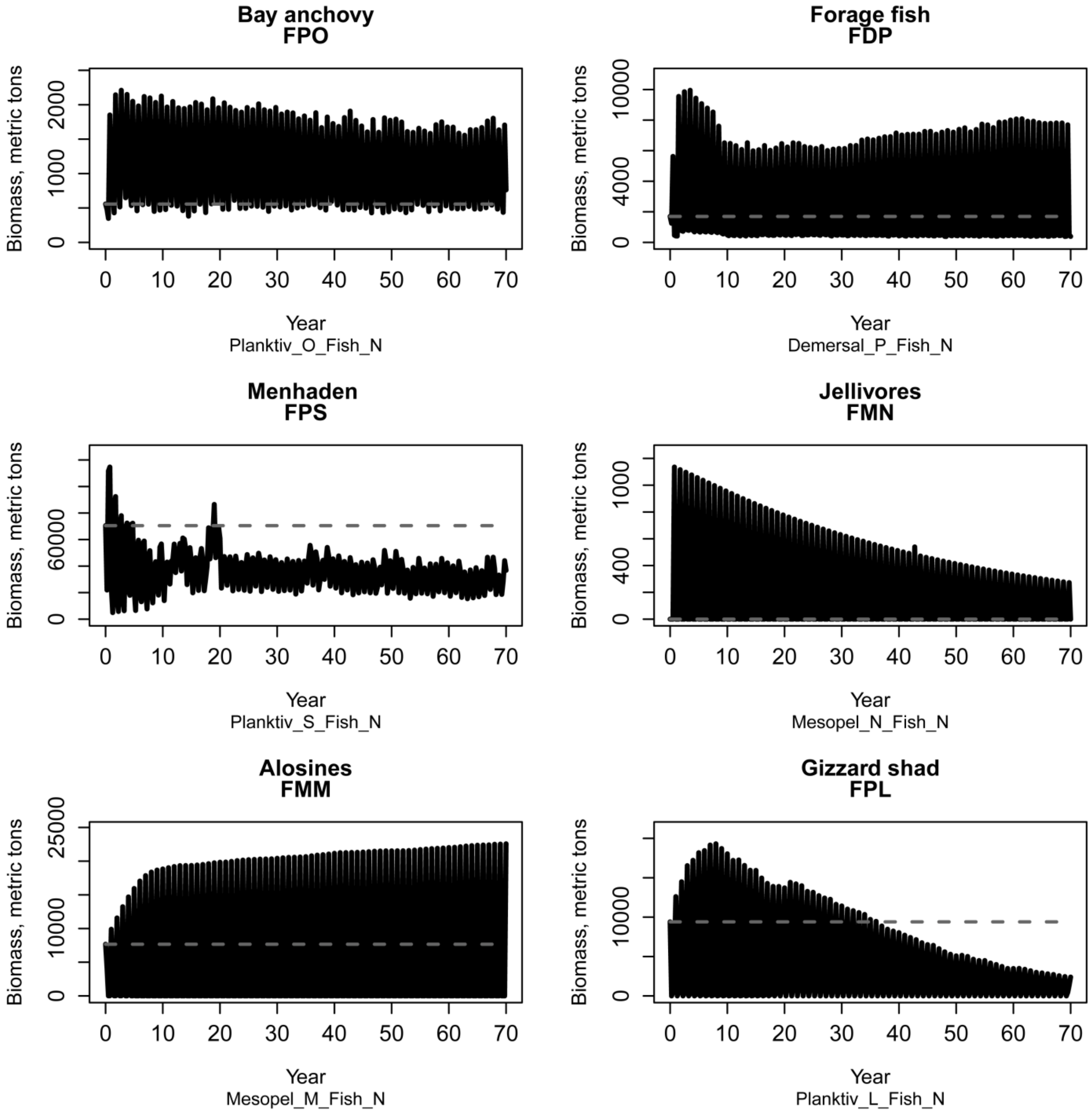

Figure 8f. Biomass results for each functional group after initial tuning phase: small-medium-sized forage fish. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

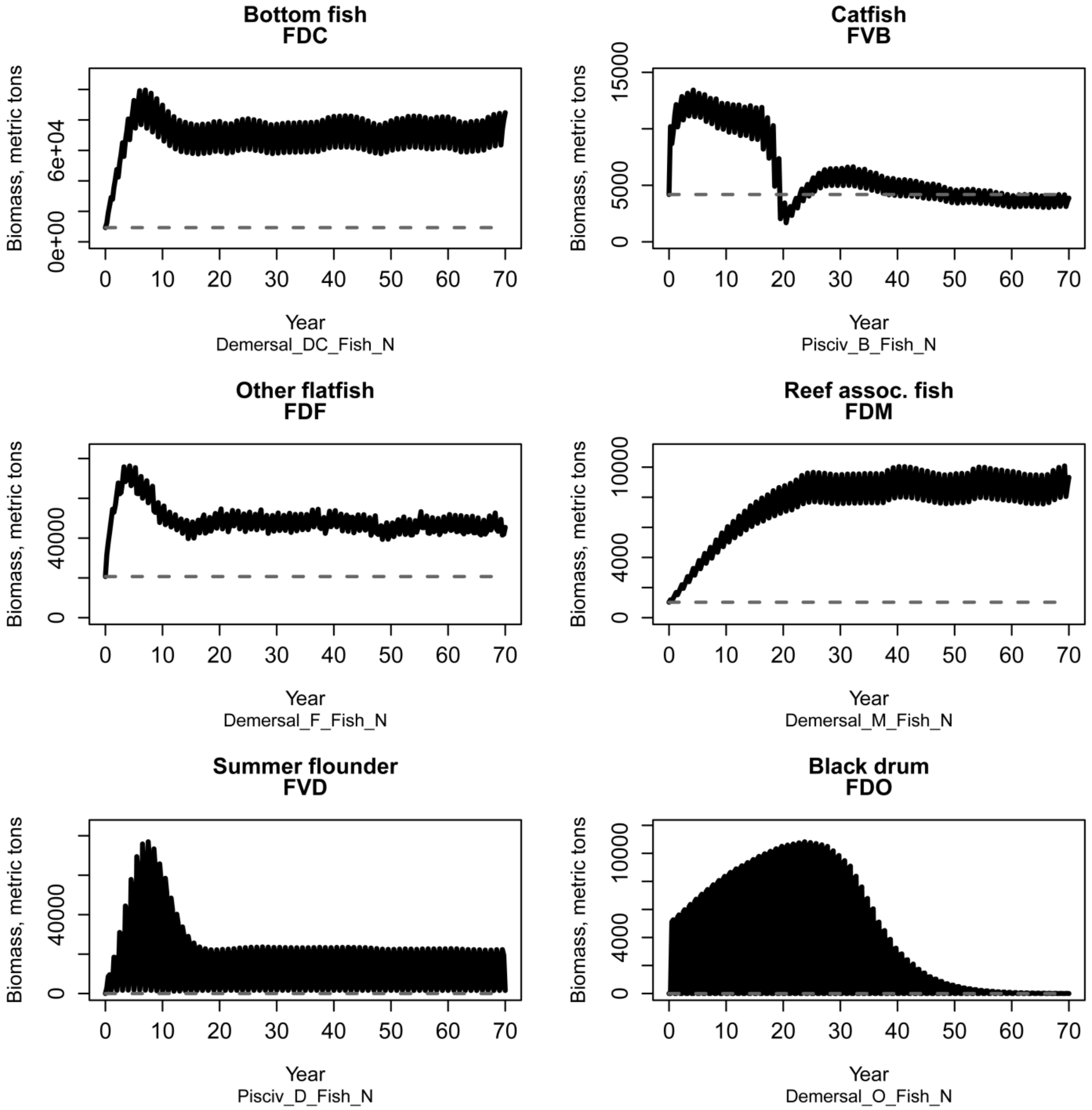

Figure 8g. Biomass results for each functional group after initial tuning phase: benthic finfish groups. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

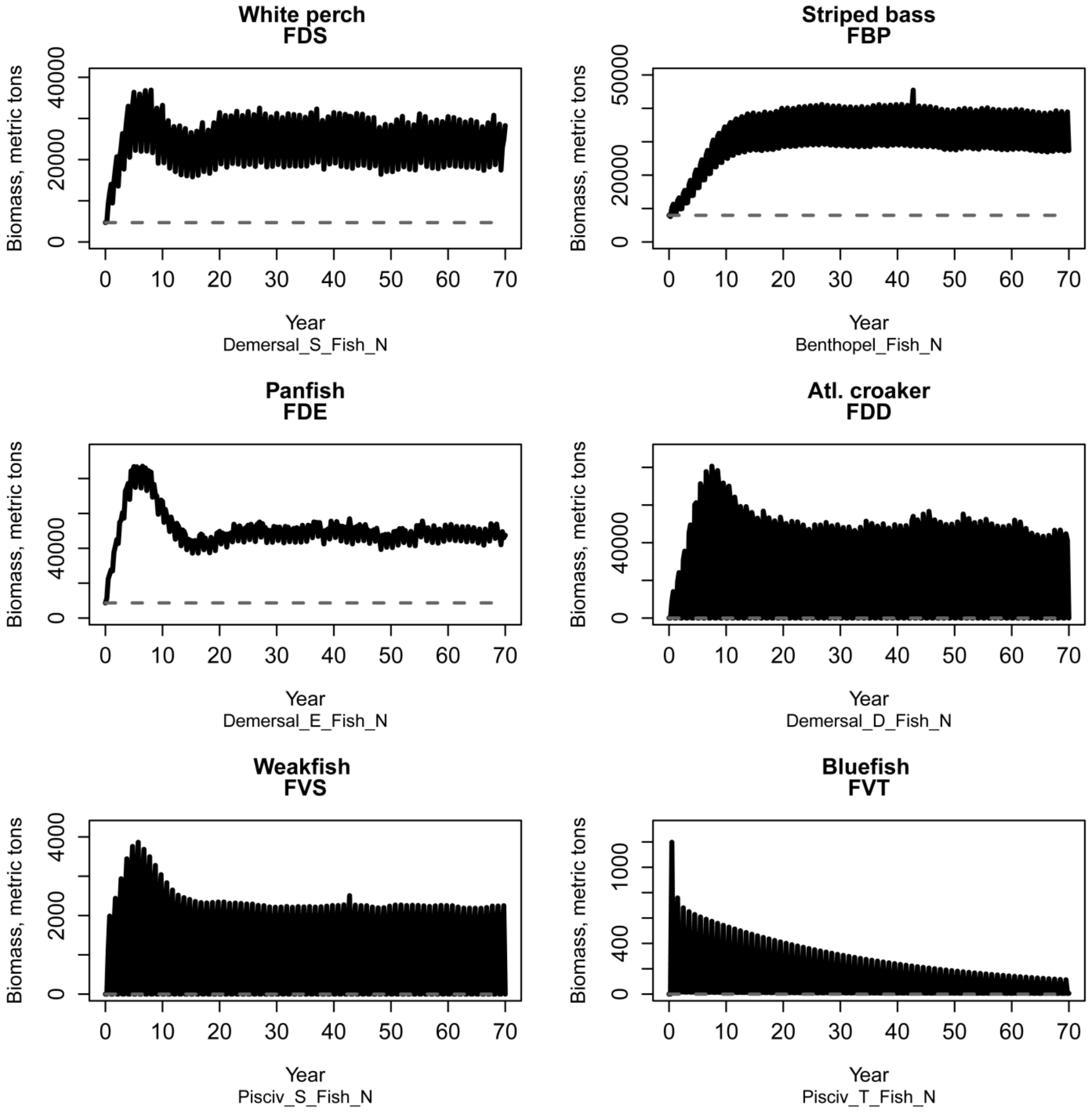

Figure 8h. Biomass results for each functional group after initial tuning phase: mixed finfish groups. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

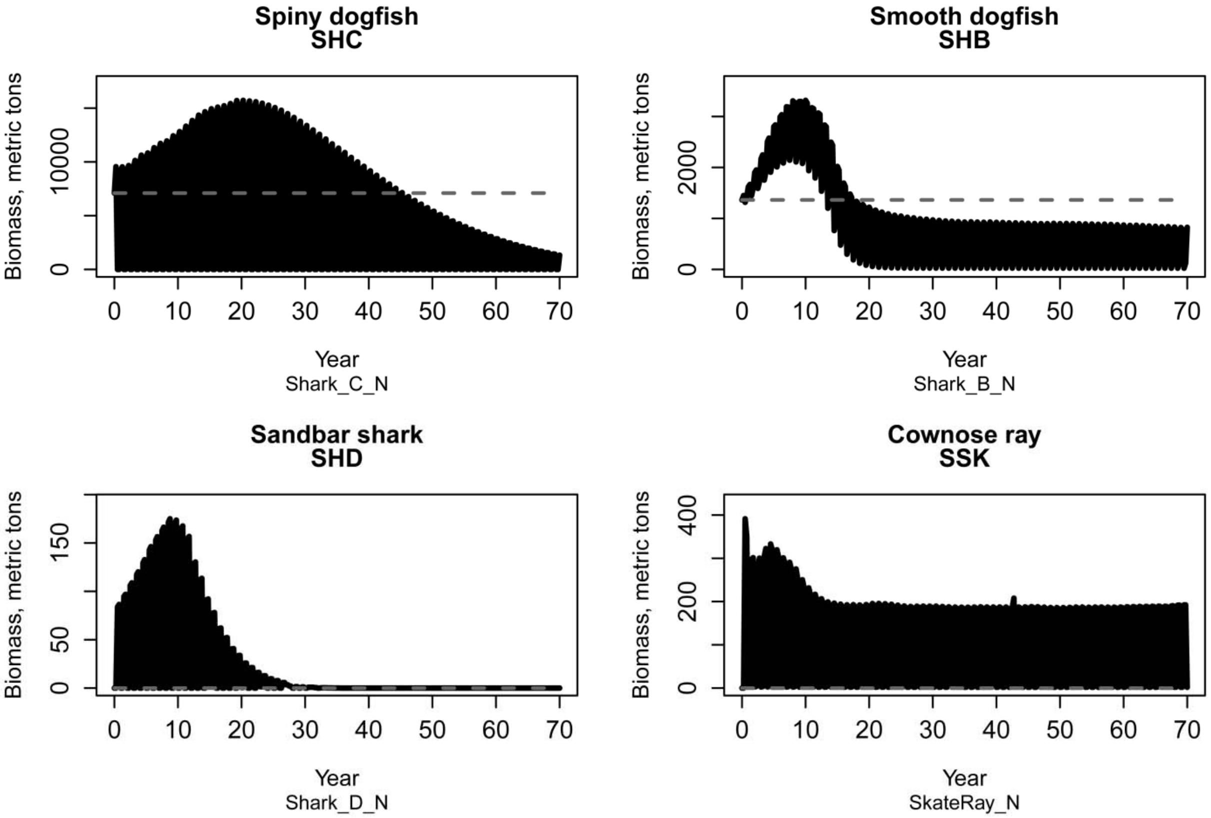

Figure 8i. Biomass results for each functional group after initial tuning phase: elasmobranch groups. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

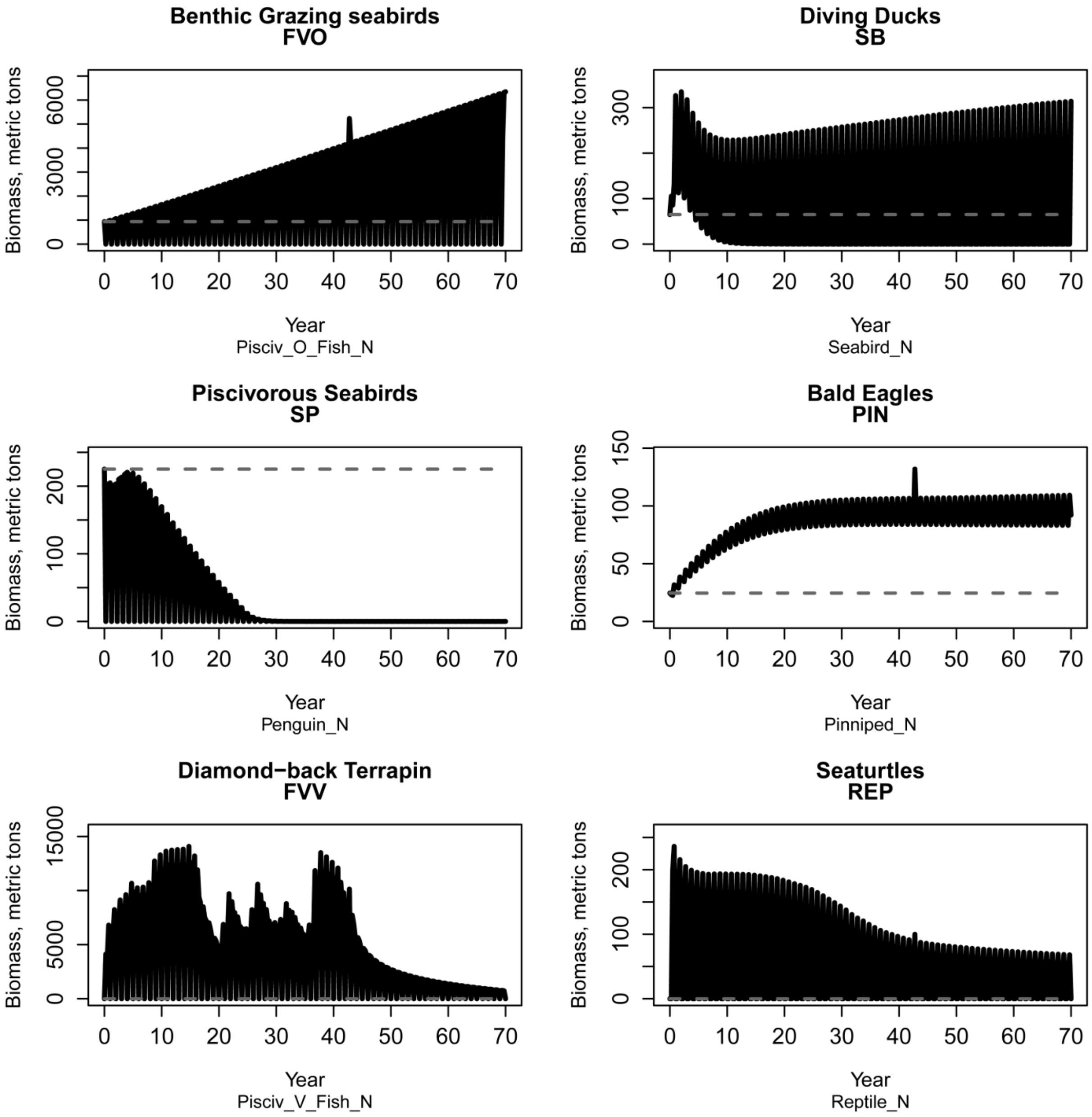

Figure 8j. Biomass results for each functional group after initial tuning phase: bird and reptile groups. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

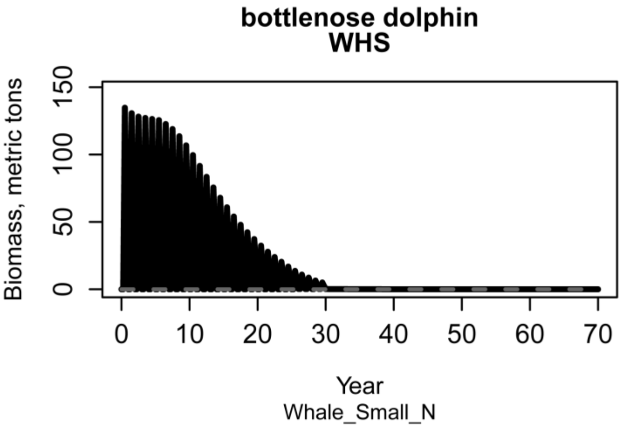

Figure 8k. Biomass results for each functional group after initial tuning phase: bottlenose dolphin. Biomass is represented in metric tons summed over the entire model extent. X-axis shows years from start of simulation. Dashed line indicates biomass estimate at the start of the simulation. Results are plotted four times per year (at a 91.25-day interval); wide bands that appear solid are due to plotting the quarterly model predictions in close proximity to one another, and represent annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

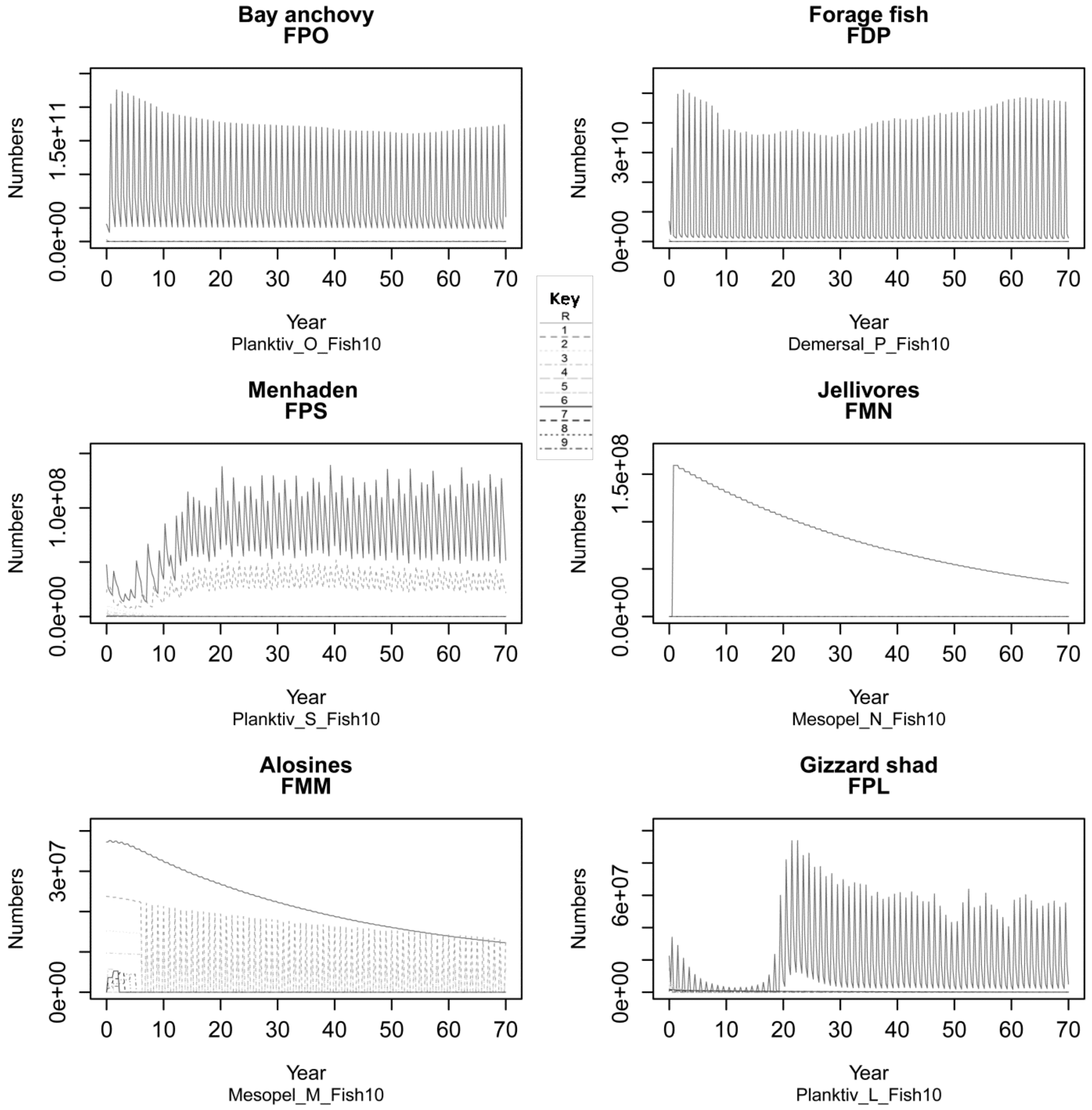

Figure 9a. Total numbers for each age class per vertebrate functional group after initial tuning phase: small-medium-sized forage fish. Numbers are summed over the entire model extent. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

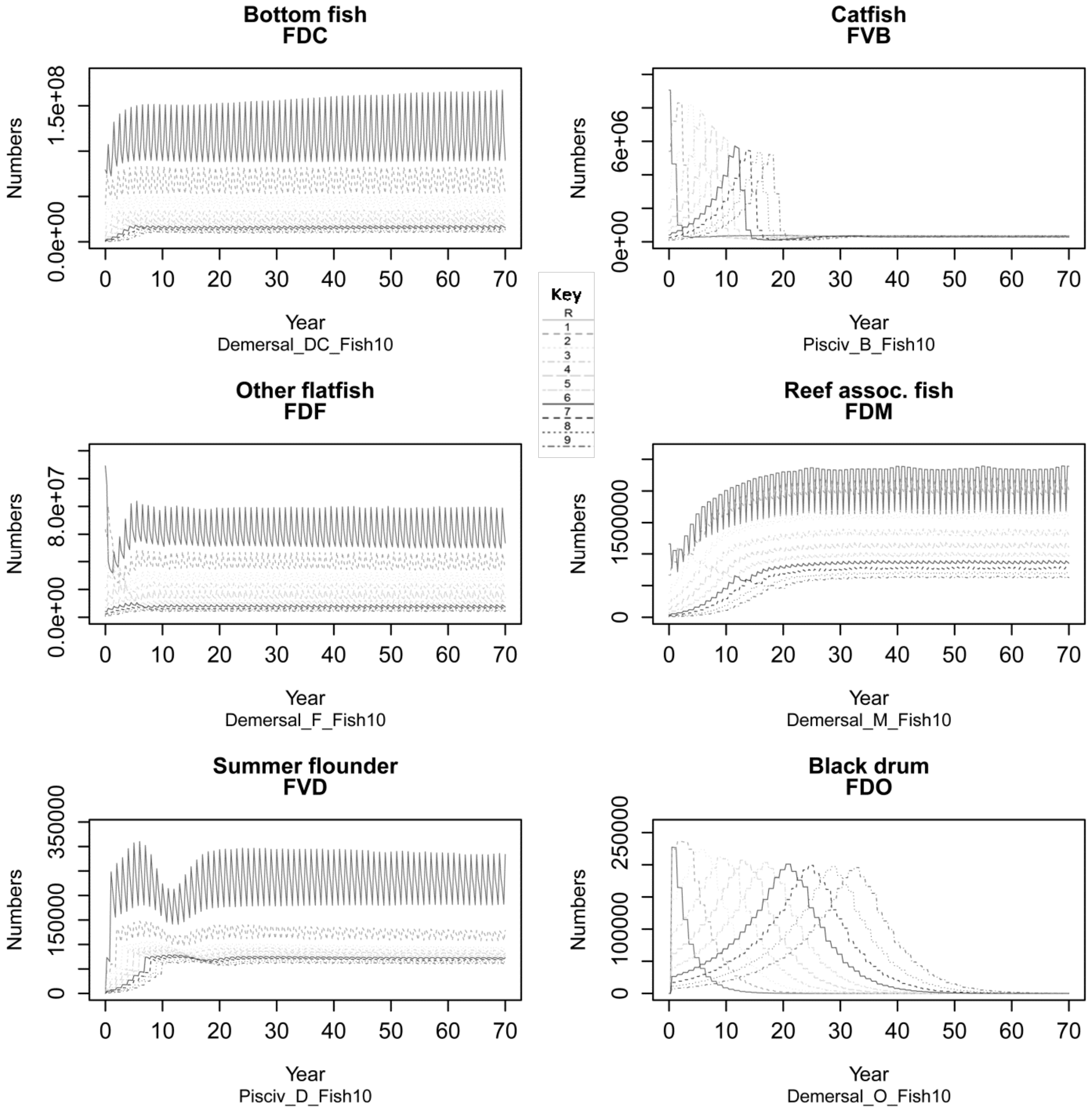

Figure 9b. Total numbers for each age class per vertebrate functional group after initial tuning phase: benthic finfish groups. Numbers are summed over the entire model extent. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

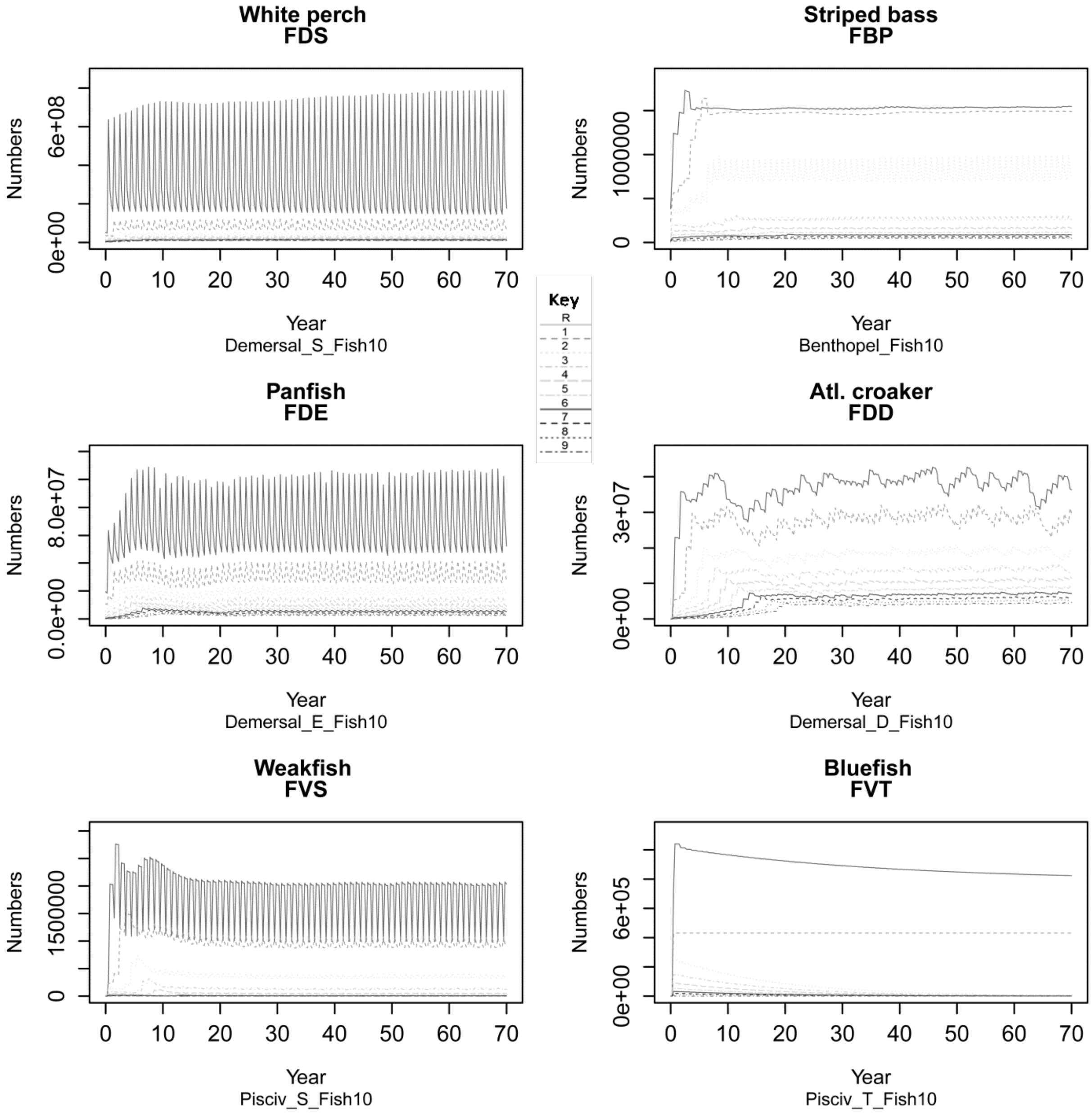

Figure 9c. Total numbers for each age class per vertebrate functional group after initial tuning phase: mixed finfish groups. Numbers are summed over the entire model extent. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

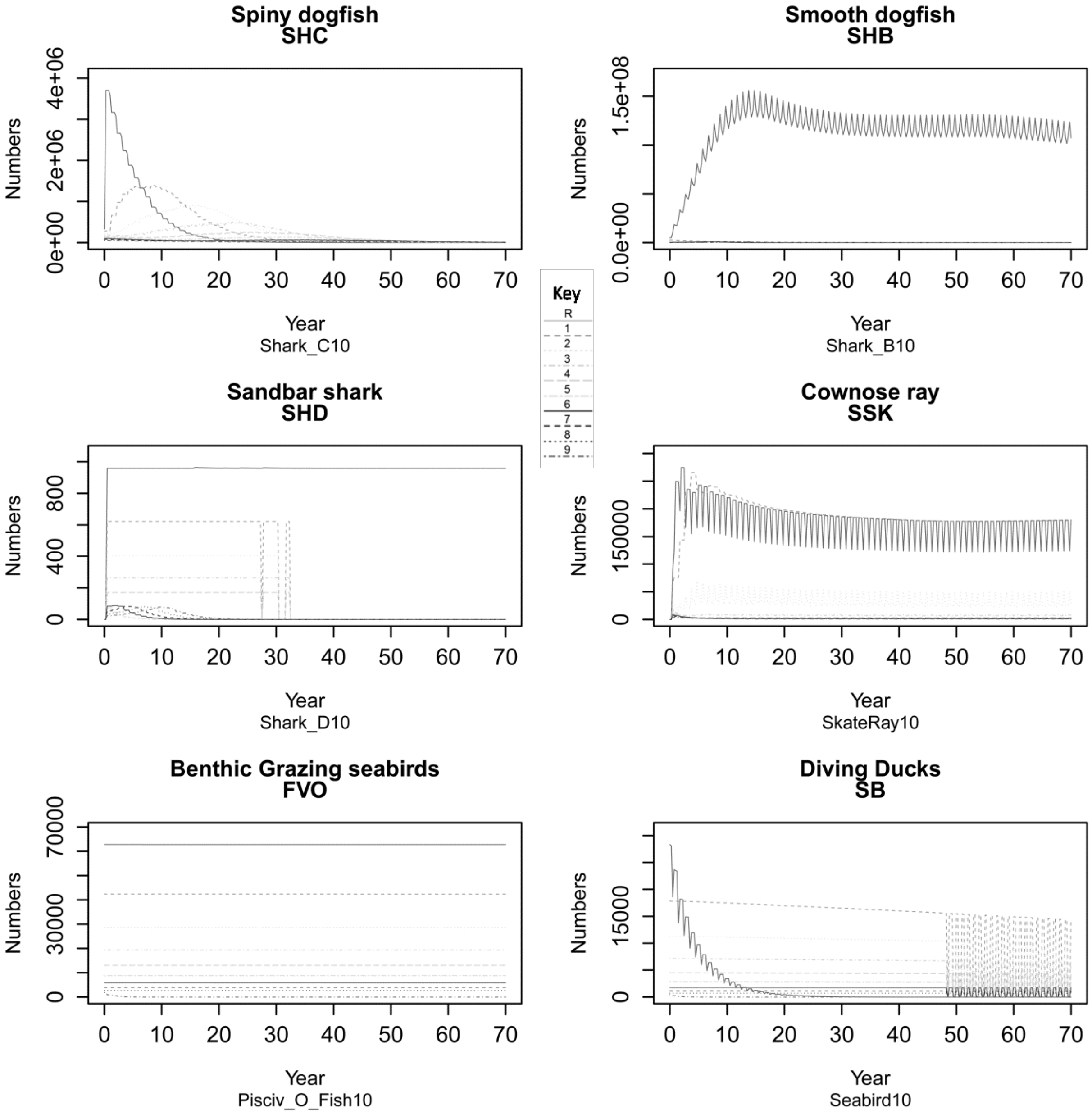

Figure 9d. Total numbers for each age class per vertebrate functional group after initial tuning phase: elasmobranchs and bird groups (continued on Fig. 8e). Numbers are summed over the entire model extent. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

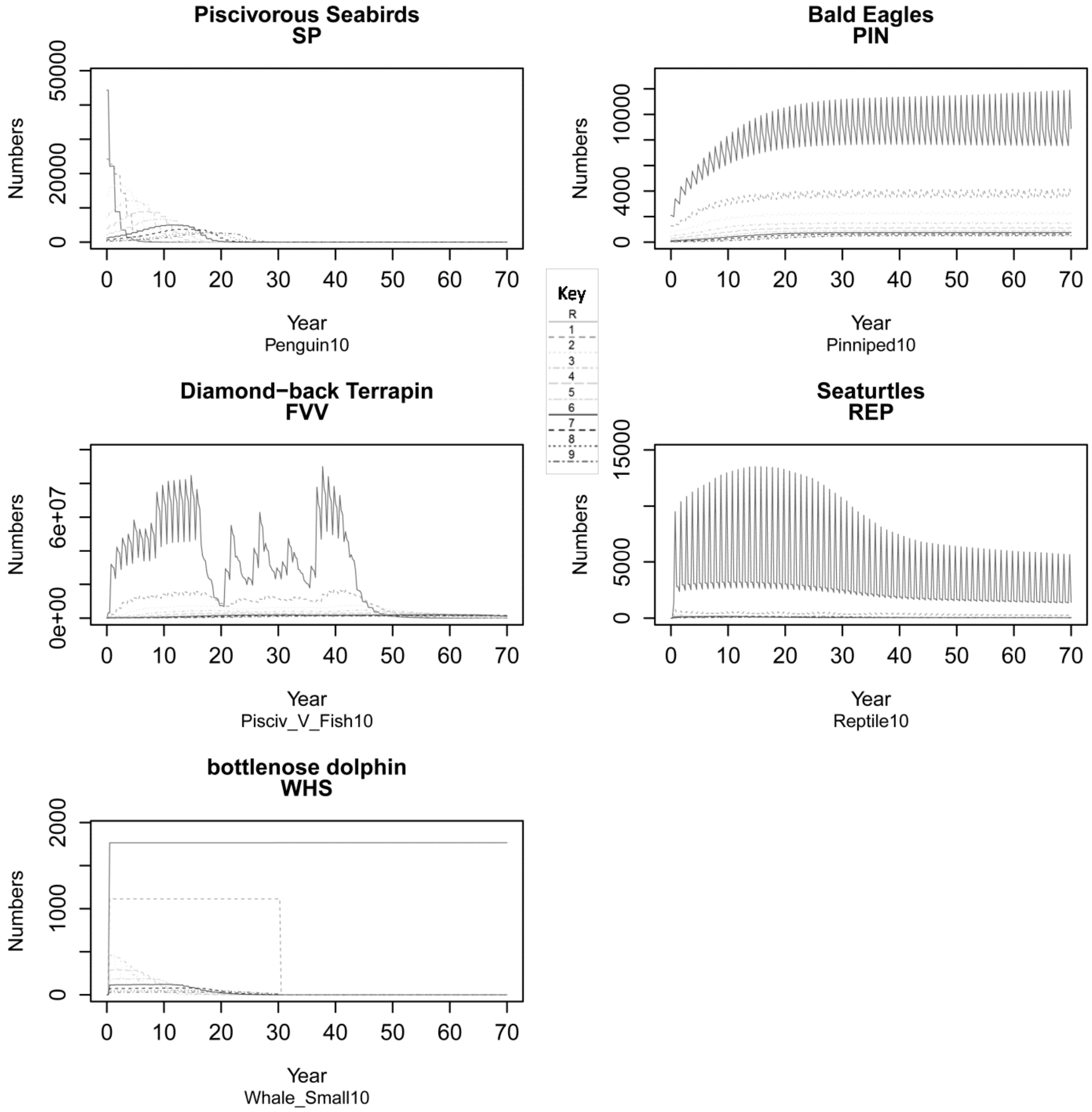

Figure 9e. Total numbers for each age class per vertebrate functional group after initial tuning phase: bird groups (continued from Fig. 9d), reptile, and mammal groups. Numbers are summed over the entire model extent. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Group names title each subplot, while group codes appear directly below names; Atlantis "long-name" for each group appears below each x-axis.

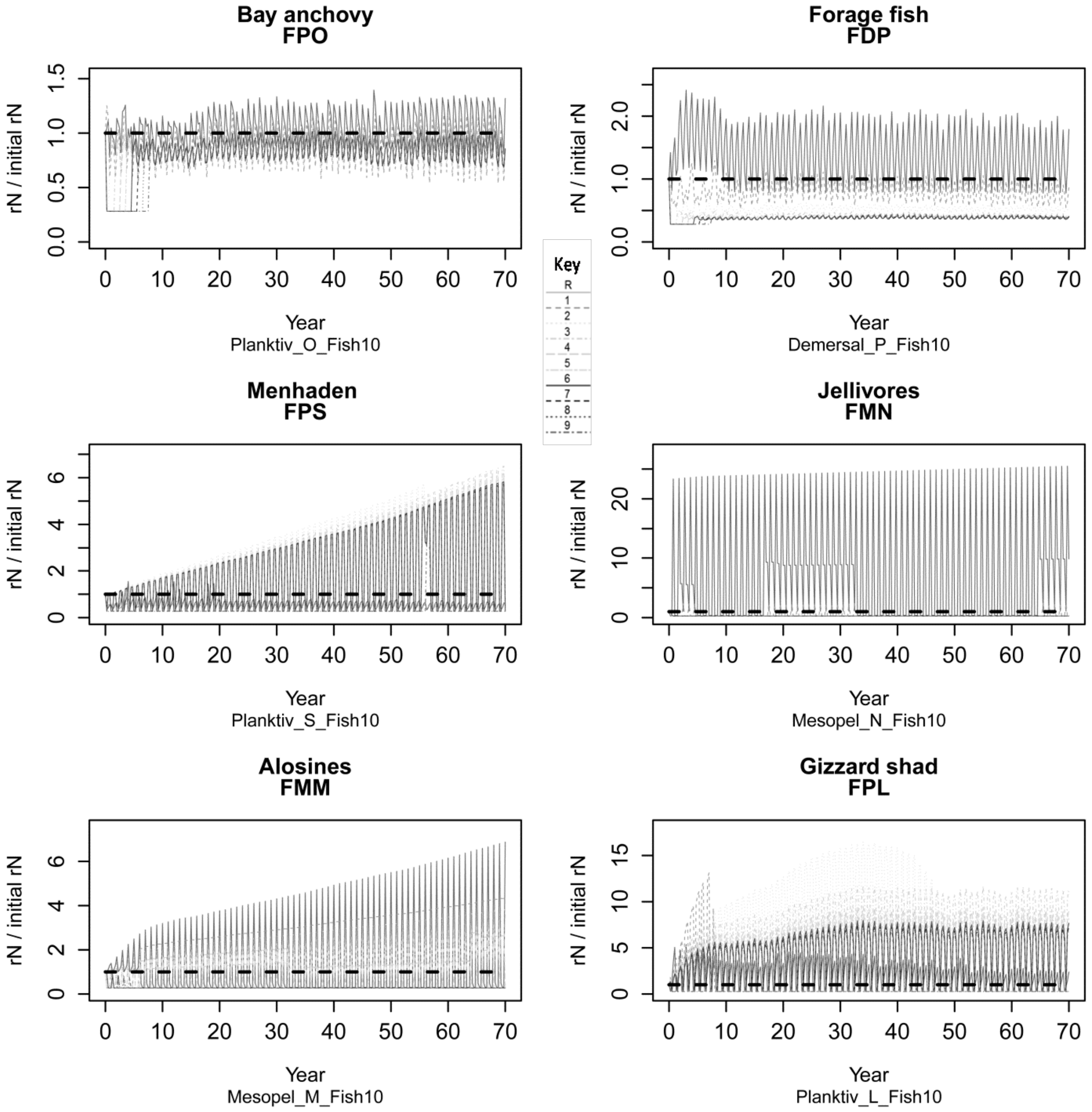

Figure 10a. Ratio of reserve nitrogen to initial reserve nitrogen for each age class per vertebrate functional group after initial tuning phase: small-medium-sized forage fish. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Reserve nitrogen represents weight-at-age that is related to muscle, fat, reproductive parts, and other soft tissue. As the ratio increases above 1, individuals become fat; as the ratio declines below 1, individuals begin to starve. X-axis shows years from start of simulation. Dashed line indicates biomass at the start of the simulation.

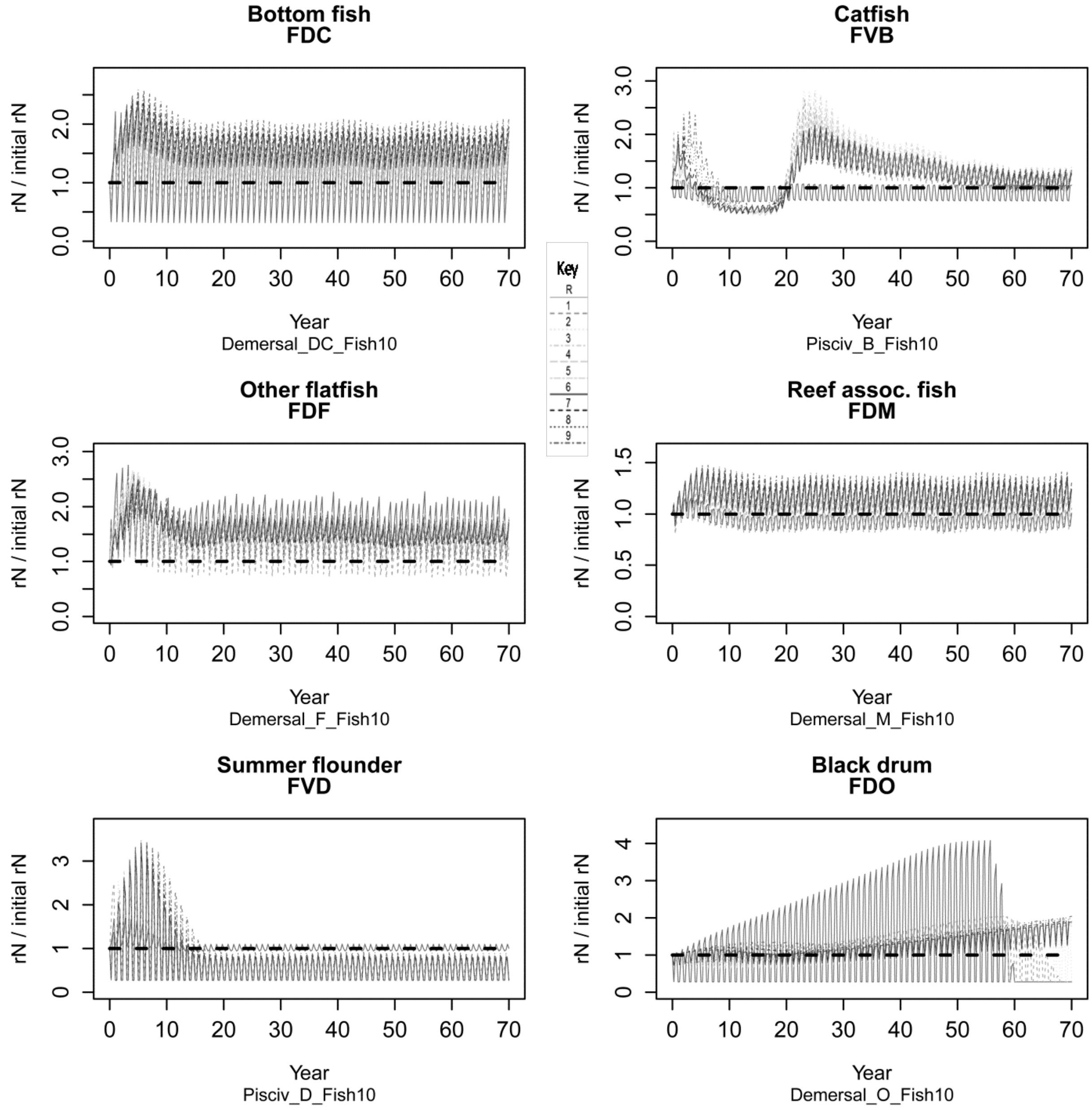

Figure 10b. Ratio of reserve nitrogen to initial reserve nitrogen for each age class per vertebrate functional group after initial tuning phase: benthic finfish. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25-day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Reserve nitrogen represents weight-at-age that is related to muscle, fat, reproductive parts, and other soft tissue. As the ratio increases above 1, individuals become fat; as the ratio declines below 1, individuals begin to starve. X-axis shows years from start of simulation. Dashed line indicates biomass at the start of the simulation.

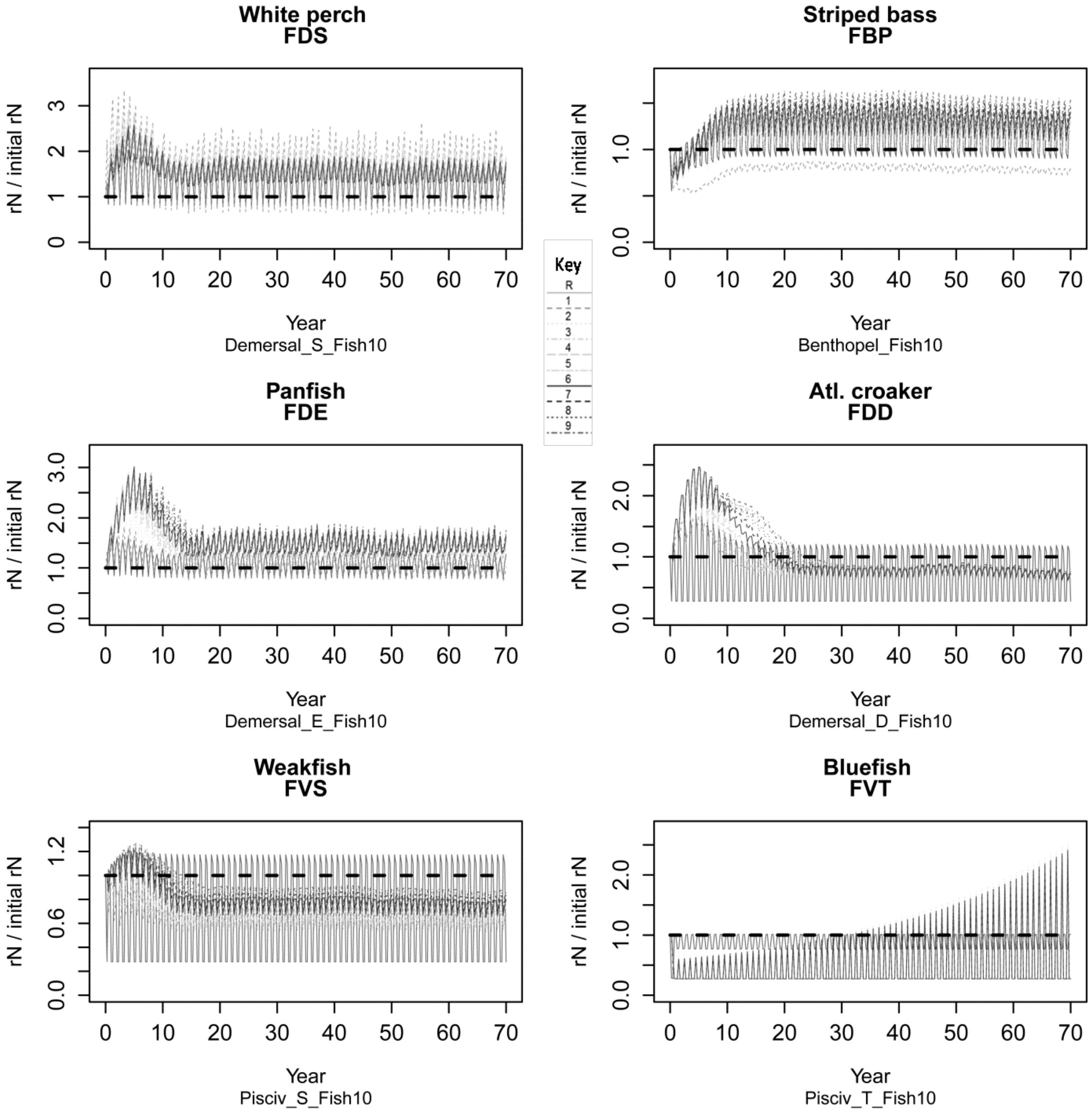

Figure 10c. Ratio of reserve nitrogen to initial reserve nitrogen for each age class per vertebrate functional group after initial tuning phase: mixed finfish groups. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25 day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Reserve nitrogen represents weight-at-age that is related to muscle, fat, reproductive parts, and other soft tissue. As the ratio increases above 1, individuals become fat; as the ratio declines below 1, individuals begin to starve. X-axis shows years from start of simulation. Dashed line indicates biomass at the start of the simulation.

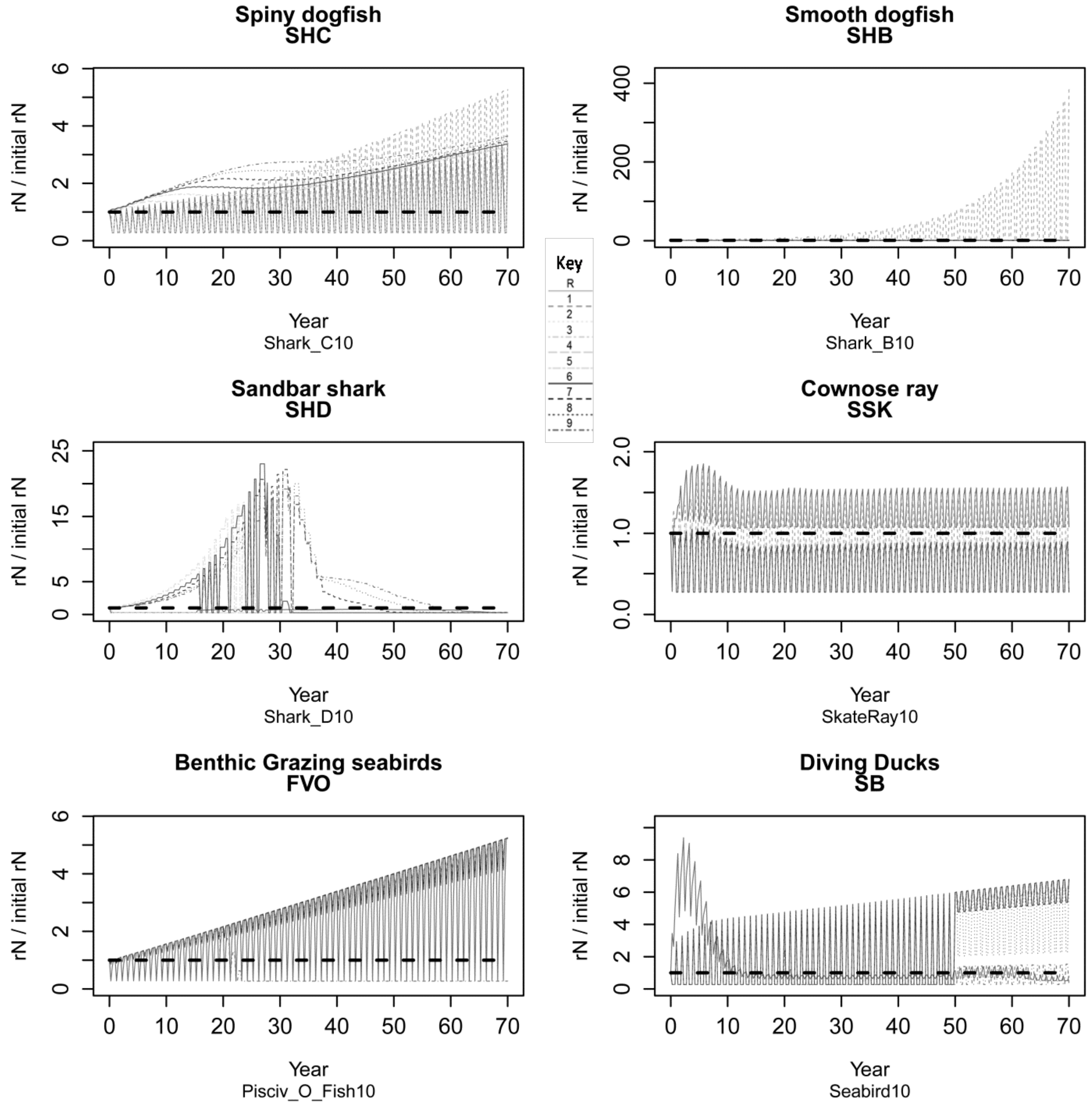

Figure 10d. Ratio of reserve nitrogen to initial reserve nitrogen for each age class per vertebrate functional group after initial tuning phase: elasmobranchs and bird groups (continued on Fig. 10e). In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25 day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Reserve nitrogen represents weight-at-age that is related to muscle, fat, reproductive parts, and other soft tissue. As the ratio increases above 1, individuals become fat; as the ratio declines below 1, individuals begin to starve. X-axis shows years from start of simulation. Dashed line indicates biomass at the start of the simulation.

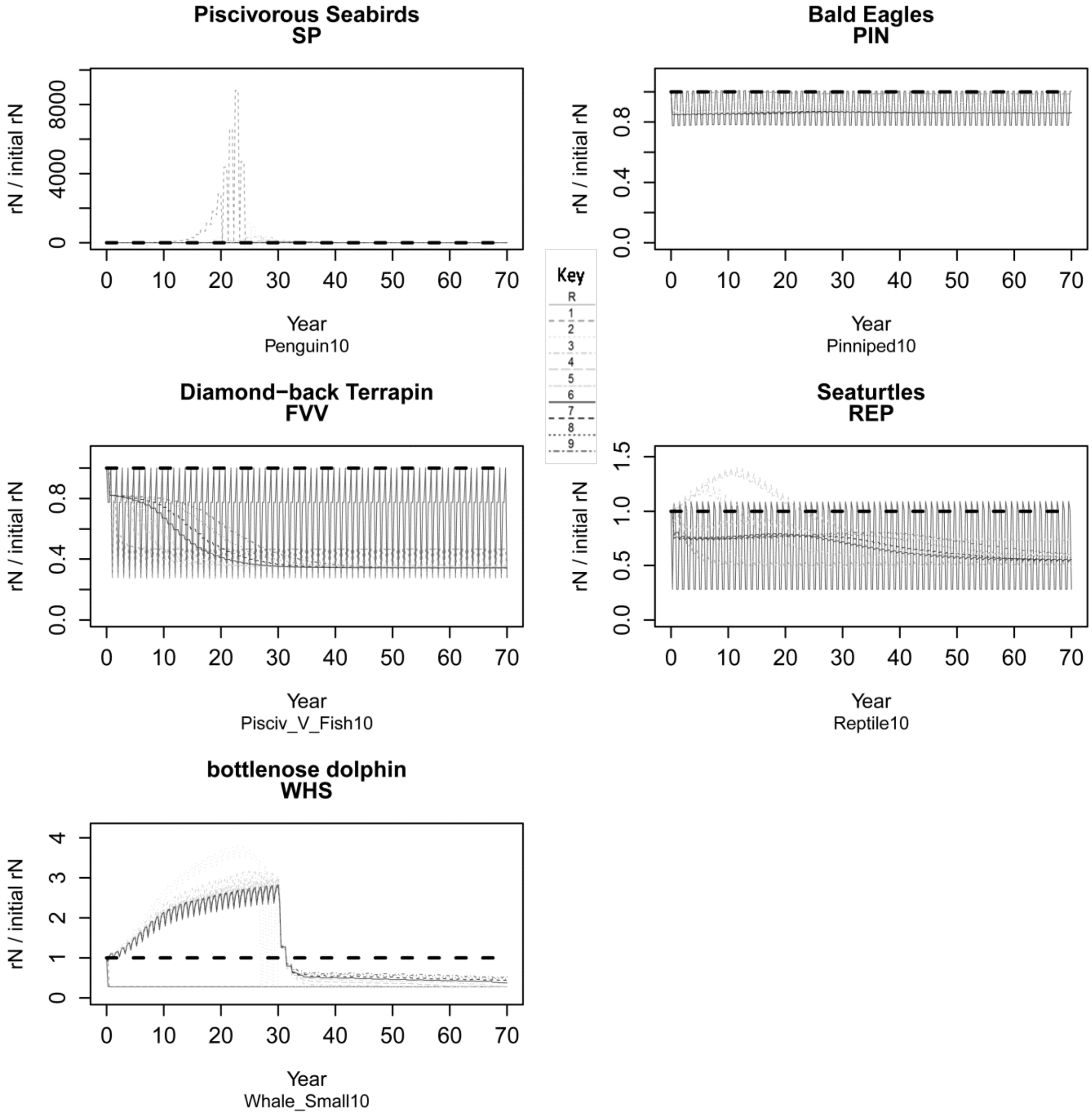

Figure 10e. Ratio of reserve nitrogen to initial reserve nitrogen for each age class per vertebrate functional group after initial tuning phase: birds (continued from Fig. 10d), reptiles and mammal groups. In key, "R" represents the age class of new recruits. X-axis shows years from start of simulation. Results are plotted four times per year (at a 91.25 day interval); the wide range of quarterly values seen in some plots represents annual variation predicted for each group. Reserve nitrogen represents weight-at-age that is related to muscle, fat, reproductive parts, and other soft tissue. As the ratio increases above 1, individuals become fat; as the ratio declines below 1, individuals begin to starve. X-axis shows years from start of simulation. Dashed line indicates biomass at the start of the simulation.

Table 1. CAM polygon characteristics. Boxes aggregate Chesapeake areas by location, salinity, depth, and bottom type (mainstem boxes only). Box 0 is a non-dynamic "boundary box" necessary to allow for the exchange of water nutrients and migratory groups to and from the dynamic model domain, but other processes are not explicitly modeled for this box. "---" indicates characteristic is not modeled for that box.

Box	Description	Aggregated Salinity Range (ppt)	Aggregated Depth Range	Bottom Type	Area (square km)
0	---	---	---	---	---
1	Lower bay	10-18	10-41m	Soft	482.2
2	Lower bay	18-30	10-31m	Soft	299.8
3	Lower bay	18-30	10-31m	Soft	61.6
4	Lower bay	18-30	0-10m	Soft	111.2
5	Lower bay	18-30	0-10m	Soft	40.4
6	Lower bay	18-30	0-10m	Soft	48.9
7	Lower bay	18-30	10-14m	Hard	159.8
8	Lower bay	18-30	10-14m	Hard	171.1
9	Lower bay	18-30	0-10m	Hard	89.6
10	Lower bay	18-30	0-10m	Hard	216.5
11	Lower bay	18-30	0-10m	Hard	75.7
12	Lower bay	18-30	0-10m	Hard	672.2
13	Lower bay	10-18	0-10m	Soft	97.0
14	Lower bay	10-18	0-10m	Soft	139.2
15	Lower bay	10-18	2-10m	Hard	307.6
16	Lower bay	10-18	2-10m	Hard	331.0
17	Lower bay	10-18	0-2m	Hard	63.0
18	Lower bay	10-18	0-2m	Hard	129.0
19	James R.	18-30	0-23m	---	106.8
20	James R.	10-18	2-10m	---	97.7
21	James R.	10-18	0-2m	---	25.7
22	James R.	10-18	0-2m	---	32.8
23	James R.	1-10	0-2m	---	75.6
24	James R.	1-10	0-2m	---	78.7
25	James R.	1-10	2-10m	---	99.8
26	Rappahannock R.	10-18	10-22m	---	42.9
27	Rappahannock R.	10-18	2-10m	---	54.2
28	Rappahannock R.	10-18	2-10m	---	51.3
29	Rappahannock R.	1-10	0-2m	---	22.0
30	Rappahannock R.	1-10	0-2m	---	27.2
31	Rappahannock R.	1-10	2-15m	---	55.5
32	Potomac R.	10-18	10-24m	---	163.8
33	Potomac R.	10-18	2-10m	---	101.7
34	Potomac R.	1-10	2-16m	---	409.0

Box	Description	Aggregated Salinity Range (ppt)	Aggregated Depth Range	Bottom Type	Area (square km)
35	Potomac R.	1-10	0-2m	---	37.6
36	Potomac R.	1-10	0-2m	---	34.9
37	Rappahannock R.	10-18	0-2m	---	21.3
38	Rappahannock R.	10-18	0-2m	---	25.8
39	Lower bay	10-18	10-13m	Hard	210.6
40	Mid-bay	10-18	10-50m	Soft	738.3
41	Mid-bay	10-18	10-31m	Soft	59.1
42	Mid-bay	10-18	10-47m	Hard	182.5
43	Mid-bay	10-18	2-10m	Soft	99.6
44	Mid-bay	10-18	2-10m	Soft	44.6
45	Mid-bay	10-18	2-10m	Soft	21.0
46	Mid-bay	10-18	2-10m	Soft	101.8
47	Mid-bay	10-18	2-10m	Soft	5.6
48	Mid-bay	10-18	2-10m	Soft	13.3
49	Mid-bay	10-18	2-10m	Hard	182.2
50	Mid-bay	10-18	2-10m	Hard	39.0
51	Mid-bay	10-18	2-10m	Hard	100.6
52	Mid-bay	10-18	2-10m	Hard	273.5
53	Mid-bay	10-18	2-10m	Hard	108.5
54	Mid-bay	10-18	2-10m	Hard	39.5
55	Mid-bay	10-18	0-2m	Hard	50.1
56	Mid-bay	10-18	0-2m	Hard	47.2
57	Mid-bay	10-18	0-2m	Hard	13.2
58	Mid-bay	10-18	0-2m	Hard	13.3
59	Upper bay	1-10	10-28m	Soft	99.1
60	Mid-bay	10-18	2-10m	Hard	24.2
61	Upper bay	1-10	2-10m	Soft	396.8
62	Upper bay	1-10	2-10m	Hard	46.1
63	Upper bay	1-10	2-10m	Hard	69.3
64	Upper bay	1-10	0-2m	Hard	27.3
65	Upper bay	1-10	0-2m	Hard	33.0
66	Potomac R.	10-18	2-10m	---	98.4
67	Potomac R.	10-18	0-2m	---	7.4
68	Potomac R.	10-18	0-2m	---	37.0
69	York R.	10-18	10-25m	---	25.0
70	York R.	10-18	2-10m	---	28.7
71	York R.	10-18	2-10m	---	28.7
72	York R.	10-18	0-2m	---	28.7
73	York R.	10-18	0-2m	---	29.8
74	York R.	1-10	2-18m	---	14.7
75	York R.	1-10	0-2m	---	3.9

Box	Description	Aggregated Salinity Range (ppt)	Aggregated Depth Range	Bottom Type	Area (square km)
76	York R.	1-10	0-2m	---	5.3
77	Patuxent R.	10-18	2-10m	---	7.5
78	Patuxent R.	10-18	2-10m	---	6.5
79	Patuxent R.	10-18	0-2m	---	3.2
80	Patuxent R.	10-18	0-2m	---	3.8
81	Patuxent R.	10-18	10-38m	---	11.7
82	Patuxent R.	1-10	2-24m	---	51.8
83	Patuxent R.	1-10	0-2m	---	12.4
84	Patuxent R.	1-10	0-2m	---	13.8
85	Nanticoke R.	10-18	2-13m	---	21.5
86	Nanticoke R.	1-10	2-17m	---	16.9
87	Nanticoke R.	10-18	0-2m	---	9.9
88	Nanticoke R.	10-18	0-2m	---	10.5
89	Nanticoke R.	1-10	0-2m	---	11.4
90	Nanticoke R.	1-10	0-2m	---	8.6
91	Mid-bay	10-18	0-2m	Hard	24.7
92	Choptank R.	1-10	2-15m	---	31.4
93	Choptank R.	1-10	0-2m	---	10.7
94	Choptank R.	1-10	0-2m	---	8.8
95	Choptank R.	10-18	2-18m	---	149.9
96	Choptank R.	10-18	0-2m	---	36.6
97	Choptank R.	10-18	0-2m	---	37.4

Table 2. Volume (m^3) for each layer of each box in CAM. The occurrence of a '0' indicates that box is too shallow to include all possible water column layers. The first water column layer listed is always the deepest found in that box. For example, Box 4 is deep enough to have only two water column layers (≤ 5 m). Box 0 is a non-dynamic "boundary box" necessary to allow for the exchange of water nutrients and migratory groups to and from the dynamic model domain, but other processes are not explicitly modeled for this box.

Box	Deepest	-->	-->	Shallowest	Sediment
0	---	---	---	---	---
1	7,232,440,497	2,410,813,499	1,928,650,799	482,162,700	482,162,700
2	2,997,555,316	1,498,777,658	1,199,022,126	299,755,532	299,755,532
3	615,570,495	307,785,248	246,228,198	61,557,049	61,557,049
4	445,062,296	111,265,574	0	0	111,265,574
5	161,712,741	40,428,185	0	0	40,428,185
6	195,468,170	48,867,043	0	0	48,867,043
7	319,568,070	798,920,175	639,136,140	159,784,035	159,784,035
8	342,229,624	855,574,061	684,459,249	171,114,812	171,114,812
9	358,559,219	89,639,805	0	0	89,639,805
10	865,857,426	216,464,356	0	0	216,464,356
11	302,794,457	75,698,614	0	0	75,698,614
12	2,688,955,636	672,238,909	0	0	672,238,909
13	387,949,358	96,987,339	0	0	96,987,339
14	556,657,723	139,164,431	0	0	139,164,431
15	307,595,336	1,230,381,344	307,595,336	0	307,595,336
16	330,999,553	1,323,998,211	330,999,553	0	330,999,553
17	75,550,026	0	0	0	62,958,355
18	154,791,180	0	0	0	128,992,650
19	213,554,009	533,885,021	427,108,017	106,777,004	106,777,004
20	97,692,554	390,770,215	97,692,554	0	97,692,554
21	30,828,677	0	0	0	25,690,564
22	39,414,504	0	0	0	32,845,420
23	90,668,711	0	0	0	75,557,259
24	94,498,031	0	0	0	78,748,359
25	99,807,722	399,230,887	99,807,722	0	99,807,722
26	257,402,306	214,501,921	171,601,537	42,900,384	42,900,384
27	54,235,259	216,941,038	54,235,259	0	54,235,259
28	51,313,916	205,255,665	51,313,916	0	51,313,916
29	26,407,689	0	0	0	22,006,408
30	32,696,149	0	0	0	27,246,791
31	55,537,289	222,149,156	55,537,289	0	55,537,289
32	1,310,515,287	819,072,054	655,257,643	163,814,411	163,814,411
33	101,730,746	406,922,986	101,730,746	0	101,730,746
34	817,967,575	1,635,935,150	408,983,788	0	408,983,788
35	45,100,858	0	0	0	37,584,048

Box	Deepest	-->	-->	Shallowest	Sediment
36	41,865,444	0	0	0	34,887,870
37	25,532,397	0	0	0	21,276,998
38	31,003,173	0	0	0	25,835,978
39	210,612,703	1,053,063,515	842,450,812	210,612,703	210,612,703
40	14,765,505,492	3,691,376,373	2,953,101,098	738,275,275	738,275,275
41	591,018,059	295,509,030	236,407,224	59,101,806	59,101,806
42	3,285,326,065	912,590,574	730,072,459	182,518,115	182,518,115
43	99,621,473	398,485,893	99,621,473	0	99,621,473
44	44,647,653	178,590,613	44,647,653	0	44,647,653
45	20,986,387	83,945,548	20,986,387	0	20,986,387
46	101,779,118	407,116,473	101,779,118	0	101,779,118
47	5,591,884	22,367,537	5,591,884	0	5,591,884
48	13,277,868	53,111,471	13,277,868	0	13,277,868
49	182,160,753	728,643,013	182,160,753	0	182,160,753
50	38,994,586	155,978,345	38,994,586	0	38,994,586
51	100,645,556	402,582,223	100,645,556	0	100,645,556
52	273,536,805	1,094,147,221	273,536,805	0	273,536,805
53	108,536,308	434,145,234	108,536,308	0	108,536,308
54	39,492,938	157,971,753	39,492,938	0	39,492,938
55	60,091,729	0	0	0	50,076,441
56	56,657,022	0	0	0	47,214,185
57	15,830,311	0	0	0	13,191,926
58	15,994,325	0	0	0	13,328,604
59	891,577,464	495,320,813	396,256,651	99,064,163	99,064,163
60	24,163,439	96,653,758	24,163,439	0	24,163,439
61	396,755,756	1,587,023,025	396,755,756	0	396,755,756
62	46,074,747	184,298,989	46,074,747	0	46,074,747
63	69,251,550	277,006,199	69,251,550	0	69,251,550
64	32,773,913	0	0	0	27,311,594
65	39,584,138	0	0	0	32,986,782
66	98,389,781	393,559,126	98,389,781	0	98,389,781
67	8,915,039	0	0	0	7,429,199
68	44,451,794	0	0	0	37,043,162
69	199,982,885	124,989,303	99,991,443	24,997,861	24,997,861
70	28,667,075	114,668,300	28,667,075	0	28,667,075
71	28,683,206	114,732,823	28,683,206	0	28,683,206
72	34,380,685	0	0	0	28,650,571
73	35,791,690	0	0	0	29,826,408
74	44,011,033	58,681,378	14,670,344	0	14,670,344
75	4,709,022	0	0	0	3,924,185
76	6,346,339	0	0	0	5,288,615

Box	Deepest	-->	-->	Shallowest	Sediment
77	7,467,975	29,871,902	7,467,975	0	7,467,975
78	6,466,912	25,867,649	6,466,912	0	6,466,912
79	3,817,966	0	0	0	3,181,638
80	4,582,315	0	0	0	3,818,596
81	164,098,208	58,606,503	46,885,202	11,721,301	11,721,301
82	51,766,993	258,834,966	207,067,972	51,766,993	51,766,993
83	14,874,537	0	0	0	12,395,447
84	16,583,202	0	0	0	13,819,335
85	85,960,268	21,490,067	0	0	21,490,067
86	33,826,145	67,652,291	16,913,073	0	16,913,073
87	11,915,243	0	0	0	9,929,370
88	12,611,911	0	0	0	10,509,926
89	13,627,140	0	0	0	11,355,950
90	10,312,560	0	0	0	8,593,800
91	29,644,825	0	0	0	24,704,021
92	31,357,529	125,430,114	31,357,529	0	31,357,529
93	12,789,683	0	0	0	10,658,070
94	10,592,645	0	0	0	8,827,204
95	449,556,912	599,409,216	149,852,304	0	149,852,304
96	43,932,084	0	0	0	36,610,070
97	44,921,439	0	0	0	37,434,533

Table 3. Initial concentrations for water quality parameters applied to the Chesapeake Atlantis Model, summarized by Segment (2003 segmentation scheme: http://www.chesapeakebay.net/maps/map/chesapeake_bay_2003_segmentation_scheme_codes, accessed August 2013) and based on 5 years of EPA observations made during the months of December and January (2000–2004). The number of usable samples available for each Bay segment is shown (*n*) for each water quality parameter. Chlorophyll a observations (CHLA) were used to estimate initial concentrations of picophytoplankton, large phytoplankton, and dinoflagellates (CAM groups PS, PL, and DF, respectively). Dissolved inorganic nitrogen observations (DIN) were used to estimate NH3, NO2, and NO3 concentrations. Particulate nitrogen (PN) and dissolved organic nitrogen (DON) observations were used to estimate refractory and labile detritus (CAM groups DR and DL, respectively). Silica observations (SIF) were used directly to estimate initial silica concentrations for the model. Standard deviation for each Bay Segment mean is shown in parentheses; "---" indicates no data available.

	CHLA			**DIN**			**PN**			**DON**			**SIF**		
CBSEG 2003	***n***	**mean**	**std**	***n***	**mean**	**std**	***n***	**mean**	**std**	***n***	**mean**	**std**	***n***	**mean**	**std**
BACOH	11	19.94	(10.55)	11	1.99	(0.84)	11	0.49	(0.17)	11	0.96	(0.25)	11	2.81	(1.09)
BIGMH	18	11.27	(10.98)	23	0.03	(0.05)	18	0.20	(0.09)	23	0.36	(0.06)	18	0.10	(0.02)
BOHOH	12	14.98	(10.95)	12	1.21	(0.41)	12	0.30	(0.11)	12	0.38	(0.14)	12	2.34	(0.66)
BSHOH	11	6.81	(10.41)	11	0.99	(0.5)	9	0.19	(0.08)	11	0.41	(0.14)	9	2.90	(1.36)
C&DOH	11	2.26	(0.69)	11	1.49	(0.27)	11	0.33	(0.17)	11	0.40	(0.19)	11	1.98	(0.91)
CB2OH	85	4.13	(3.98)	90	0.95	(0.41)	90	0.17	(0.13)	90	0.25	(0.08)	90	1.52	(0.79)
CB3MH	90	8.20	(6.54)	90	0.48	(0.41)	90	0.20	(0.12)	89	0.27	(0.06)	90	0.86	(0.64)
CB4MH	180	9.71	(6.94)	194	0.21	(0.26)	180	0.18	(0.1)	194	0.29	(0.04)	180	0.48	(0.5)
CB5MH	221	9.90	(7.33)	243	0.12	(0.17)	222	0.17	(0.09)	242	0.29	(0.06)	222	0.34	(0.4)
CB6PH	97	13.14	(10.14)	100	0.05	(0.05)	96	0.14	(0.06)	100	0.20	(0.03)	98	0.14	(0.13)
CB7PH	196	8.21	(7.61)	204	0.05	(0.05)	133	0.14	(0.09)	204	0.19	(0.05)	134	0.09	(0.09)
CB8PH	60	7.21	(5.14)	61	0.03	(0.03)	59	0.11	(0.05)	61	0.17	(0.04)	60	0.13	(0.14)
CHKOH	8	8.37	(7.34)	18	0.24	(0.14)	16	0.20	(0.07)	18	0.27	(0.05)	16	2.63	(1.1)
CHOOH	19	4.62	(5.25)	19	2.60	(0.92)	19	0.37	(0.17)	19	0.43	(0.15)	19	4.99	(2.31)
CHSMH	60	8.57	(5.71)	47	0.47	(0.32)	45	0.21	(0.09)	47	0.31	(0.08)	45	0.99	(0.66)
CHSOH	22	8.92	(14.13)	22	3.18	(1.16)	22	0.25	(0.18)	22	0.32	(0.3)	22	6.17	(1.78)
CRRMH	9	11.49	(13.7)	29	0.02	(0.03)	18	0.14	(0.08)	29	0.25	(0.02)	16	0.20	(0.11)
EASMH	45	10.31	(7.66)	51	0.18	(0.19)	45	0.22	(0.12)	51	0.32	(0.06)	45	0.58	(0.58)
EBEMH	28	11.09	(7.7)	38	0.25	(0.15)	36	0.16	(0.1)	38	0.27	(0.05)	16	0.81	(0.75)
ELIPH	46	11.86	(7.32)	76	0.17	(0.15)	69	0.16	(0.1)	76	0.25	(0.05)	51	0.54	(0.63)
ELKOH	10	2.25	(1.21)	10	1.46	(0.2)	10	0.25	(0.11)	9	0.38	(0.13)	10	2.16	(0.8)
FSBMH	22	12.74	(6.61)	23	0.12	(0.11)	22	0.34	(0.13)	23	0.50	(0.13)	22	0.29	(0.29)
GUNOH	8	8.63	(12.79)	10	0.98	(0.69)	10	0.20	(0.2)	10	0.38	(0.17)	10	2.07	(1.26)
JMSMH	17	7.75	(4.45)	49	0.09	(0.14)	32	0.13	(0.06)	49	0.22	(0.05)	36	0.79	(1.29)
JMSOH	16	7.63	(9.07)	31	0.33	(0.18)	30	0.19	(0.1)	31	0.24	(0.08)	30	1.93	(1.63)

CBSEG 2003	CHLA			DIN			PN			DON			SIF		
	n	**mean**	**std**	***n***	**mean**	**std**	***n***	**mean**	**std**	***n***	**mean**	**std**	***n***	**mean**	**std**
JMSPH	24	8.61	(4.6)	35	0.06	(0.09)	30	0.12	(0.06)	35	0.20	(0.04)	31	0.46	(0.65)
LAFMH	17	10.48	(4.97)	43	0.10	(0.12)	34	0.19	(0.11)	43	0.23	(0.05)	34	0.55	(0.7)
LCHMH	28	9.88	(7.12)	31	0.19	(0.2)	28	0.23	(0.12)	31	0.33	(0.06)	28	0.52	(0.51)
MAGMH	21	21.53	(36.85)	21	0.36	(0.3)	21	0.43	(0.56)	21	0.37	(0.15)	21	0.83	(0.73)
MANMH	20	10.03	(5.81)	26	0.09	(0.17)	20	0.23	(0.09)	26	0.40	(0.08)	20	0.47	(0.57)
MIDOH	17	11.90	(13.18)	18	0.60	(0.38)	18	0.29	(0.23)	18	0.36	(0.08)	18	1.28	(0.68)
MOBPH	62	10.03	(9.9)	66	0.02	(0.02)	62	0.13	(0.08)	66	0.21	(0.03)	62	0.19	(0.16)
MPNOH	10	3.17	(2.24)	20	0.25	(0.08)	18	0.24	(0.13)	20	0.30	(0.08)	20	3.02	(1.24)
NANMH	16	6.61	(3.27)	16	1.34	(0.87)	16	0.46	(0.29)	16	0.47	(0.14)	16	2.71	(1.58)
PATMH	35	10.32	(8.43)	35	0.59	(0.31)	35	0.23	(0.17)	35	0.34	(0.12)	35	0.93	(0.61)
PAXMH	210	13.71	(10.73)	243	0.11	(0.17)	205	0.20	(0.11)	243	0.30	(0.04)	210	0.86	(0.87)
PAXOH	54	15.28	(43.67)	55	1.08	(0.46)	54	0.43	(0.49)	55	0.31	(0.08)	54	4.90	(1.47)
PIAMH	14	16.00	(12.35)	12	0.03	(0.04)	12	0.14	(0.07)	12	0.21	(0.02)	12	0.12	(0.06)
PMKOH	9	5.59	(4.1)	18	0.30	(0.14)	16	0.45	(0.41)	18	0.27	(0.04)	18	3.08	(1.37)
POCMH	10	10.58	(5.68)	12	0.04	(0.06)	10	0.21	(0.07)	12	0.34	(0.08)	10	0.40	(0.48)
POCOH	2	10.97	(0.7)	3	0.43	(0.31)	3	0.26	(0.07)	3	0.54	(0.1)	3	3.22	(0.44)
POTMH	642	16.40	(18.62)	211	0.26	(0.3)	121	0.23	(0.12)	211	0.38	(0.1)	121	0.75	(0.86)
POTOH	60	4.07	(4.57)	60	1.20	(0.37)	60	0.18	(0.12)	59	0.35	(0.1)	60	1.76	(1.09)
RHDMH	12	12.71	(7.81)	15	0.19	(0.19)	12	0.30	(0.14)	15	0.33	(0.05)	12	1.24	(0.97)
RPPMH	65	11.56	(13.36)	167	0.13	(0.21)	116	0.18	(0.17)	167	0.25	(0.06)	124	1.01	(1.2)
RPPOH	10	4.75	(6.04)	24	0.62	(0.31)	20	0.20	(0.11)	24	0.34	(0.29)	22	2.84	(1.66)
SASOH	27	16.20	(9.66)	27	1.54	(0.52)	23	0.35	(0.17)	27	0.37	(0.14)	27	2.73	(0.71)
SBEMH	80	9.34	(9.93)	80	0.40	(0.24)	80	0.13	(0.09)	80	0.40	(0.11)	---	---	---
SEVMH	18	11.09	(9.27)	18	0.31	(0.28)	18	0.24	(0.12)	18	0.36	(0.11)	18	0.89	(0.68)
SOUMH	16	8.91	(7.1)	16	0.22	(0.26)	16	0.24	(0.1)	16	0.32	(0.04)	16	1.14	(0.88)
TANMH	69	14.99	(11.44)	77	0.11	(0.13)	69	0.24	(0.11)	77	0.35	(0.07)	69	0.20	(0.22)
WBEMH	29	11.96	(8.23)	50	0.08	(0.1)	38	0.21	(0.13)	50	0.24	(0.03)	20	0.52	(0.68)
WICMH	20	5.23	(3.3)	20	1.11	(0.58)	20	0.23	(0.08)	20	0.49	(0.16)	20	2.73	(1.77)
WSTMH	14	7.34	(5.5)	14	0.35	(0.31)	14	0.21	(0.09)	14	0.32	(0.05)	14	1.18	(0.93)
YRKMH	21	10.37	(8.1)	56	0.18	(0.13)	38	0.29	(0.27)	53	0.26	(0.07)	49	1.62	(0.91)
YRKPH	21	7.20	(3.6)	61	0.05	(0.06)	35	0.17	(0.11)	61	0.21	(0.05)	46	0.49	(0.44)

Table 4. Distribution of Bay Segments_2003 data in CAM boxes.

CBSEG_2003	Number of CAM boxes informed by segment	CAM boxes incorporating segment data	Segment description
BACOH	3	61, 63, 64	Back R.-oligohaline region
BIGMH	3	41, 50, 58	Big Annemessex R.-mesohaline region
BOHOH	3	61, 62, 65	Bohemia R.-oligohaline region
BSHOH	3	61, 63, 64	Bush R.-oligohaline region
C&DOH	3	61, 62, 65	C&D canal-oligohaline region
CB2OH	2	59, 61	Chesapeake Bay-oligohaline region
CB3MH	2	59, 62	Chesapeake Bay-mesohaline region
CB4MH	5	40, 46, 51, 52, 53	Chesapeake Bay-mesohaline region
CB5MH	11	1, 16, 18, 39, 40, 42, 44, 47, 48, 52, 54	Chesapeake Bay-mesohaline region
CB6PH	9	1, 2, 3, 4, 5, 9, 13, 16, 18	Chesapeake Bay-polyhaline region
CB7PH	6	1, 2, 7, 8, 12, 14	Chesapeake Bay-polyhaline region
CB8PH	4	7, 6, 10, 11	Chesapeake Bay-polyhaline region
CHKOH	1	23	Chickahominy R.-oligohaline region
CHOMH1	3	95, 96, 97	Choptank R.-mesohaline region 1
CHOMH2	3	95, 96, 97	Choptank R.-mesohaline region 2
CHOOH	3	92, 93, 94	Choptank R.-oligohaline region
CHSMH	3	61, 62, 65	Chester R.-mesohaline region
CHSOH	1	65	Chester R.-oligohaline region
CRRMH	2	27, 37	Corrotoman R.-mesohaline region
EASMH	4	40, 46, 51, 91	Eastern Bay-mesohaline region
EBEMH	2	20, 22	East Branch Elizabeth R.-mesohaline region
ELIPH	1	19	Elizabeth R.-polyhaline region
ELKOH	3	61, 62, 65	Elk R.-oligohaline region
FSBMH	2	43, 57	Fishing Bay-mesohaline region
GUNOH	3	61, 63, 64	Gunpowder R.-oligohaline region
HNGMH	2	44, 49	Honga R.-mesohaline region
JMSMH	3	20, 21, 22	James R.-mesohaline region
JMSOH	3	23, 24, 25	James R.-oligohaline region
JMSPH	1	19	James R.-polyhaline region
LAFMH	2	20, 22	Lafayette R.-mesohaline region
LCHMH	3	45, 52, 56	Little Choptank R.-mesohaline region
LYNPH	1	11	Lynnhaven R.-polyhaline region
MAGMH	3	46, 53, 55	Magothy R.-mesohaline region
MANMH	3	41, 50, 58	Manokin R.-mesohaline region
MIDOH	3	61, 63, 64	Middle R.-oligohaline region
MOBPH	4	3, 4, 5, 10	Mobjack Bay-polyhaline region
MPNOH	2	74, 75	Mattaponi R.-oligohaline region
NANMH	3	85, 87, 88	Nanticoke R.-mesohaline region
NANOH	3	86, 89, 90	Nanticoke R.-oligohaline region
PATMH	3	46, 55, 64	Patapsco R.-mesohaline region
PAXMH	6	47, 77, 78, 79, 80, 81	Patuxent R.-mesohaline region
PAXOH	3	82, 83, 84	Patuxent R.-oligohaline region

CBSEG_2003	Number of CAM boxes informed by segment	CAM boxes incorporating segment data	Segment description
PIAMH	3	26, 28, 38	Piankatank R.-mesohaline region
PMKOH	2	74, 76	Pamunkey R.-oligohaline region
POCMH	3	14, 15, 17	Pocomoke R.-mesohaline region
POCOH	3	14, 15, 17	Pocomoke R.-oligohaline region
POTMH	7	32, 33, 54, 60, 66, 67, 68	Potomac R.-mesohaline region
POTOH	3	34, 35, 36	Potomac R.-oligohaline region
RHDMH	3	46, 53, 55	Rhode R.-mesohaline region
RPPMH	5	26, 27, 28, 37, 38	Rappahannock R.-mesohaline region
RPPOH	3	29, 30, 31	Rappahannock R.-oligohaline region
SASOH	3	61, 62, 65	Sassafras R.-oligohaline region
SBEMH	2	20, 22	South Branch Elizabeth R.-mesohaline region
SEVMH	3	46, 53, 55	Severn R.-mesohaline region
SOUMH	3	46, 53, 55	South R.-mesohaline region
TANMH	4	14, 15, 17, 49	Tangier Sound-mesohaline region
WBEMH	2	20, 22	W. Branch Elizabeth R.-mesohaline region
WICMH	3	41, 50, 58	Wicomico R.-mesohaline region
WSTMH	3	46, 53, 55	West R.-mesohaline region
YRKMH	5	69, 70, 71, 72, 73	York R.-mesohaline region
YRKPH	5	69, 70, 71, 72, 73	York R.-polyhaline region

Table 5. Primary producer functional groups and basic life history parameterization. Growth, clearance, lysis, and mortality rates are post-calibration values. Maximum initial concentration and biomass (bay-wide, wet-weight) are estimates from January 1, 2002, used to initialize the model. "Q-mort" is quadratic mortality, used in the model to limit uncontrolled, explosive growth of any particular group. "Excess. DIN mort." is extra mortality due to excess dissolved inorganic nitrogen. "Refuge habitat" indicates whether the group can be used by other groups to decrease its availability to predators, see main text for further details; "---" indicates setting not applicable to that group.

Common name	**Group code**	**Species**	**2D/ 3D**	**Units**	**Initial concen-tration (max)**	**Biomass (mt)**	**Maximum growth rate (mgN/day)**	**Clearance (mg3/mgN/ day)**	**Lysis (mgN/day)**	**Q-mort (/day)**	**Excess. DIN mort.**	**Refuge habitat ?**
Marsh grass	MA	Saltmarsh cordgrass, *Spartina alterniflora*, and giant cordgrass *Spartina cynosuroides*	2D	mgN/m^2	28,963.0	4,005,682	0.200	--	0.00100	--	--	Yes
Seagrass (SAV)	SG	Genera: *Zostera, Ruppia, Potamogeton* and "freshwater mixed" as described by Moore et al. (2000)	2D	mgN/m^2	472.6	85,140	0.020	--	0.01000	--	0.000001	Yes
Large phytoplankton	PL	Phytoplankton in size range 2–200 um (e.g., Diatoms, cryptophyes)	3D	mgN/m^3	121.6	687,613	2.700	--	0.00001	0.001	--	No

Common name	Group code	Species	2D/ 3D	Units	Initial concen-tration (max)	Biomass (mt)	Maximum growth rate (mgN/day)	Clearance (mg3/mgN/ day)	Lysis (mgN/day)	Q-mort (/day)	Excess. DIN mort.	Refuge habitat ?
Picophytoplankton	PS	Phytoplankton in size range 0.2–2 um (e.g., cyanobacteria)	3D	mgN/m^3	18.6	105,052	1.000	--	0.01200	0.001	--	No
Dinoflagellates	DF	Mixotrophs	3D	mgN/m^3	20.3	114,602	0.585	0.275	0.00900	0.001	--	No
Microphytobenthos	MB	Benthic algae	2D	mgN/m^2	377.5	189,720	0.100	--	0.00100	--	--	No

Table 6. Habitat composition (proportions) of boxes in the Chesapeake Atlantis Model. '0' indicates habitat type is not found in that CAM box. "NA" = not applicable. Biogenic habitat proportions shown here correspond to *Cover* (Equation 18) available for refuge to prey as described in Habitat Associations.

					Biogenic habitats		
CAM box	**Rock or artificial reef**	**Sand**	**Mud**	**Woody debris**	**SAV**	**Marsh**	**Oyster**
0	NA	NA	NA	NA	NA	NA	NA
1	0.005	0	0.995	0	0	0	0
2	0.005	0	0.995	0	0	0	0
3	0.005	0	0.995	0	0	0	0
4	0.055	0	0.775	0.035	0.035	0.100	0
5	0.055	0	0.775	0.035	0.035	0.100	0
6	0.055	0	0.775	0.035	0.035	0.100	0
7	0.005	0.995	0	0	0	0	0
8	0.005	0.995	0	0	0	0	0
9	0.080	0.720	0	0.050	0.025	0.075	0.050
10	0.080	0.720	0	0.050	0.025	0.075	0.050
11	0.080	0.720	0	0.050	0.025	0.075	0.050
12	0.080	0.720	0	0.050	0.025	0.075	0.050
13	0.055	0	0.775	0.035	0.035	0.100	0
14	0.055	0	0.775	0.035	0.035	0.100	0
15	0.010	0.940	0	0	0	0	0.050
16	0.010	0.940	0	0	0	0	0.050
17	0.150	0.500	0	0.100	0.050	0.150	0.050
18	0.150	0.500	0	0.100	0.050	0.150	0.050
19	0.008	0.283	0.607	0	0.035	0	0.067
20	0.010	0.400	0.490	0	0	0	0.100
21	0.100	0.080	0.250	0.150	0.100	0.300	0.020
22	0.100	0.080	0.250	0.150	0.100	0.300	0.020
23	0.100	0.080	0.250	0.150	0.100	0.300	0.020
24	0.100	0.080	0.250	0.150	0.100	0.300	0.020
25	0.010	0.400	0.490	0	0	0	0.100
26	0.005	0.050	0.945	0	0	0	0
27	0.010	0.400	0.490	0	0	0	0.100
28	0.010	0.400	0.490	0	0	0	0.100
29	0.100	0.080	0.250	0.150	0.100	0.300	0.020
30	0.100	0.080	0.250	0.150	0.100	0.300	0.020
31	0.008	0.225	0.718	0	0	0	0.050
32	0.005	0.050	0.945	0	0	0	0
33	0.010	0.400	0.490	0	0	0	0.100
34	0.008	0.225	0.718	0	0	0	0.050
35	0.100	0.080	0.250	0.150	0.100	0.300	0.020
36	0.100	0.080	0.250	0.150	0.100	0.300	0.020
37	0.100	0.080	0.250	0.150	0.100	0.300	0.020
38	0.100	0.080	0.250	0.150	0.100	0.300	0.020
39	0.005	0.995	0	0	0	0	0

					Biogenic habitats		
CAM box	**Rock or artificial reef**	**Sand**	**Mud**	**Woody debris**	**SAV**	**Marsh**	**Oyster**
40	0.005	0	0.995	0	0	0	0
41	0.005	0	0.995	0	0	0	0
42	0.005	0.995	0	0	0	0	0
43	0.010	0	0.990	0	0	0	0
44	0.010	0	0.990	0	0	0	0
45	0.010	0	0.990	0	0	0	0
46	0.010	0	0.990	0	0	0	0
47	0.010	0	0.990	0	0	0	0
48	0.010	0	0.990	0	0	0	0
49	0.010	0.940	0	0	0	0	0.050
50	0.010	0.940	0	0	0	0	0.050
51	0.010	0.940	0	0	0	0	0.050
52	0.010	0.940	0	0	0	0	0.050
53	0.010	0.940	0	0	0	0	0.050
54	0.010	0.940	0	0	0	0	0.050
55	0.150	0.500	0	0.100	0.050	0.150	0.050
56	0.150	0.500	0	0.100	0.050	0.150	0.050
57	0.150	0.500	0	0.100	0.050	0.150	0.050
58	0.150	0.500	0	0.100	0.050	0.150	0.050
59	0.005	0	0.995	0	0	0	0
60	0.010	0.940	0	0	0	0	0.050
61	0.010	0	0.990	0	0	0	0
62	0.010	0.940	0	0	0	0	0.050
63	0.010	0.940	0	0	0	0	0.050
64	0.150	0.500	0	0.100	0.050	0.150	0.050
65	0.150	0.500	0	0.100	0.050	0.150	0.050
66	0.010	0.400	0.490	0	0	0	0.100
67	0.100	0.080	0.250	0.150	0.100	0.300	0.020
68	0.100	0.080	0.250	0.150	0.100	0.300	0.020
69	0.005	0.050	0.945	0	0	0	0
70	0.010	0.400	0.490	0	0	0	0.100
71	0.010	0.400	0.490	0	0	0	0.100
72	0.100	0.080	0.250	0.150	0.100	0.300	0.020
73	0.100	0.080	0.250	0.150	0.100	0.300	0.020
74	0.008	0.225	0.718	0	0	0	0.050
75	0.100	0.080	0.250	0.150	0.100	0.300	0.020
76	0.100	0.080	0.250	0.150	0.100	0.300	0.020
77	0.010	0.400	0.490	0	0	0	0.100
78	0.010	0.400	0.490	0	0	0	0.100
79	0.100	0.080	0.250	0.150	0.100	0.300	0.020
80	0.100	0.080	0.250	0.150	0.100	0.300	0.020
81	0.005	0.050	0.945	0	0	0	0
82	0.008	0.225	0.718	0	0	0	0.050
83	0.100	0.080	0.250	0.150	0.100	0.300	0.020
84	0.100	0.080	0.250	0.150	0.100	0.300	0.020
85	0.008	0.225	0.718	0	0	0	0.050

					Biogenic habitats		
CAM box	**Rock or artificial reef**	**Sand**	**Mud**	**Woody debris**	**SAV**	**Marsh**	**Oyster**
86	0.008	0.225	0.718	0	0	0	0.050
87	0.100	0.080	0.250	0.150	0.100	0.300	0.020
88	0.100	0.080	0.250	0.150	0.100	0.300	0.020
89	0.100	0.080	0.250	0.150	0.100	0.300	0.020
90	0.100	0.080	0.250	0.150	0.100	0.300	0.020
91	0.150	0.500	0	0.100	0.050	0.150	0.050
92	0.008	0.225	0.718	0	0	0	0.050
93	0.100	0.080	0.250	0.150	0.100	0.300	0.020
94	0.100	0.080	0.250	0.150	0.100	0.300	0.020
95	0.008	0.225	0.718	0	0	0	0.050
96	0.100	0.080	0.250	0.150	0.100	0.300	0.020
97	0.100	0.080	0.250	0.150	0.100	0.300	0.020

Table 7. Expected microphytobenthos (CHLA) concentrations in sediments of the Chesapeake Bay, based on M. Kemp (personal communication) and field observations presented in Rizzo and Wetzel (1985). Concentrations are mg CHLA/m^2. “Soft” includes all sediments other than clean sand. Bottom type was not identified in tributaries; therefore, intermediate CHLA concentrations were assumed for tributary boxes.

	Water Column Depth		
	0–2 m	**> 2–8 m**	**> 8 m**
Mainstem:			
Soft	60	20	0
Sand	100	60	0
Tributaries:	80	40	0

Table 8. Invertebrate functional groups and basic life history parameterization. "2D" or "3D" indicate how many spatial dimensions that the group is modeled in. Growth, clearance, and mortality rates are post-calibration values. Maximum initial concentration and initial biomass (bay-wide, wet-weight) are estimates from January 1, 2002, estimates used to initialize the model; however, biomass for each group is not available until the day of the year that group migrates into the model. "Q-mort" is quadratic mortality, used in the model to limit uncontrolled, explosive growth of any particular group. "Refuge habitat" indicates whether the group can be used by other groups to decrease its availability to predators, see main text for further details.

Group name	**Group code**	**Group description, species included**	**2D/ 3D**	**Units**	**Initial concen-tration (max)**	**Initial biomass (mt)**	**Max. growth rate (mgN/day)**	**Clearance (mg^3/mgN /day)**	**Q-mort (/day)**	**Refuge habitat ?**
Ctenophores	ZG	*Mnemiopsis leidyi*	3D	mgN/m^3	0.08	998	0.04	0.004	0.001	No
Sea nettles	ZL	*Chrysaora quinquecirrha*	3D	mgN/m^3	0.07	926	0.02	0.08	0.001	No
Meso-zooplankton	ZM	Zooplankton in size range 200–20,000 um (0.2–20 mm), e.g., copepods, cladocera	3D	mgN/m^3	2.09	26,410	2.3	0.3	1.00E-05	No
Micro-zooplankton	ZS	Zooplankton in size range 20–200 um (0.02–0.2 mm), e.g., ciliates, dinoflagellates, nanoflagellates, gymnodioids, protozoa	3D	mgN/m^3	1.65	20,844	1.9	0.45	0.0001	No
Deep benthic filter feeders	BFD	Benthic filter feeders (e.g., hard clam, arcs, filter feeding poycheates, sessile tunicates; see Table 10 for complete list)	2D	mgN/m^2	680.65	829,445	0.04	0.004	1.00E-08	No
Shallow benthic filter feeders	BFS	*Macoma spp.* (saltwater clams)	2D	mgN/m^2	97.25	118,507	0.02	0.008	1.00E-09	No

Group name	Group code	Group description, species included	2D/ 3D	Units	Initial concen-tration (max)	Initial biomass (mt)	Max. growth rate (mgN/day)	Clearance (mg^3/mgN /day)	Q-mort (/day)	Refuge habitat ?
Other benthic filter feeders	BFF	Oyster (*Crassostrea virginica*)	2D	mgN/m^2	4,176.60	181,555	0.04	0.002	1.00E-08	Yes
Benthic carnivores	BC	Benthic predators that compete with fish (e.g., polychaetes, nematodes, burrowing crustacea, flatworms et al.; see Table 10 for complete list)	3D	mgN/m^3	52.00	63,352	0.03	0.0002	1.00E-06	No
Benthic deposit feeders	BD	Benthic detritivores and omnivores (e.g., amphipods, isopods, small crustacea, snails, et al. (see Table 10 for complete list)	3D	mgN/m^3	60.30	73,452	0.06	0.007	1.00E-09	No
Meiobenthos	BO	Major taxonomic groups include copepods, nematodes, nauplii, foraminifera, newly settled clams, polychaetes, et.al (following Metcalfe, 2005)	3D	mgN/m^3	5.72	35,266	0.2	0.02	1.00E-07	No
Brief squid	CEP	*Lolliguncula brevis*	3D	mgN/m^3	1.80	1,027	0.1	0.0019	1.00E-06	No
Juvenile squid	jCEP	Juvenile brief squid	3D	mgN/m^3	0	0	0.03	0.0015	1.00E-06	No
Blue crab	PWN	*Callinectes sapidus*	3D	mgN/m^3	31.70	38,627	0.01	0.001	1.00E-05	No
Juvenile crab	jPWN	Juvenile blue crab	3D	mgN/m^3	0	0	0.09	0.004	1.00E-05	No

Table 9. Biological characteristics and timing of invertebrate migrators in CAM. Sea nettles and crab do not actually leave the Bay system over the winter, but rather encyst (sea nettles) and enter torpor (crabs); both conditions effectively remove these groups from the model domain and are consequently modeled as migrations. "NA" = not applicable.

Common name	Group code	Day group moves into model	Day group leaves the model	Day spawning begins for group	Period (days) spawning occurs	Average biomass of new recruits (mgN/m^3)
Sea nettles	ZL	91	319	NA	NA	NA
Brief squid	CEP	74	335	182	90	NA
Juvenile squid	jCEP	91	0	NA	NA	0.1
Crab	PWN	91	305	182	90	NA
Juvenile crab	jPWN	91	305	NA	NA	0.0227

Table 10. Species composition of the four aggregate benthic invertebrate groups in CAM based on the Benthic-Index of Biological Integrity (B-IBI) of the Chesapeake Bay Program: benthic deposit feeders (BD), Macoma *spp.* (BFS), benthic carnivores (BC), and benthic filter feeders (BFD). These groups are a subset of species collected during the Long-Term Benthic survey during 2002–2009 that represented either 90% of the total abundance (ABUN), 90% of the total biomass (BIOM), or both. National Oceanic Data Center (NODC) taxonomic codes are superseded by Taxonomic Serial Number (TSN) designations; "---" indicates no TSN exists for that species. Abbreviations for the B-IBI are IN = Interface Feeder, CO = Carnivore and Omnivore, SU=Suspension Feeder, P=Predator, and M= Macoma clams.

Scientific Name	**NODC**	**TSN**	**Family**	**Group Code Name**	**B-IBI Trophic Group**	**Qualifying Measure**
Benthic deposit feeders (BD):						
Apoprionospio pygmaea	5001433599	66847	Spionidae	Annelida : Polychaeta	IN	ABUN&BIOM
Asabellides oculata	5001670802	67786	Ampharetidae	Annelida : Polychaeta	IN	ABUN
Boccardiella ligerica	5001432802	67012	Spionidae	Annelida : Polychaeta	IN	ABUN
Hobsonia florida	5001670309	67755	Ampharetidae	Annelida : Polychaeta	IN	ABUN
Loimia medusa	5001682001	68015	Terebellidae	Annelida : Polychaeta	IN	ABUN&BIOM
Magelona spp.	50014401	67043	Magelonidae	Annelida : Polychaeta	IN	ABUN
Marenzelleria viridis	5001430602	573739	Spionidae	Annelida : Polychaeta	IN	ABUN&BIOM
Monticellina dorsobranchialis	5001509897	204530	Cirratulidae	Annelida : Polychaeta	IN	ABUN
Paraonis fulgens	5001410302	66697	Paraonidae	Annelida : Polychaeta	IN	ABUN
Paraprionospio pinnata	5001431701	66937	Spionidae	Annelida : Polychaeta	IN	ABUN&BIOM
Polycirrus eximius	5001680804	67963	Terebellidae	Annelida : Polychaeta	IN	ABUN
Polydora cornuta	5001430448	204501	Spionidae	Annelida : Polychaeta	IN	ABUN
Prionospio perkinsi	5001430517	66854	Spionidae	Annelida : Polychaeta	IN	ABUN
Spiochaetopterus costarum	5001490302	67107	Chaetopteridae	Annelida : Polychaeta	IN	ABUN&BIOM
Spiophanes bombyx	5001431001	66897	Spionidae	Annelida : Polychaeta	IN	ABUN&BIOM
Streblospio benedicti	5001431801	66939	Spionidae	Annelida : Polychaeta	IN	ABUN&BIOM
Tharyx sp. A Morris	5001500399	---	Cirratulidae	Annelida : Polychaeta	IN	ABUN&BIOM
Acanthohaustorius millsi	6169220602	93982	Haustoriidae	Arthropoda : Amphipoda	IN	ABUN
Ameroculodes species complex	61693799	---	Oedicerotidae	Arthropoda : Amphipoda	IN	ABUN
Apocorophium lacustre	6169159798	656749	Corophiidae	Arthropoda : Amphipoda	IN	ABUN
Gammarus daiberi	6169210705	93779	Gammaridae	Arthropoda : Amphipoda	IN	ABUN&BIOM
Gammarus fasciatus	6169210706	93780	Gammaridae	Arthropoda : Amphipoda	CO	ABUN
Lepidactylus dytiscus	6169220901	93998	Haustoriidae	Arthropoda : Amphipoda	IN	ABUN

Scientific Name	NODC	TSN	Family	Group Code Name	B-IBI Trophic Group	Qualifying Measure
Leptocheirus plumulosus	6169060701	93486	Aoridae	Arthropoda : Amphipoda	IN	ABUN&BIOM
Listriella barnardi	6169330301	94213	Liljeborgiidae	Arthropoda : Amphipoda	IN	ABUN
Listriella clymenellae	6169330302	94214	Liljeborgiidae	Arthropoda : Amphipoda	IN	ABUN
Melita nitida	6169211006	93812	Melitidae	Arthropoda : Amphipoda	IN	ABUN
Monocorophium tuberculatum	6169159999	656762	Corophiidae	Arthropoda : Amphipoda	IN	ABUN
Paracaprella tenuis	6171010901	95434	Caprellidae	Arthropoda : Amphipoda	CO	ABUN
Protohaustorius wigleyi	6169221202	94010	Haustoriidae	Arthropoda : Amphipoda	IN	ABUN
Rhepoxynius epistomus	6169421501	94728	Phoxocephalidae	Arthropoda : Amphipoda	IN	ABUN
Leucon americanus	6154040110	90790	Leuconidae	Arthropoda : Cumacea	IN	ABUN
Oxyurostylis smithi	6154050801	90923	Diastylidae	Arthropoda : Cumacea	IN	ABUN
Biffarius biformis	6183049999	552845	Callianassidae	Arthropoda : Decapoda	CO	BIOM
Panopeus herbstii	6189020801	98778	Xanthidae	Arthropoda : Decapoda	CO	BIOM
Rhithropanopeus harrisii	6189020901	98790	Xanthidae	Arthropoda : Decapoda	CO	ABUN&BIOM
Cyathura polita	6160010201	542646	Anthuridae	Arthropoda : Isopoda	CO	ABUN&BIOM
Edotea triloba	6162020703	92627	Idoteidae	Arthropoda : Isopoda	CO	ABUN
Sphaeroma quadridentatum	6161020702	92339	Sphaeromatidae	Arthropoda : Isopoda	CO	ABUN
Synidotea spp.	61620202	92566	Idoteidae	Arthropoda : Isopoda	CO	ABUN
Squilla empusa	6191010101	99143	Squillidae	Arthropoda : Stomatopoda	CO	BIOM
Ceriantheopsis americanus	3743010201	51991	Cerianthidae	Cnidaria : Anthozoa	CO	BIOM
Diadumene leucolena	3760080103	52749	Diadumenidae	Cnidaria : Anthozoa	CO	ABUN
Leptosynapta tenuis	8178010202	158432	Synaptidae	Echinodermata : Holothuroidea	IN	ABUN&BIOM
Microphiopholis atra	8129031201	---	Amphiuridae	Echinodermata : Ophiuroidea	IN	ABUN&BIOM
Tellina agilis	5515310205	81088	Tellinidae	Mollusca : Bivalvia	IN	ABUN&BIOM
Acteocina canaliculata	5110040103	76117	Scaphandridae	Mollusca : Gastropoda	CO	ABUN&BIOM
Hydrobiidae	510313	70493	Hydrobiidae	Mollusca : Gastropoda	CO	ABUN&BIOM
Littoridinops tenuipes	5103130501	70528	Hydrobiidae	Mollusca : Gastropoda	CO	ABUN
Nassarius trivittatus	5105080103	74109	Nassariidae	Mollusca : Gastropoda	CO	BIOM
Polinices duplicatus	5103760407	72918	Naticidae	Mollusca : Gastropoda	CO	BIOM
Rictaxis punctostriatus	5110010403	76083	Acteonidae	Mollusca : Gastropoda	CO	ABUN
Macoma *spp.*(BFS):						
Macoma balthica	5515310116	567846	Tellinidae	Mollusca : Bivalvia	M	ABUN&BIOM
Macoma mitchelli	5515310119	81054	Tellinidae	Mollusca : Bivalvia	M	ABUN&BIOM

Scientific Name	NODC	TSN	Family	Group Code Name	B-IBI Trophic Group	Qualifying Measure
Macoma tenta	5515310120	81055	Tellinidae	Mollusca : Bivalvia	M	BIOM
Benthic carnivores (BC):						
Aglaophamus verrilli	5001250303	66052	Nephtyidae	Annelida : Polychaeta	P	ABUN&BIOM
Bhawania heteroseta	5001080302	65159	Chrysopetalidae	Annelida : Polychaeta	P	ABUN
Brania clavata	5001230902	65761	Syllidae	Annelida : Polychaeta	P	ABUN
Brania wellfleetensis	5001230903	65762	Syllidae	Annelida : Polychaeta	P	ABUN
Cabira incerta	5001220401	65565	Pilargidae	Annelida : Polychaeta	P	ABUN
Eteone heteropoda	5001130207	65266	Phyllodocidae	Annelida : Polychaeta	P	ABUN
Glycera americana	5001270104	66106	Glyceridae	Annelida : Polychaeta	P	ABUN&BIOM
Glycera dibranchiata	5001270105	66107	Glyceridae	Annelida : Polychaeta	P	BIOM
Glycinde solitaria	5001280104	66132	Goniadidae	Annelida : Polychaeta	P	ABUN&BIOM
Laeonereis culveri	5001240801	65965	Nereididae	Annelida : Polychaeta	P	ABUN
Neanthes succinea	5001240309	65918	Nereididae	Annelida : Polychaeta	P	ABUN&BIOM
Nephtys bucera	5001250114	66027	Nephtyidae	Annelida : Polychaeta	P	BIOM
Nephtys picta	5001250117	66030	Nephtyidae	Annelida : Polychaeta	P	ABUN&BIOM
Phyllodoce arenae	5001131410	65366	Phyllodocidae	Annelida : Polychaeta	P	ABUN&BIOM
Podarkeopsis levifuscina	5001211999	555698	Hesionidae	Annelida : Polychaeta	P	ABUN
Pseudeurythoe paucibranchiata	5001100301	65176	Amphinomidae	Annelida : Polychaeta	P	ABUN
Sigambra tentaculata	5001220201	65552	Pilargidae	Annelida : Polychaeta	P	ABUN&BIOM
Carinoma tremaphoros	4302020101	57429	Carinomidae	Nemertina	P	ABUN
Micrura leidyi	4303020505	57477	Lineidae	Nemertina	P	BIOM
Nemertina	43	57411	Unidentified	Nemertina	P	ABUN&BIOM
Stylochus ellipticus	3906030101	54089	Stylochidae	Platyhelminthes : Turbellaria	P	ABUN
Turbellaria	3901	53964	Unidentified	Platyhelminthes : Turbellaria	P	ABUN
Benthic filter feeders (BFD):						
Chaetopterus variopedatus	5001490101	67097	Chaetopteridae	Annelida : Polychaeta	SU	BIOM
Ampelisca spp.	61690201	93321	Ampeliscidae	Arthropoda : Amphipoda	SU	ABUN&BIOM
Ampelisca verrilli	6169020110	93331	Ampeliscidae	Arthropoda : Amphipoda	SU	ABUN&BIOM
Molgula lutulenta	8406030120	159581	Molgulidae	Chordata : Ascidiacea	SU	ABUN&BIOM
Molgula manhattensis	8406030108	159557	Molgulidae	Chordata : Ascidiacea	SU	ABUN&BIOM
Branchiostoma caribaeum	8500010101	159682	Branchiostomidae	Chordata : Cephalochordata	SU	ABUN&BIOM

Scientific Name	NODC	TSN	Family	Group Code Name	B-IBI Trophic Group	Qualifying Measure
Aligena elevata	5515100602	80685	Kelliidae	Mollusca : Bivalvia	SU	ABUN
Anadara ovalis	5506010202	79342	Arcidae	Mollusca : Bivalvia	SU	BIOM
Anadara transversa	5506010201	79340	Arcidae	Mollusca : Bivalvia	SU	BIOM
Corbicula fluminea	5515450201	81387	Corbiculidae	Mollusca : Bivalvia	SU	ABUN&BIOM
Crassostrea virginica	5510020102	79872	Ostreidae	Mollusca : Bivalvia	SU	BIOM
Ensis directus	5515290301	81022	Solenidae	Mollusca : Bivalvia	SU	ABUN&BIOM
Gemma gemma	5515471301	81511	Veneridae	Mollusca : Bivalvia	SU	ABUN&BIOM
Geukensia demissa	5507011501	79555	Mytilidae	Mollusca : Bivalvia	SU	BIOM
Ischadium recurvum	5507011601	79561	Mytilidae	Mollusca : Bivalvia	SU	BIOM
Mercenaria mercenaria	5515471101	81496	Veneridae	Mollusca : Bivalvia	SU	BIOM
Mulinia lateralis	5515250301	80959	Mactridae	Mollusca : Bivalvia	SU	ABUN&BIOM
Mytilopsis leucophaeata	5515370201	81335	Dreissenidae	Mollusca : Bivalvia	SU	ABUN
Mytilus edulis	5507010101	79454	Mytilidae	Mollusca : Bivalvia	SU	BIOM
Parvilucina crenella	5515010102	80388	Lucinidae	Mollusca : Bivalvia	SU	ABUN&BIOM
Rangia cuneata	5515250401	80962	Mactridae	Mollusca : Bivalvia	SU	ABUN&BIOM
Tagelus plebeius	5515330201	81272	Solecurtidae	Mollusca : Bivalvia	SU	BIOM
Phoronis spp.	77000102	155462	Phoronidae	Phoronida	SU	ABUN&BIOM

Table 11. Biomass estimates (wet weight) for vertebrate functional groups at start of model run (2002), specific to Chesapeake Bay, and information sources used. Estimates for aggregate groups represent summary values weighted by relative abundance of each species in the group in Chesapeake Bay. Preliminary biomass estimates were based on a variety of available sources shown in the final column of the table. Preliminary biomass estimates were fed into an Ecopath model that was built expressly for balancing the initial CAM groups; "---" indicates no information was available to use for Ecopath; consequently, starting biomass for such groups was estimated solely by the Ecopath model. Balanced Ecopath estimates for all birds, reptiles, and bottlenose dolphin differed only slightly from preliminary biomass estimates, so the preliminary estimates were used as starting biomass for CAM in these instances. Landings data were obtained from the NOAA Office of Science and Technology for the calendar year 2002 (personal communication; commercial: M. Lewis, 1/19/11; recreational: L. Dolinger-Few, 1/31/11). Bird data obtained from the Cornell Lab of Ornithology at: http://bna.birds.cornell.edu/bna/species (accessed October 2010). SA = stock assessment.

Common name	**Scientific name**	**Group code**	**Prelim. biomass (mt)**	**Starting biomass (mt)**	**Source(s) for biomass estimates**
Gizzard shad	*Dorosoma cepedianum*	FPL	57	9,399	Landings data
Bay anchovy	*Anchoa mitchilli*	FPO	---	9,710	Ecopath
Atl. menhaden	*Brevoortia tyrannus*	FPS	6,200	177,915	2006 ASMFC SA; landings data
Summer flounder	*Paralichthys dentatus*	FVD	1,088	4,965	2006 NMFS SA Update, age 2–7; landings data
Weakfish	*Cynoscion regalis*	FVS	254	1,470	2009 48th SAW; landings data
Catfish:		FVB	282	4,187	Landings data
- Channel catfish	*Ictalurus punctatus*				
- Blue catfish	*Ictalurus furcatus*				
- White catfish	*Ameiurus catus*				
- Flathead catfish	*Pylodictis olivaris*				
- Black bullhead	*Ameiurus melas*				
Bluefish	*Pomatomus saltatrix*	FVT	1,630	1,365	2003 ASMFC SA; landings data
Alosines:		FMM	53	12,494	Landings data
- American shad	*Alosa sapidissima*				
- Alewife	*Alosa pseudoharengus*				
- Blueback shad	*Alosa aestivalis*				
- Hickory shad	*Alosa mediocris*				
Butterfish	*Peprilus triacanthus*	FMN	0.23	1,234	Landings data
Striped bass	*Morone saxatilis*	FBP	15,962	15,962	Landings data

Common name	Scientific name	Group code	Prelim. biomass (mt)	Starting biomass (mt)	Source(s) for biomass estimates
Atl. croaker	*Micropogonias undulatus*	FDD	16,976	6,227	2010 ASMFC SA; landings data
Panfish:		FDE	721	8,662	Landings data
- Spot	*Leiostomus xanthurus*				
- Yellow perch	*Perca flavescens*				
- Bluegill	*Lepomis macrochirus*				
- Silver Perch	*Bairdiella chrysoura*				
White perch	*Morone americana*	FDS	979	4,715	Landings data
Reef assoc. fish:		FDM	119	1,027	2006 ASMFC Tautog SA; landings data
- Atlantic spadefish	*Chaetodipterus faber*				
- Tautog	*Tautoga onitis*				
- Black seabass	*Centropristis striata*				
- Oyster toadfish	*Opsanus tau*				
Forage fish:		FDP	0.16	20,051	Landings data
- Atlantic silverside	*Menidia menidia*				
- Mummichog	*Fundulus heteroclitus*				
Bottom fish:		FDC	3.35	9,308	Landings data
- Spotted hake	*Urophycis regia*				
- Inshore lizardfish	*Synodus foetens*				
- Northern searobin	*Prionotus carolinus*				
Black drum	*Pogonias cromis*	FDO	21	5,029	Landings data
Other flatfish:		FDF	---	20,691	Ecopath
- Windowpane	*Scophthalmus aquosus*				
- Hogchoker	*Trinectes maculatus*				
- Blackcheek tonguefish	*Symphurus plagiusa*				
- Winter flounder	*Pseudopleuronectes americanus*				
Smooth dogfish	*Mustelus canis*	SHB	3	1,363	Landings data
Sandbar shark	*Carcharhinus plumbeus*	SHD	55	152	Landings data
Spiny dogfish	*Squalus acanthias*	SHC	1,363	7,099	2010 TRAC status report - Atlantic coast females; landings data
Cownose ray	*Rhinoptera bonasus*	SSK	6	480	Landings data

Common name	Scientific name	Group code	Prelim. biomass (mt)	Starting biomass (mt)	Source(s) for biomass estimates
Benthic grazing seabirds: - Canada goose - Mallard - Redhead - Tundra swan - Mute swan	*Branta canadensis* *Anas platyrhynchos* *Aythya americana* *Cygnus columbianus* *Cygnus olor*	FVO	1,076	1,076	D. Forsell, USF&W (unpublished data); Cornell Lab of Ornithology
Diving ducks: - Surf scoter - Long-tailed duck	*Melanitta perspicillata* *Clangula hyemalis*	SB	56	56	D. Forsell, USF&W (unpublished data); Cornell Lab of Ornithology
Piscivorous seabirds: - Osprey - Great blue heron - Brown pelican - Double-crested cormorant	*Pandion haliaetus* *Ardea herodias* *Pelecanus occidentalis* *Phalacrocorax auritus*	SP	218	218	D. Forsell, USF&W (unpublished data); Cornell Lab of Ornithology
Bald eagles	*Haliaeetus leucocephalus*	PIN	24	24	D. Forsell, USF&W (unpublished data); Cornell Lab of Ornithology
Diamond-back terrapin	*Malaclemys terrapin*	FVV	4,132	4,132	Expert knowledge (Randy Chambers, College of William & Mary)
Sea turtles: - Loggerhead - Kemp's Ridley - Leatherback	*Caretta caretta* *Lepidochelys kempii* *Dermochelys coriacea*	REP	193	193	Byles (1989); Keinath (1993); Plotkin (1995); Coles (1999); Kobell (2010)
Bottlenose dolphin	*Tursiops truncatus*	WHS	322	322	Trites and Pauly (1998); Barco et al. (1999); Neuenhoff et al. (2010)

Table 12. Vertebrate life history parameterization. Parameters for aggregate groups represent summary values weighted by relative abundance of each species in the group. Natural mortality, *M*, was used only to set up the initial age structure for model runs. Likewise, *k*, *L*inf were used only to parameterize initial size structure, where *k* is the VonBertalanffy growth coefficient and *L*inf is theoretical maximum size (cm). Growth of birds and dolphin were assumed to follow a Gompertz growth curve; "a" and "b" are constants of the length–weight relationship ($W=aL^b$). "A_m" values indicate age class of group at first maturity and are post-calibration values. "A_r" is age at recruitment to the modeled population (i.e., approximate age of transformation from larval to juvenile stage). BHalpha and BHbeta are based on the Beverton-Holt recruitment model, but these values are specific to the Atlantis model, where BHalpha is the estimate of the maximum number of recruits that can be produced (system-wide), and BHbeta is the biomass of mature adults (both sexes) that produces one-half Bhalpha. R_{Fixed} is the fixed number of new recruits per individual (per year). Linear mortality is set at '0' for all vertebrates and is not included in the table. Quadratic mortality values are included in the model to limit uncontrolled, explosive growth of any particular group. Efficiency is the portion of food not immediately lost to sloppy feeding by each group. "NA" = not applicable. Additional details for life history parameterization and references are found in Appendix C. Common name corresponding to code for each vertebrate group modeled can be found in Table 11 or Table 13.

Code	***M* (*per year*)**	***k***	***L*inf**	**Max age (yr)**	**a**	**b**	**A_m**	**A_r (days)**	**BHalpha**	**BHbeta**	**R_{fixed}**	**Juvenile quadratic mortality (per day)**	**Adult quadratic mortality (per day)**	**Efficiency**
FPL	0.41	0.18	43.60	10.0	0.020	2.99	3	60	7.51E+09	1.04E+10	NA	1.0E-10	5.0E-11	0.70
FPO	2.30	0.52	11.00	2.0	0.010	3.00	1	60	1.05E+15	1.02E+08	NA	8.5E-12	1.0E-09	0.80
FPS	0.75	0.48	36.90	10.0	0.130	3.11	2	60	7.51E+10	1.21E+11	NA	1.0E-10	1.0E-15	0.80
FVD	0.46	0.84	137.00	10.0	0.010	3.12	2	60	1.00E+07	1.14E+09	NA	1.0E-07	5.0E-08	0.65
FVS	0.27	0.26	82.30	17.0	0.010	2.98	1	60	8.56E+07	6.64E+09	NA	1.0E-10	1.0E-10	0.65
FVB	0.16	0.06	77.60	17.8	0.011	3.08	3	60	3.77E+06	2.87E+08	NA	1.0E-20	1.0E-13	0.55
FVT	0.35	0.17	97.53	9.0	0.020	2.89	2	60	3.54E+06	6.19E+11	NA	1.0E-10	1.0E-12	0.10
FMM	0.49	0.47	49.10	10.3	0.007	2.80	4	24	3.00E+08	1.20E+11	NA	1.0E-12	6.0E-11	0.80
FMN	0.80	0.80	23.15	1.5	0.011	3.17	1	30	3.95E+09	2.03E+11	NA	1.0E-15	1.0E-16	0.60
FBP	0.14	0.15	119.25	30.0	0.010	3.09	2	60	2.92E+07	1.92E+10	NA	1.0E-10	1.0E-07	0.50
FDD	0.88	0.57	40.90	17.0	0.004	3.20	1	60	8.20E+08	2.65E+10	NA	1.0E-11	1.0E-09	0.70
FDE	0.67	1.08	26.59	7.8	0.015	3.07	2	60	4.80E+09	8.33E+09	NA	1.0E-09	1.0E-09	0.55
FDS	0.38	0.07	52.00	12.0	0.010	3.12	3	60	3.40E+10	1.05E+09	NA	1.0E-09	1.0E-09	0.80
FDM	0.33	0.33	38.73	16.5	0.040	2.74	1	26	3.72E+07	8.37E+10	NA	1.0E-10	1.0E-08	0.30

Code	***M* (*per year*)**	***k***	***L*inf**	**Max age (yr)**	**a**	**b**	**A_m**	**A_r (days)**	**BHalpha**	**BHbeta**	**R_{fixed}**	**Juvenile quadratic mortality (per day)**	**Adult quadratic mortality (per day)**	**Efficiency**
FDP	3.45	1.24	14.55	1.5	0.010	3.02	1	30	1.34E+13	6.24E+09	NA	1.0E-10	5.0E-08	0.60
FDC	0.63	0.30	34.84	7.0	0.010	3.03	2	60	5.66E+09	1.11E+10	NA	1.0E-09	1.0E-09	0.50
FDO	0.09	0.15	94.80	43.0	0.020	2.95	1	60	1.53E+09	5.10E+09	NA	1.0E-09	1.0E-13	0.50
FDF	0.56	0.31	28.74	8.5	0.024	2.96	4	60	2.74E+09	2.83E+10	NA	1.0E-09	5.0E-09	0.80
SHB	0.11	0.04	150.00	16.0	0.230	3.10	2	60	NA	NA	2.50	2.0E-11	1.0E-13	0.50
SHD	0.12	0.06	267.00	32.0	0.010	3.27	5	60	NA	NA	6.00	1.0E-17	1.0E-11	0.70
SHC	0.09	0.06	123.00	75.0	0.004	3.06	3	60	NA	NA	5.00	1.0E-12	1.0E-11	0.70
SSK	0.17	0.08	124.00	18.0	0.005	3.19	2	60	NA	NA	2.00	3.0E-10	5.0E-06	0.80
FVO	0.28	NA	92.15	23.5	0.118	2.19	1	68	NA	NA	3.00	5.0E-15	1.0E-11	0.10
SB	0.27	NA	44.77	20.0	0.091	2.42	1	48	NA	NA	3.65	1.0E-07	1.0E-07	0.30
SP	0.20	NA	113.88	15.3	0.099	2.20	1	58	NA	NA	6.00	1.0E-13	1.0E-15	0.70
PIN	0.20	NA	87.89	28.0	0.004	2.60	2	119	NA	NA	1.50	1.0E-05	1.0E-05	0.10
FVV	0.16	0.15	32.11	40.0	0.035	3.00	2	71	NA	NA	17.00	5.0E-09	5.0E-09	0.10
REP	0.29	0.08	98.97	60.8	0.153	3.00	5	56	NA	NA	40.00	5.0E-05	6.5E-08	0.10
WHS	0.11	NA	385.01	40.0	0.123	2.43	2	105	NA	NA	0.13	2.0E-13	4.0E-07	0.50

Table 13. Post-calibration growth parameter settings used in the functional response for each vertebrate functional group and age class (mgN/day) in CAM (corresponds to parameter "mum" in bio.prm file).

		Age class									
Common name	**Group code**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Gizzard shad	FPL	6.12	21.83	42.88	132.40	179.54	224.74	266.61	304.49	338.19	367.78
Bay anchovy	FPO	0.01	0.03	0.06	0.10	0.15	0.20	0.25	0.30	0.35	0.40
Atl. menhaden	FPS	123.46	123.43	196.16	250.48	287.78	312.32	328.09	338.07	344.34	348.26
Summer flounder	FVD	1000.82	8573.78	11186.32	12427.40	12983.43	13226.82	13332.33	13377.89	13397.52	13405.98
Weakfish	FVS	16.45	652.89	991.35	1227.54	1380.44	1475.77	1534.02	1569.21	1590.33	1602.96
Catfish	FVB	2.94	162.87	445.99	738.42	1066.17	1412.90	1766.09	2116.43	2457.20	2783.73
Bluefish	FVT	218.55	375.54	362.41	553.93	746.72	931.36	1102.58	1257.87	1396.45	1518.65
Alosines	FMM	6.00	13.00	20.00	25.00	28.00	31.00	32.00	32.40	33.00	33.60
Butterfish	FMN	0.25	2.41	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Striped bass	FBP	170.40	693.00	1117.20	1444.80	1680.00	1839.60	1940.40	2007.60	2058.00	2083.20
Atl. croaker	FDD	20.19	113.02	133.74	140.80	143.11	143.86	144.10	144.17	144.20	144.21
Panfish	FDE	20.31	53.34	63.42	67.20	68.46	68.88	68.88	68.88	68.88	68.88
White perch	FDS	0.22	2.81	6.31	10.96	16.54	22.87	29.75	37.04	44.60	52.32
Reef fish	FDM	19.30	42.72	57.84	66.72	71.28	73.68	75.12	75.60	76.08	76.32
Forage fish	FDP	0.11	0.27	0.08	0.12	0.16	0.20	0.23	0.26	0.29	0.32
Bottom fish	FDC	2.09	6.78	12.13	17.15	21.47	25.00	27.80	29.98	31.65	32.91
Black drum	FDO	20.82	51.32	73.98	88.22	96.56	101.29	103.93	105.40	106.20	106.64
Other flatfish	FDF	4.92	21.50	26.88	52.50	46.44	75.10	59.28	89.04	66.60	96.60
Smooth dogfish	SHB	0.50	2.04	4.52	7.76	11.58	15.84	20.41	25.17	30.04	34.94
Sandbar shark	SHD	40.48	369.33	866.06	2806.94	3945.32	5077.72	6159.36	7163.87	8077.96	8897.18
Spiny dogfish	SHC	29.70	251.90	399.42	510.07	586.54	637.20	669.98	690.90	704.14	712.47
Cownose ray	SSK	4.68	56.12	118.61	193.51	274.46	356.82	437.36	513.99	585.46	651.12
Benthic grazing seabirds	FVO	2577.71	2577.71	2577.71	2577.71	2577.71	2577.71	2577.71	2577.71	2577.71	2577.71
Diving ducks	SB	1000.00	1100.00	1100.00	1100.00	1100.00	1100.00	1100.00	1100.00	1100.00	1000.00

		Age class									
Common name	**Group code**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Piscivorous seabirds	SP	1226.67	404.80	404.80	1226.67	1226.67	1226.67	1226.67	1226.67	1226.67	1226.67
Bald eagles	PIN	4400.00	4400.00	4620.00	4620.00	4620.00	4620.00	4620.00	4620.00	4620.00	4400.00
Diamond-back terrapin	FVV	3.62	9.06	13.16	15.75	17.28	18.15	18.63	18.90	19.05	19.13
Sea turtles	REP	289.04	1243.58	2378.39	3357.32	4089.84	4599.00	4938.54	5159.53	5301.27	5391.37
Bottlenose dolphin	WHS	42234.33	52973.68	55229.68	55441.65	55469.27	55472.86	55473.33	55473.39	55473.40	55473.40

Table 14. Post-calibration clearance rates used in the functional response for each vertebrate functional group and age class (mg^3/mgN/day).

		Age class									
Common name	**Group code**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Gizzard shad	FPL	0.61	2.18	4.29	13.24	17.95	22.47	26.66	30.45	33.82	36.78
Bay anchovy	FPO	0.00	0.01	0.01	0.02	0.02	0.03	0.04	0.05	0.06	0.07
Atl. menhaden	FPS	12.35	12.34	19.62	25.05	28.78	31.23	32.81	33.81	34.43	34.83
Summer flounder	FVD	100.08	857.38	1118.63	1242.74	1298.34	1322.68	1333.23	1337.79	1339.75	1340.60
Weakfish	FVS	2.63	104.46	158.62	196.41	220.87	236.12	245.44	251.07	254.45	256.47
Catfish	FVB	0.29	16.29	44.60	73.84	106.62	141.29	176.61	211.64	245.72	278.37
Bluefish	FVT	21.86	37.55	36.24	55.39	74.67	93.14	110.26	125.79	139.64	151.86
Alosines	FMM	0.60	1.30	2.00	2.50	2.80	3.10	3.20	3.24	3.30	3.36
Butterfish	FMN	0.02	0.24	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
Striped bass	FBP	27.26	110.88	178.75	231.17	268.80	294.34	310.46	321.22	329.28	333.31
Atl. croaker	FDD	2.02	11.30	13.37	14.08	14.31	14.39	14.41	14.42	14.42	14.42
Panfish	FDE	3.25	8.53	10.15	10.75	10.95	11.02	11.02	11.02	11.02	11.02
White perch	FDS	0.04	0.45	1.01	1.75	2.65	3.66	4.76	5.93	7.14	8.37
Reef fish	FDM	3.09	6.84	9.25	10.68	11.40	11.79	12.02	12.10	12.17	12.21
Forage fish	FDP	0.01	0.03	0.01	0.01	0.02	0.02	0.02	0.03	0.03	0.03
Bottom fish	FDC	0.21	1.08	1.94	2.74	3.44	4.00	4.45	4.80	5.06	5.27
Black drum	FDO	2.08	5.13	7.40	8.82	9.66	10.13	10.39	10.54	10.62	10.66
Other flatfish	FDF	0.79	3.44	4.30	8.40	7.43	12.02	9.48	14.25	10.66	15.46
Smooth dogfish	SHB	0.08	0.33	0.72	1.24	1.85	2.53	3.27	4.03	4.81	5.59
Sandbar shark	SHD	4.05	36.93	86.61	280.69	394.53	507.77	615.94	716.39	807.80	889.72
Spiny dogfish	SHC	2.97	25.19	39.94	51.01	58.65	63.72	67.00	69.09	70.41	71.25
Cownose ray	SSK	0.47	8.98	18.98	30.96	43.91	57.09	69.98	82.24	93.67	104.18
Benthic grazing seabirds	FVO	257.77	257.77	257.77	257.77	257.77	257.77	257.77	257.77	257.77	257.77
Diving ducks	SB	150.00	150.00	150.00	150.00	150.00	150.00	150.00	150.00	150.00	150.00
Piscivorous seabirds	SP	122.67	40.48	40.48	122.67	122.67	122.67	122.67	122.67	122.67	122.67
Bald eagles	PIN	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00
Diamond-back terrapin	FVV	0.36	0.91	1.32	1.58	1.73	1.81	1.86	1.89	1.91	1.91
Sea turtles	REP	28.90	124.36	237.84	335.73	408.98	459.90	493.85	515.95	530.13	539.14
Bottlenose dolphin	WHS	4223.43	5297.37	5522.97	5544.16	5546.93	5547.29	5547.33	5547.34	5547.34	5547.34

Table 15. Timing of reproductive and migration events for vertebrate groups in CAM. The terrapin group (FVV) remains in the Bay system throughout the year; however, for modeling, it is assumed the group effectively migrates when they overwinter buried in the mud, since they do not actively affect other groups in the model during this period. Striped bass (FBP) is the only population that has a partial migration in CAM (we assume one-half the population is resident year-round in the Bay); all other migrating populations move as a whole. DOY = day of the year. NA indicates that the timing parameter does not apply to that non-migratory group.

Group code	Group migrates	Juveniles migrate in (DOY)	Juveniles migrate out (DOY)	Adults migrate in (DOY)	Adults spawn (or mate) (DOY)	Spawning (mating) duration (days)	Adults migrate out (DOY)
FPL	Yes	196	46	258	60	90	46
FPO	No	NA	NA	NA	152	90	NA
FPS	Yes	319	277	105	335	90	288
FVD	Yes	15	319	105	244	90	319
FVS	Yes	105	319	105	121	90	319
FVB	No	NA	NA	NA	91	60	NA
FVT	Yes	288	319	105	182	30	196
FMM	Yes	288	46	46	50	60	94
FMN	Yes	196	319	105	121	90	319
FBP	Yes	74	319	74	60	90	319
FDD	Yes	105	288	105	182	150	288
FDE	No	NA	NA	NA	60	60	NA
FDS	Yes	105	74	105	90	90	74
FDM	No	NA	NA	NA	121	60	NA
FDP	No	NA	NA	NA	91	90	NA
FDC	No	NA	NA	NA	15	90	NA
FDO	Yes	105	319	105	91	60	319
FDF	No	NA	NA	NA	91	60	NA
SHB	Yes	319	166	319	121	120	166
SHD	Yes	135	288	135	121	30	288
SHC	Yes	319	105	319	305	60	105
SSK	Yes	135	288	135	180	21	288
FVO	Yes	166	46	166	91	100	46
SB	Yes	364	0	319	121	70	46
SP	Yes	105	15	105	60	90	15
PIN	No	NA	NA	NA	74	60	NA
FVV	Yes	74	288	74	121	60	288
REP	Yes	135	319	135	182	180	319
WHS	Yes	105	258	105	60	180	258

Table 16. Pre-calibration prey availability matrix. A '0' indicates there can be no availability of the prey to the predator in the model. Predator groups are listed on the left side of the matrix while prey groups are listed along the top. As availability increases, a predator's impact on prey abundance increases, given both spatial overlap of predator and prey, and limited habitat populations (BFF, SG, MA), which provide refuge from predation for many prey groups. Where data was lacking, but the authors believe a predator-prey relationship exists (e.g., soft-bodied invertebrate remains are not typically identifiable in vertebrate gut content studies), a small, arbitrary number was added to predator diet to allow such groups to interact in the model. When no prey information was available for a particular predator, assumed prey items were all assigned a uniform availability.

[Editor's note: Table 16, too large to be included in this print version, is available as an Excel file linked from the online PDF of this report.]

Table 17. Post-calibration prey availability matrix. A '0' indicates there can be no availability of the prey to the predator in the model. Predator groups are listed on the left side of the matrix while prey groups are listed along the top. As availability increases, a predator's impact on prey abundance increases, given both spatial overlap of predator and prey, and limited habitat populations (BFF, SG, MA), which provide refuge from predation for many prey groups. Where data was lacking, but the authors believe a predator-prey relationship exists (e.g., soft-bodied invertebrate remains are not typically identifiable in vertebrate gut content studies), a very small, arbitrary number was added to predator diet to allow such groups to interact in the model. When no prey information was available for a particular predator, assumed prey items were all assigned a uniform availability.

[Editor's note: Table 17, too large to be included in this print version, is available as an Excel file linked from the online PDF of this report.]

Table 18. Habitat dependencies for age-structured groups in CAM. For any group, a '1' for one or more of the habitat types indicates at that at least one of the indicated habitats must occur in a CAM box to allow the group to move into that CAM box.

							Biogenic habitats		
Common name	**Code**	**Prey age**	**Rock or artificial reef**	**Sand**	**Mud**	**Woody debris**	**SAV**	**Marsh**	**Oyster reef**
Brief squid	CEP	Juvenile	1	1	1	0	1	0	1
		Adult	1	1	1	0	1	0	1
Blue crab	PWN	Juvenile	0	0	1	1	1	1	0
		Adult	1	1	1	1	1	1	1
Atlantic menhaden	FPS	Juvenile	0	0	0	0	1	1	0
		Adult	1	1	1	0	1	1	1
Gizzard shad	FPL	Juvenile	0	0	0	0	1	1	0
		Adult	1	1	1	0	1	1	1
Bay anchovy	FPO	Juvenile	0	0	0	0	1	1	0
		Adult	0	0	0	0	1	1	0
Summer flounder	FVD	Juvenile	0	0	0	0	1	1	0
		Adult	0	1	1	0	1	1	0
Terrapin	FVV	Juvenile	0	0	0	1	0	1	0
		Adult	0	0	0	1	0	1	0
Weakfish	FVS	Juvenile	0	0	0	1	1	1	0
		Adult	1	1	1	0	1	0	1
Bluefish	FVT	Juvenile	0	0	0	0	1	1	0
		Adult	1	1	1	0	1	0	1
Benthic grazing seabirds	FVO	Juvenile	0	0	0	0	1	1	0
		Adult	0	0	1	0	1	1	0
Catfish	FVB	Juvenile	1	0	1	1	1	1	0
		Adult	0	0	1	1	1	1	0
Alosines	FMM	Juvenile	0	0	0	0	1	1	0
		Adult	0	1	1	0	1	1	0
Butterfish	FMN	Juvenile	1	1	1	0	1	0	1
		Adult	1	1	1	0	1	0	1
Striped bass	FBP	Juvenile	0	0	0	1	1	1	0
		Adult	1	1	1	0	1	1	1
Atlantic croaker	FDD	Juvenile	0	0	0	1	1	1	0
		Adult	0	1	0	0	1	1	0
White perch	FDS	Juvenile	0	0	0	1	1	1	0
		Adult	0	0	0	1	1	1	0

							Biogenic habitats		
Common name	**Code**	**Prey age**	**Rock or artificial reef**	**Sand**	**Mud**	**Woody debris**	**SAV**	**Marsh**	**Oyster reef**
Bottom fish	FDC	Juvenile	0	0	0	0	1	1	0
		Adult	1	1	1	1	1	1	1
Black drum	FDO	Juvenile	0	0	0	1	1	1	0
		Adult	0	1	1	0	1	1	0
Panfish	FDE	Juvenile	0	0	0	1	1	1	0
		Adult	0	0	0	1	1	1	0
Other flatfish	FDF	Juvenile	0	0	0	0	1	1	0
		Adult	0	1	1	0	1	1	0
Reef fish	FDM	Juvenile	1	0	0	1	1	1	1
		Adult	1	1	0	0	1	0	1
Forage fish	FDP	Juvenile	0	0	0	1	1	1	0
		Adult	0	0	0	1	1	1	0
Sandbar shark	SHD	Juvenile	1	1	1	0	1	1	1
		Adult	1	1	1	0	1	0	1
Spiny dogfish	SHC	Juvenile	1	1	1	0	1	0	1
		Adult	1	1	1	0	1	0	1
Smooth dogfish	SHB	Juvenile	0	0	0	0	0	1	0
		Adult	0	1	1	0	1	1	0
Cownose ray	SSK	Juvenile	0	1	1	0	1	1	1
		Adult	1	1	1	0	1	0	1
Diving ducks	SB	Juvenile	0	1	1	0	1	1	0
		Adult	0	1	1	0	1	1	0
Piscivorous seabirds	SP	Juvenile	0	0	0	0	1	1	0
		Adult	0	0	0	0	1	1	0
Sea turtles	REP	Juvenile	1	1	1	0	1	0	1
		Adult	1	1	1	0	1	1	1
Bald eagles	PIN	Juvenile	1	1	1	0	1	1	1
		Adult	1	1	1	0	1	1	1
Bottlenose dolphin	WHS	Juvenile	1	1	1	0	1	0	1
		Adult	1	1	1	0	1	0	1
Macoma clams	BFS	All	0	1	1	0	1	1	0
Oysters	BFF	All	0	1	0	0	0	1	1
Benthic filter feeders	BFD	All	1	1	1	1	1	1	1
Sea nettles	ZL	All	1	1	1	0	1	0	1

Common name	Code	Prey age	Rock or artificial reef	Sand	Mud	Woody debris	Biogenic habitats SAV	Marsh	Oyster reef
Ctenophores	ZG	All	1	1	1	0	1	0	1
Benthic carnivores	BC	All	1	0	1	1	1	1	1
Bottom feeders	BD	All	1	1	1	1	1	1	1
Marsh grasses	MA	All	0	0	1	0	0	1	1
SAV	SG	All	0	1	1	0	1	0	0

Table 19. Scalar values (*Acov*) used in refuge relationships of age-structured CAM groups with biogenic habitat. Higher values of *Acov* mean more protection for prey if biogenic habitat is available. See text and Figure 7 for details.

Common name	**Group code**	**Prey age**	***Acov***
Atl. Menhaden	FPS	Juvenile	0.1
		Adult	0.1
Gizzard shad	FPL	Juvenile	0.1
		Adult	0.1
Bay anchovy	FPO	Juvenile	0.1
		Adult	0.1
Weakfish	FVS	Juvenile	0.1
		Adult	1.0
Summer flounder	FVD	Juvenile	0.1
		Adult	1.0
Terrapin	FVV	Juvenile	0.1
		Adult	0.1
Bluefish	FVT	Juvenile	0.1
		Adult	1.0
Benthic grazing seabirds	FVO	Juvenile	0.1
		Adult	0.1
Catfish	FVB	Juvenile	0.1
		Adult	1.0
Alosines	FMM	Juvenile	0.1
		Adult	0.1
Butterfish	FMN	Juvenile	0.1
		Adult	1.0
Striped bass	FBP	Juvenile	0.1
		Adult	1.0
White Perch	FDS	Juvenile	0.1
		Adult	0.1
Atl. croaker	FDD	Juvenile	0.1
		Adult	0.1
Bottom fish	FDC	Juvenile	0.1
		Adult	1.0
Black drum	FDO	Juvenile	0.1
		Adult	0.1
Panfish	FDE	Juvenile	0.1
		Adult	0.1
Other flatfish	FDF	Juvenile	0.1
		Adult	0.1
Reef fish	FDM	Juvenile	0.1
		Adult	1.0
Forage fish	FDP	Juvenile	0.1
		Adult	0.1
Sandbar shark	SHD	Juvenile	1.0
		Adult	1.0
Spiny dogfish	SHC	Juvenile	1.0
		Adult	1.0
Smooth dogfish	SHB	Juvenile	0.1
		Adult	1.0
Cownose ray	SSK	Juvenile	1.0
		Adult	1.0
Diving ducks	SB	Juvenile	0.1
		Adult	0.1
Piscivorous seabirds	SP	Juvenile	0.1
		Adult	0.1
Sea turtles	REP	Juvenile	1.0
		Adult	1.0
Bald eagles	PIN	Juvenile	1.0
		Adult	1.0
Bottlenose dolphin	WHS	Juvenile	1.0
		Adult	1.0

Table 20. Production changes predicted with TMDL nutrient and sediment reductions. Production values of all ecological groups of the TMDL reduction scenario were compared to those of the base model. Percentages shown are 11-year median differences in biomass for years 60 to 70 of each scenario.

Percent difference (range)	**Count**	**Number negative (predicted loss)**	**Group common name**
0–1	25	(9)	(+): bald eagle, blue crab, benthic carnivores, benthic grazing seabirds, bottlenose dolphin, butterfish, cownose ray, ctenophores, forage fish, mesozooplankton, piscivorous seabirds, reef fish, sandbar shark, sea nettles, smooth dogfish, weakfish; (-): Atlantic menhaden, bluefish, benthic filter feeders, dissolved inorganic nitrogen, sea turtles, brief squid, terrapin, Macoma clams, large phytoplankton
> 1–3	15	(5)	(+): Atlantic croaker, bay anchovy, black drum, bottom fish, diving ducks, marsh grasses, spiny dogfish, striped bass, summer flounder, oysters; (-): bottom feeders, detritus-refractory, gizzard shad, meiobenthos, picophytoplankton
> 3–5	3	(2)	(+): white perch; (-): microzooplankton, pelagic bacteria
> 5–7	7	(3)	(+): alosines, catfish, other flatfish, panfish; (-): benthic bacteria, detritus-labile, SAV
> 7–9	0	(0)	--
> 9–11	0	(0)	--
> 11	2	(1)	(+): dinoflagellates; (-): microphytobenthos

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Appendix A: Map Information

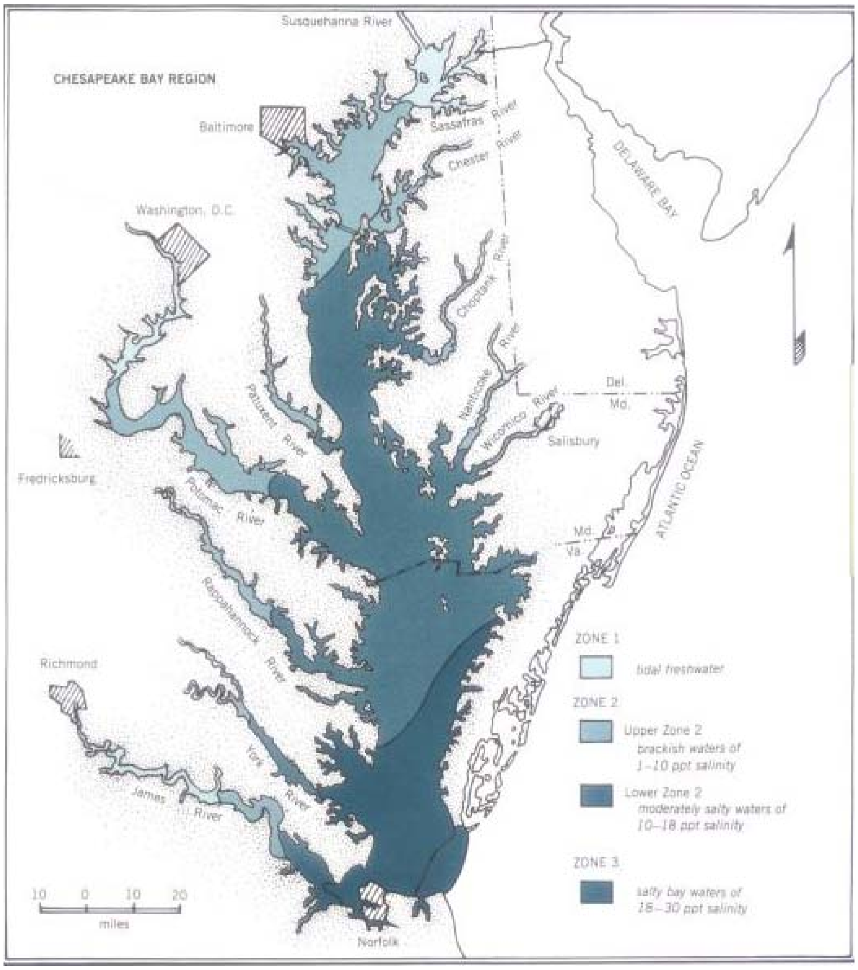
Chesapeake Bay Atlantis Model

Construction Log for Dynamic Boxes (24 AUG 2010)

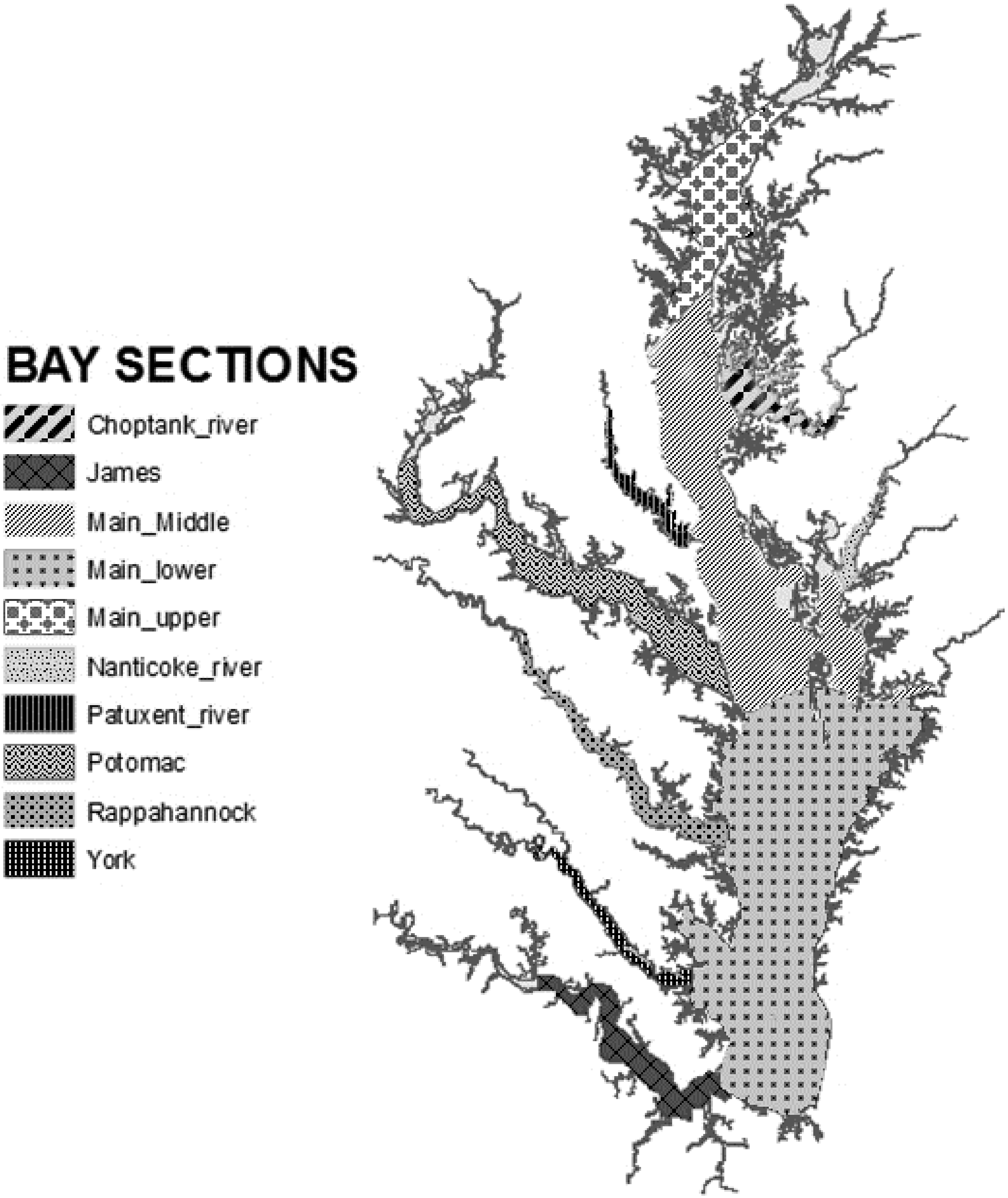
Methods:

Spatial variables

1. SALINITY (follows Lippson and Lippson, 1997)
   Model covers 3 salinity zones: 0–10 ppt, 10–18 ppt, and 18–30 ppt.

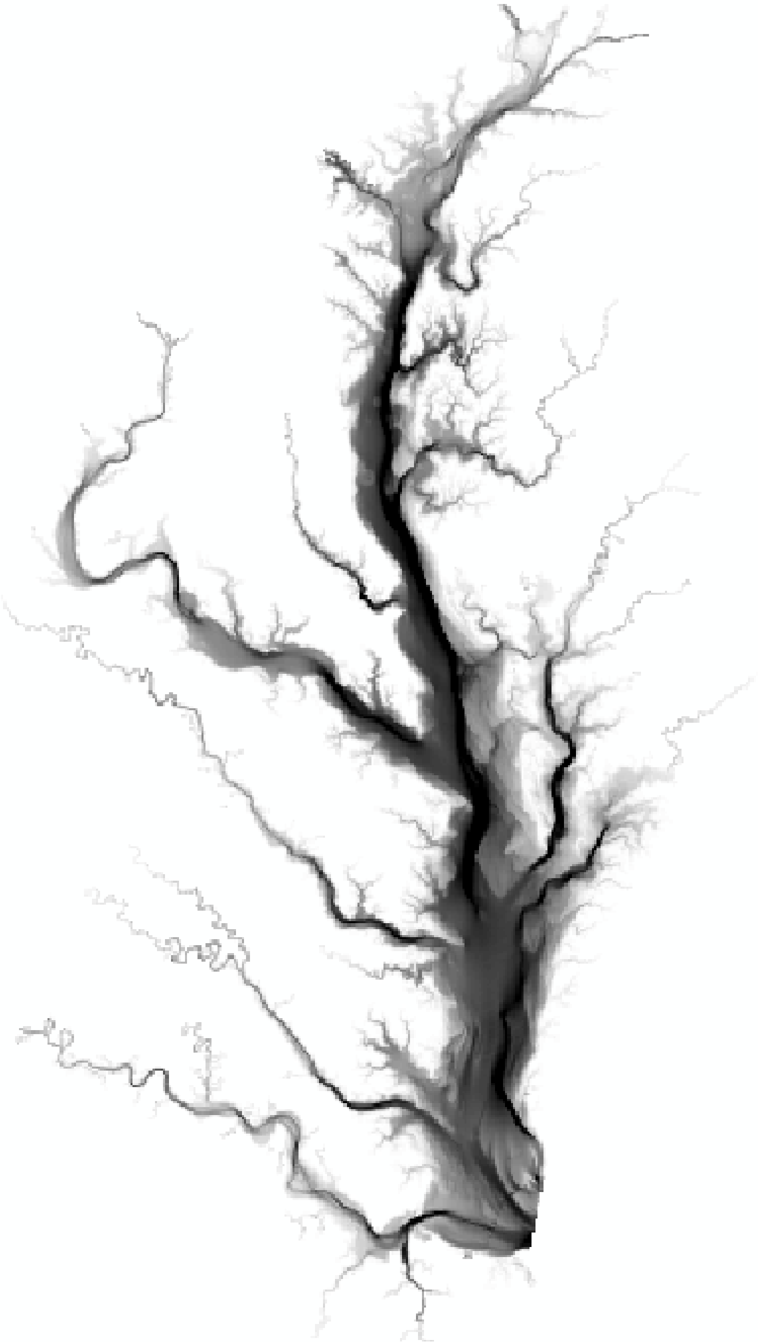


2. BAY SECTION/TRIBUTARY

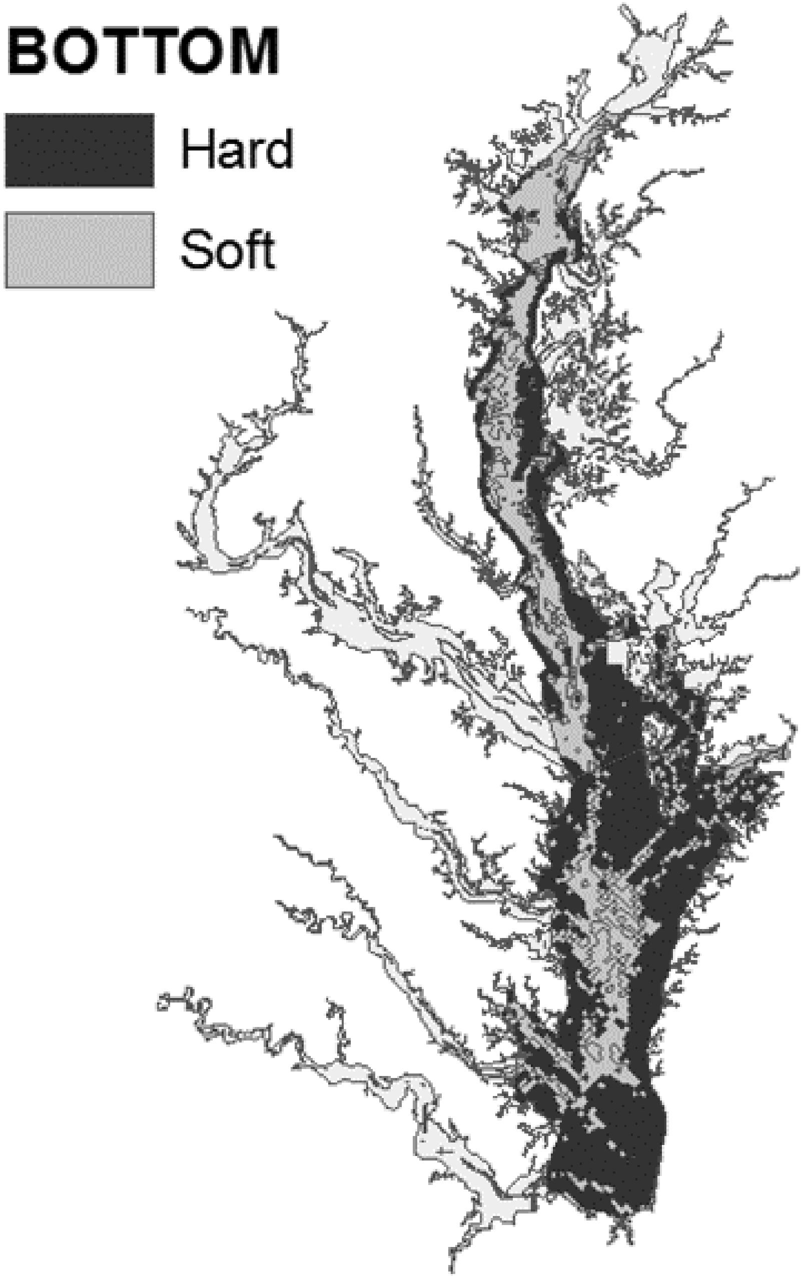


3. BATHYMETRY

Bay outline and bathymetry data derived from 10 m x 10 m grid named “bathygrid” (see Bathymetry Metadata at end of section).

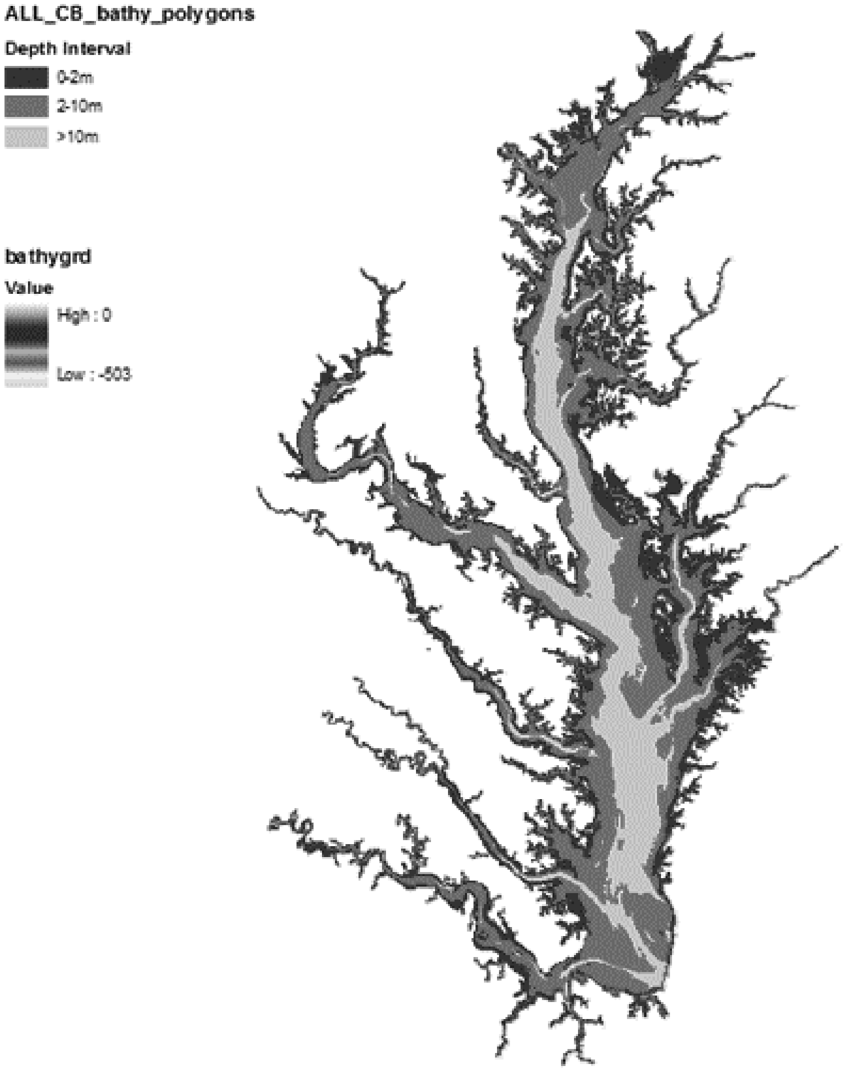


4. BOTTOM HARDNESS
   Mainstem only. Data derived from sediment grab samples. Sand bottoms classed as "Hard"; combinations of clay, silt, and sand classed as "Soft" (see Sediment Distribution Metadata at end of section).

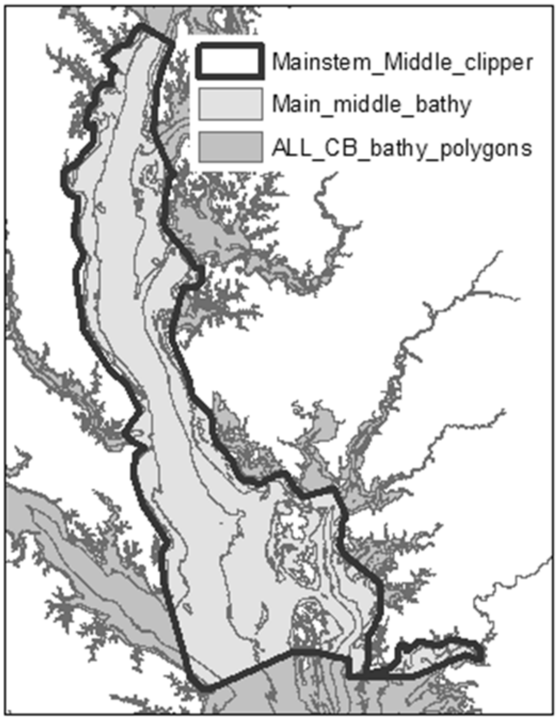


Polygon construction

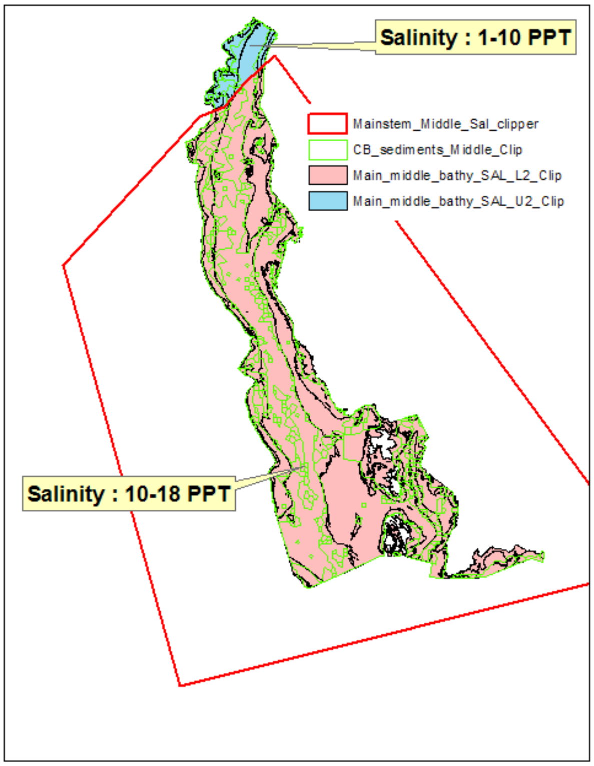
5. Create Bathymetry polygons from “bathygrid”
    - -Extract 3 sets of grid cells: 0–2 m, 2–10 m, & >10 m
    - -Convert extracted cells to polygons
    - -Merge polygons: “All_CB_bathy_polygons.shp”



6. Extract Bay Sections from bathymetry polygons by clipping.

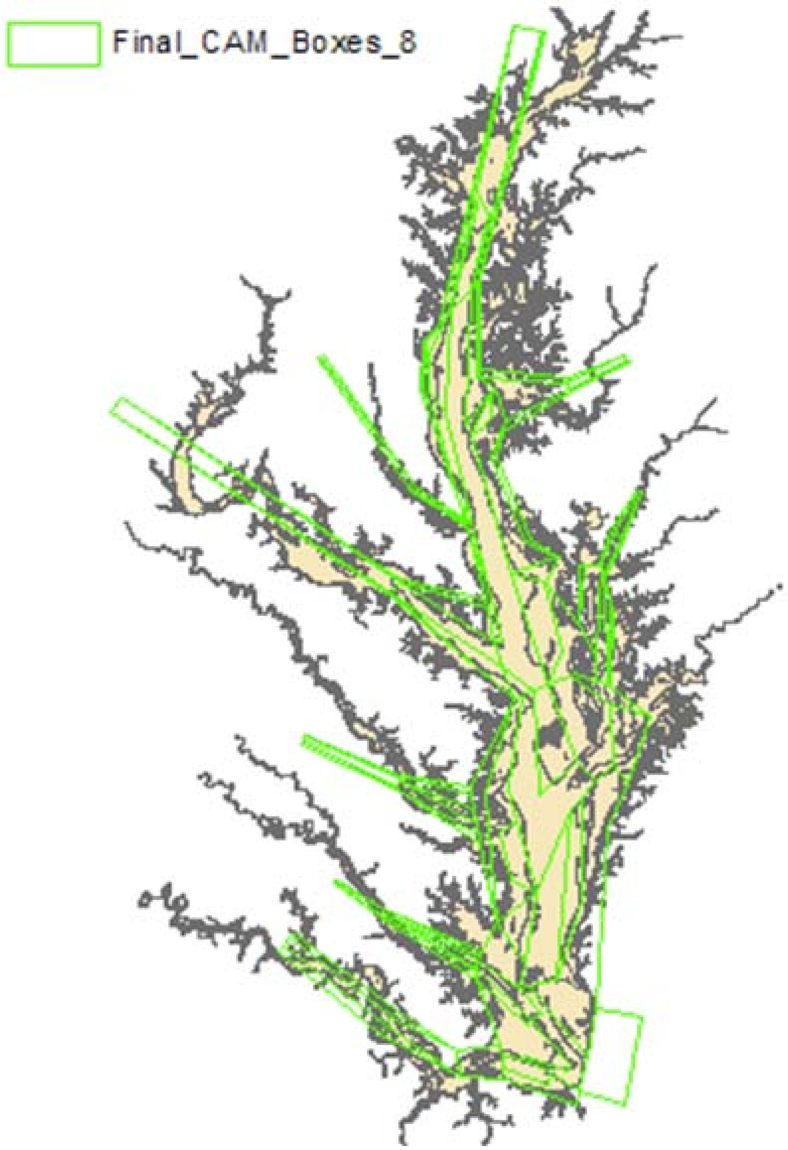


7. a) Intersect Salinity zones, Bathymetry polygons, and bottom hardness for each main Bay section with intersect tool. Intersect Tributary Sections with Salinity and Bathymetry only.

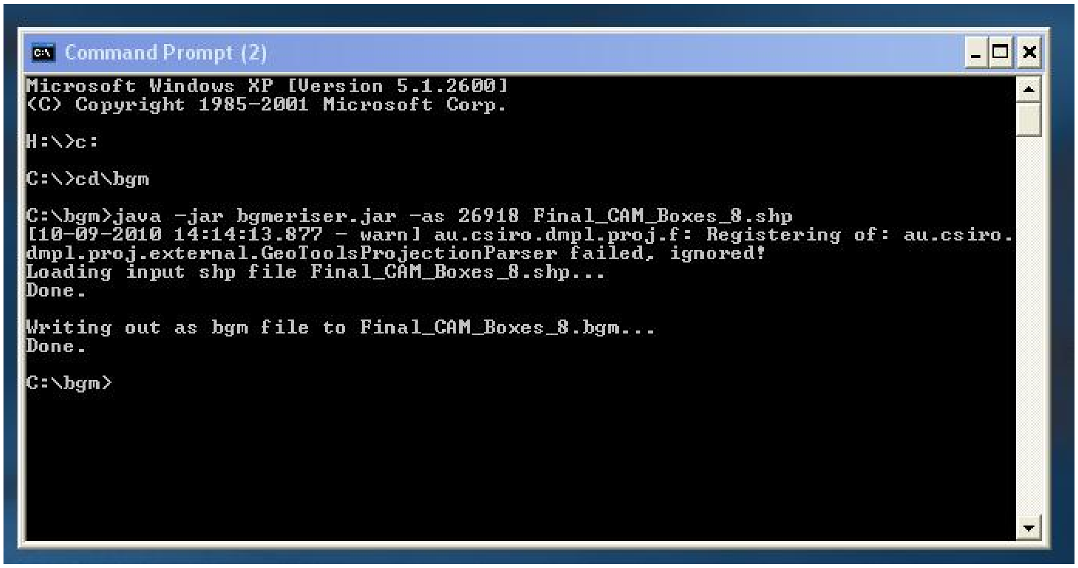


b) Summarize areas of intersection polygons by Bay Section and Tributary. For each section calculate total area by salinity zone (1–10 ppt, 10–18 ppt, 18–30 ppt), depth zone (0–2 m, >2–10 m, >10 m), and bottom hardness (Hard, Soft). If an area was less or equal to 5% of total section area it was added to areas of same salinity and most similar depth (See Table A1 for area summaries).

8. Draw model boxes based on areas and bay shape. Ensure correct topology. No overlapping polygons and no holes. There are 97 dynamic polygons and 1 border polygon in the final shapefile: Final_CAM_Boxes_8.shp.

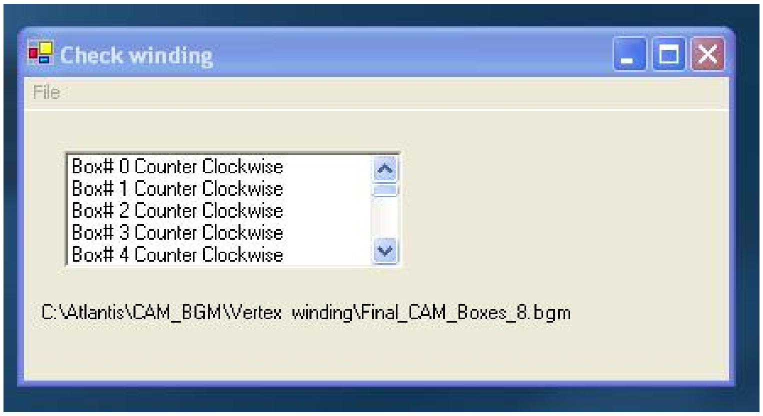


9. Convert final shapefile to BGM file with BGMeriser script.
   BGM file is named Final_CAM_Boxes_8.BGM



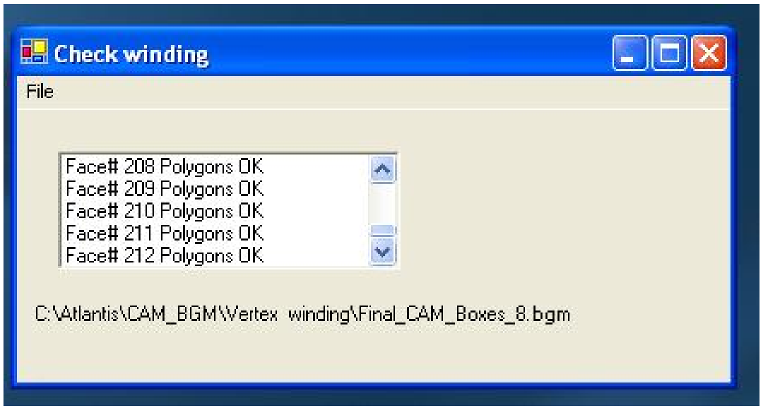
```
Microsoft Windows XP [Version 5.1.2600]
(C) Copyright 1985-2001 Microsoft Corp.

H:\>c:

C:\>cd\bgm

C:\bgm>java -jar bgmeriser.jar -as 26918 Final_CAM_Boxes_8.shp
[10-09-2010 14:14:13.877 - warn] au.csiro.dmpl.proj.f: Registering of: au.csiro.
dmpl.proj.external.GeoToolsProjectionParser failed, ignored!
Loading input shp file Final_CAM_Boxes_8.shp...
Done.

Writing out as bgm file to Final_CAM_Boxes_8.bgm...
Done.

C:\bgm>
```

10. Ensure that winding order of the vertices in the BGM file is correct with the Checkwinding.exe. All windings are counterclockwise.



```
Box# 0 Counter Clockwise
Box# 1 Counter Clockwise
Box# 2 Counter Clockwise
Box# 3 Counter Clockwise
Box# 4 Counter Clockwise
```

C:\Atlantis\CAM_BGM\Vertex winding\Final_CAM_Boxes_8.bgm



```
Face# 208 Polygons OK
Face# 209 Polygons OK
Face# 210 Polygons OK
Face# 211 Polygons OK
Face# 212 Polygons OK
```

C:\Atlantis\CAM_BGM\Vertex winding\Final_CAM_Boxes_8.bgm

Table A1. Area Summaries

Section	Salinity	Depth_m_1	Depth_m_2	Bottom	Area(kmsq)	Total_area_sect	Percent_area
Main_upper	1-10	0-2m	0-2m	Hard	61.0	675.2	9.0
Main_upper	1-10	2-10m	2-10m	Hard	114.4		16.9
Main_upper	1-10	2-10m	2-10m	Soft	398.5		59.0
Main_upper	1-10	>10m	10-28m	Soft	101.4		15.0
							100.0

Section	Salinity	Depth_m_1	Depth_m_2	Bottom	Area(kmsq)	Total_area_sect	Percent_area
Main_Middle	10-18	0-2m	0-2m	Hard	204.4	2170.2	9.4
Main_Middle	10-18	2-10m	2-10m	Hard	754.9		34.8
Main_Middle	10-18	2-10m	2-10m	Soft	228.1		10.5
Main_Middle	10-18	>10m	10-47m	Hard	182.7		8.4
Main_Middle	10-18	>10m	10-50m	Soft	800.1		36.9
						total=	100.0

Section	Salinity	Depth_m_1	Depth_m_2	Bottom	Area(kmsq)	Total_area_sect	Percent_area
Main_lower	10-18	0-2m	0-2m	Hard	185.9	3701.9	5.0
Main_lower	10-18	>10m	10-13m	Hard	210.6		5.7
Main_lower	10-18	2-10m	2-10m	Hard	639.7		17.3
Main_lower	10-18	0-10m	0-10m	Soft	237.0		6.4
Main_lower	10-18	>10m	10-41m	Soft	482.0		13.0
Main_lower	18-30	>10m	10-14m	Hard	331.1		8.9
Main_lower	18-30	0-10m	0-10m	Hard	1055.5		28.5
Main_lower	18-30	0-10m	0-10m	Soft	199.6		5.4
Main_lower	18-30	>10m	10-31m	Soft	360.6		9.7
						total=	100.0

Section	Salinity	Depth_m_1	Depth_m_2	Bottom	Area(kmsq)	Total_area_sect	Percent_area
James_river	1-10	0-2m	0-2m		153.0	517.3	29.6
James_river	1-10	>2m	2-10m		101.9		19.7
James_river	10-18	0-2m	0-2m		57.4		11.1
James_river	10-18	>2m	2-10m		98.3		19.0
James_river	18-30	>0m	0-23m		106.7		20.6
						total=	100.0

Section	Salinity	Depth_m_1	Depth_m_2	Bottom	Area(kmsq)	Total_area_sect	Percent_area
Potomac_river	1-10	0-2m	0-2m		75.4	887.4	8.5
Potomac_river	1-10	>2m	2-16m		409.0		46.1
Potomac_river	10-18	>10m	10-25m		160.0		18.0
Potomac_river	10-18	0-2m	0-2m		44.7		5.0
Potomac_river	10-18	2-10m	2-10m		198.3		22.3

						total=	100.0

Section	**Salinity**	**Depth_m_1**	**Depth_m_2**	**Bottom**	**Area(kmsq)**	**Total_area_sect**	**Percent_area**
Rappahannock_river	1-10	0-2m	0-2m		50.4	300.7	16.7
Rappahannock_river	1-10	>2m	2-15m		56.5		18.8
Rappahannock_river	10-18	>10m	10-22m		41.9		13.9
Rappahannock_river	10-18	0-2m	0-2m		47.8		15.9
Rappahannock_river	10-18	2-10m	2-10m		104.1		34.6
						total=	100.0

Section	**Salinity**	**Depth_m_1**	**Depth_m_2**	**Bottom**	**Area(kmsq)**	**Total_area_sect**	**Percent_area**
York_river	1-10	0-2m	0-2m		8.7	161.9	5.3
York_river	1-10	>2m	2-18m		14.7		9.0
York_river	10-18	>10m	10-25m		24.3		15.0
York_river	10-18	0-2m	0-2m		58.1		35.9
York_river	10-18	2-10m	2-10m		56.3		34.8
						total=	100.0

Section	**Salinity**	**Depth_m_1**	**Depth_m_2**	**Bottom**	**Area(kmsq)**	**Total_area_sect**	**Percent_area**
Choptank_river	1-10ppt	0-2m	0-2m		19.5	274.1	7.1
Choptank_river	1-10ppt	2-10m	2-15m		31.5		11.5
Choptank_river	10-18ppt	0-2m	0-2m		73.6		26.9
Choptank_river	10-18ppt	2-10m	2-18m		149.5		54.5
						total=	100.0

Section	**Salinity**	**Depth_m_1**	**Depth_m_2**	**Bottom**	**Area(kmsq)**	**Total_area_sect**	**Percent_area**
Nanticoke_river	1-10ppt	0-2m	0-2m		19.6	77.8	25.3
Nanticoke_river	1-10ppt	2-10m	2-17m		17.1		22.0
Nanticoke_river	10-18ppt	0-2m	0-2m		20.0		25.8
Nanticoke_river	10-18ppt	2-10m	2-13m		21.0		27.0
						total=	100.0

Section	**Salinity**	**Depth_m_1**	**Depth_m_2**	**Bottom**	**Area(kmsq)**	**Total_area_sect**	**Percent_area**
Patuxent_river	1-10ppt	0-2m	0-2m		26.9	110.5	24.4
Patuxent_river	1-10ppt	2-10m	2-24m		51.0		46.1
Patuxent_river	10-18ppt	0-2m	0-2m		7.2		6.5
Patuxent_river	10-18ppt	2-10m	2-10m		14.0		12.7
Patuxent_river	10-18ppt	>10m	10-38m		11.4		10.3
						total=	100.0

Bathymetry Metadata

Bathymetry for CAM was based on a 10 m x 10 m grid originally created by Patrick Nowlan, 25 June, 1999. The grid was composed of Chesapeake Bay Program (CBP) bathymetry tins. After the tins were gridded they were merged using the GRID merge function. It is an integer grid to save space and multiplied by 10 to preserve the first decimal place. Depth units are meters; measures are precise to 0.1 m. The original source was the NOAA bathymetry soundings for the Chesapeake Bay and tidal tributaries. Soundings for the shallow waters (less than 2 meters) were edited when the 1- and 2-meter contours were developed at CBP. Soundings that looked out of place or seemed out of a reasonable range were verified using NOAA nautical charts. The quality checks for water greater than 2 meters was not comprehensive; it was only an examination of potential outliers. Bathymetry sounds are incomplete for the Elizabeth River, so this section of the grid coverage is known to be invalid. Grid values were standardized to the Mean Lower Low Water (MLLW) datum.

Sediment Distribution Metadata

This dataset merges Chesapeake Bay sediment grab sample data collected by the Maryland Geological Survey (MGS) and the Virginia Institute of Marine Science (VIMS) during 1976-1984 (see http://www.mgs.md.gov/coastal_geology/baysedata.html and http://pubs.usgs.gov/ds/2005/118/metadata/GOV/vasedsfaq.htm). Data classifications are based on CMECS (Coastal and Marine Ecological Classification Standard); further information, as well as metadata for sediment distribution in XML format, is found at: http://www.habitat.noaa.gov/chesapeakebay/gis/chesapeake_bay_cmecs_geodatabase/

Purpose: Create a Bay-wide GIS coverage of sediment distribution represented by interpolated polygons.

Supplemental Information: Percent sand, clay, and silt data in addition to coordinate data were taken from MGS and VIMS datasets and classified with the Shepard's ternary model (http://www.mgs.md.gov/coastal/vmap/shepard.html) to create the following categories: sand, clay, silt, sandy clay, sandy silt, clayey sand, clayey silt, silty sand, silty clay and sand-clay-silt.

Categorical grid interpolation was done with ArcGIS/Spatial Analyst grid tools in several steps.
1: Rectangular neighborhood 3x3 cells, majority (most frequent category).
2: Circular neighborhood radius = 3 cells, majority.
3: Boundary clean, no sort, run expansion and shrink 2 times.

Interpolation error was assessed with a raster calculator by subtracting the point raster from the interpolated raster. Of 6130 cells in the uninterpolated raster, 96% were spatially coincident with cells of equivalent value in the interpolated raster.

Appendix B: Biological Processes Modeled in Atlantis

Table B1. Biological processes and factors modeled in Atlantis. Row labels refer to process modeled, column labels indicate groups in Atlantis. Row labels refer to process modeled, column labels indicate groups in Atlantis. Abbreviations not defined within table (in order of appearance): “Y” – indicates factor is modeled, “PAB” – pelagic attached bacteria, “PFB” – pelagic free-living bacteria, “AEB” – aerobic benthic bacteria, “ANB” – anaerobic benthic bacteria, “DO” – dissolved oxygen, “wc” – water column, “sed” – sediment, “N” – nitrogen, “DON” – dissolved organic nitrogen, “N2” – nitrogen gas, “DC” – carrion detritus, “pprey” – predator-prey availability matrix, “PN” – particulate nitrogen, “DIN” – dissolved inorganic nitrogen. The Chesapeake Atlantis Model simulates all groups except the last 2 columns (CORAL and MACROBEN).

[See online version of this report to enlarge table for readability.]

Factors & Groups modeled:

				Detritus		Bacteria		Nutrients			Primary Producers (P*X*)						Consumers										
		If no "Y" then one setting for entire Bay	If no "Y" then one setting for all layers	Detritus-Labile	Detritus-Refractory	Pelagic Bacteria	Benthic Bacteria	Ammonia	Nitrite-Nitrate	Silicon/ Silicate	Marsh	SAV	Phytoplankton Small	Phytoplankton Large	Micro-phytobenthos	Dinoflagellates (mixotrophic)	Zooplankton Small	Meso zooplankton	Ctenophores	Sea Nettles	Invert Predators	Invert Omnivores	Meiobenthos	Benthic Filter feeders (Macoma, suspension feeders, & oysters) "BF*x*"	General Consumers: Crab, Fish, Birds, Reptiles & Mammal	Coral	Large Benthic Invertebrate
	Process	**By Box?**	**By Layer?**	**DL**	**DR**	**PB (2 types: PAB, PFB)**	**BB (2 types: AEB, ANB)**	**NH3**	**NO**	**Si**	**MA**	**SG**	**PS**	**PL**	**MB**	**DF**	**ZS**	**ZM**	**ZG**	**ZL**	**BC**	**BD**	**BO**	**BFS, BFD, BFF**	**C*X***	**CORAL**	**MACROBEN**
Nutrient Cycling	**Excretion (NH3, NO)**	Y	Y			Y (decreases DO)							Y (NH3 + NO)	Y (NH3 + NO)		Y (NH3 + NO)	Y	Y	Y	Y	Y	Y	Y	Y (wc only)	Y (decreases DO)	Y	Y
	Remineralization ("Rnet"=NH produced by Denitrification & other pathways)	Y	Y	Bacterial remineralization	Bacterial remineralization	minor (decreases DO)	major (decreases DO)			Y																	
	Denitrification (NO, not NH3)	Y	Y			Y	Y	Y	Y																		
	Nitrification	Y	Y			minor (NH3 + NO)	major (NH3 + NO)	Y	Y		wc	sed			wc and sed												
	Uptake N [also Si for PL and MB]	Y	Y			Y					wc (NH3 + NO)	sed (NH3 + NO)	wc	wc (N + Si)	wc and sed (NH, NO, and Si)	wc											
	DON production	Y	Y			Y	Y																				
	DON remineralization & uptake	Y	Y			Y	Y																				
	N2 fixing	Y	Y			minor	major																				
	Waste (detritus)	Y	Y			Y					Y	Y				Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Detritus-Labile production	Y	Y	Y (a fraction is recycled during remineralization, plus a fraction of both DR and DC are converted to DL)	Y (a fraction is recycled during remineralization , plus a fraction of DL is converted to	Y	Y				Y (wc only via lysis)	Y (sed only via lysis)	Y (via lysis in both wc and sed)	Y (via lysis in both wc and sed)	Y (via lysis in both wc and sed)	Y (via lysis in both wc and sed)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding, plus moves detritus from wc to sediments)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)	Y (via mortality and sloppy feeding)
	Detritus-Labile consumption	Y	Y			Y	Y									Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)
	Detritus-Refractory prod.	Y	Y	Y	Y						Y (via mortality)	Y (via mortality)	Y (via mortality)	Y (via mortality)	Y (via mortality)	Y (via mortality)	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding	Y From mortality and sloppy feeding
	Detritus-Refractory consump.+burial	Y	Y			Y	Y									Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey + burial)	Y (consump. depends on pprey)	Y (consump. depends on pprey)	Y (consump. depends on pprey)
Growth Limiting Factors	**Nutrient limitation (N, Si)**	Y	Y								N	N	N	N, Si	N, Si	N										Y (zooxanthellae component)	
	Oxygen limitation/ Oxygen mortality	Y	Y			Y	Y						Y	Y		Y					Y	Y	Y	Y	Y	Y (host component)	Y
	Space limitation	Y	Y			Y (optional, if use cubic formulation)	Y (optional, if use cubic formulation)				Y	Y	Y	Y	Y	Y							Y	Y		Y	
	Turbidity	Y	Y								Y (via potential shading)	Y (via potential shading; also - optional, can be stressed by fouling and	Y (via potential shading)	Y (via potential shading)	Y (via potential shading)	Y (via potential shading)								Y (optional, growth can be slowed)		Y (as energy used to clean host)	
	Resuspension	Y	Y								Y (can be stressed by excess bottom stress degrading leaves)		Y	Y	Y	Y	Y (optional)	Y (optional)	Y (optional)	Y (optional)			Y (optional)				
	Light availability/shading	Y	Y								Y (result of sediment, phytoplankton, detritus and water color)	Y (result of sediment, phytoplankton, detritus and water color)	Y (result of sediment, phytoplankton, detritus and water color)	Y (result of sediment, phytoplankton, detritus and water color)	Y (result of sediment, phytoplankton, detritus and water color)	Y (result of sediment, phytoplankton, detritus and water color)											
Mortality	**Predation**	Y	Y								Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Lysis (producer mortality, to detritus)	Y	Y								Y	Y	Y	Y	wc	Y											
	Mortality (linear)	Y				Y	Y				Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Mortality (quadratic)	Y															Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Mortality (Fishing on consumers = 0 for all in base model)	Y									Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)
	Other Mortality										The degree of bottom stress can degrade leaves (optional)	Excessive DIN causes mortality (optional, via impicit representation of epiphyte effects)	Cells degrade in sediments by both linear mortality and lysis	Cells degrade in sediments by both linear mortality and lysis	Cells degrade in sediments by both linear mortality and lysis	Cells degrade in sediments by both linear mortality and lysis										Bleaching	
Movement	**Movement (box to box)**												Y (advection)	Y (advection)	Y (advection)	Y (advection)	Y (advection)	Y (Advection and optional directed movement)	Y (Advection and optional directed movement)	Y (Advection and optional directed movement)	Y (Advection for resuspended animals; and optional [untested] directed movement)	Y (Advection for resuspended animals; and optional [untested] directed movement)	Y (Advection for resuspended animals; and optional [untested] directed movement)		Y (Directed)	Larval (Advection)	Y (optional directed movement)
	Vertical movement																		Y (Directed)	Y (Directed)					Y (Directed)		
Variable type:	**Need to set starting value? (if no "Y" initial value internally calculated)**			Y (DON + PN)	Y (PN)			Y (DIN)	Y (DIN)	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
Modeled Domain	**Water column**			Y	Y	Y		Y	Y	Y		Y (optional)	Y	Y	Y (if resuspended, but not active; can be eaten)	Y	Y	Y	Y	Y			Y		Y		
	Epibenthic							Y	Y		Y	Y (there is a variant that allows for above ground, below ground and epiphyte biomass												Y	Y	Y	Y
	Sediment			Y	Y		Y	Y	Y	Y		Y (optional)	Can exist here once settled waiting for resuspension, but not active (can be eaten)	Can exist here once settled waiting for resuspension, but not active (can be eaten)	Y						Y	Y			Y		
Other Factors and Processes Modeled	**Other processes**															Toxic effects on other species (optional)										Rugosity, calcification	
	Persistent through time			Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Explicit overwintering behaviour (Optional - encysted, or inactive overwintering stage)												Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y		Y
	bioturbation	Y	Y																		Y	Y		Y	Y (If a benthic invertebrate)		Y
	bioirrigation	Y	Y																		Y	Y	Y	Y	Y (If a benthic invertebrate)		Y
	Explicit reproduction																Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y (optional)	Y	Y	Y (optional)
	Growth	Y	Y			Y (tied to magnitude of detritus pool)	Y (tied to magnitude of detritus pool)				Y (increases DO in wc)	Y (increases DO in both wc and sed)	Y (increases DO in wc)	Y (increases DO in wc)	Y (increases DO in both wc and sed)	Y (increases DO in wc)	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Predator - consumes other groups	Y	Y													Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Refuge for consumers (prey)	Y	Y (epi)								Y	Y												Y (BFF)		Y	

Appendix C: Vertebrate Life History

CAM represents vertebrate biomass in 29 functional groups: 18 finfish, 4 elasmobranch, 4 bird, 2 reptile, and 1 mammal (Table 11). Functional group types include both individual species and aggregate groups of species; in total, 58 vertebrate species are included in CAM. Each vertebrate group is divided into 10 age classes, with each class representing one-tenth of the overall life span of the group. Initial biomass for most vertebrate groups was based on a preliminary, balanced Ecopath model for the system (with no fishing) that was developed for this purpose. Preliminary biomass estimates used in the Ecopath model were, in turn, based on a wide variety of sources including (in descending order of use): landings data, stock assessments, available literature, unpublished data, and expert opinion (Table 11). Weight-length conversions were based on the relationship

$$W = aL^b \tag{C.1}$$

where W is weight in grams, L is length in mm, and a and b are constants.

Fish

Life history parameters for finfish and sharks came primarily from FishBase (Froese and Pauly, 2013). When multiple species occurred within a functional group, each parameter value was weighted according to the biomass of each constituent species or group of species. Life history parameters are summarized primarily in Tables 12, 13, 14, and 15. When life history parameter estimates for fish were not available from FishBase, estimates were taken directly from the literature. Estimates of k, a, and b (for length-weight relationship) for blueback shad come from Bozeman and Van Den Avyle (1989); k for blackcheek tonguefish (in aggregate group FDF) comes from Terwilliger and Munroe (1999); Winemiller and Rose (1992) provided maximum ages for American shad and tautog (in aggregate groups FMM and FDM, respectively), age at maturity for winter flounder (in aggregate group FDF), and both maximum age and age at maturity for white perch, summer flounder, bay anchovy, small forage fish (FDP); and for spot, blueback shad, black seabass, from aggregate groups FDE, FMM, and FDM, respectively.

For species for which the natural mortality rate (M) was not available but a longevity estimate ($Tmax$) was available, and we calculated M assuming that only 1% of the population should reach maximum longevity:

$$M = \frac{\ln(0.01)}{-Tmax} \tag{C.2}$$

When no $Tmax$ value was present, but the asymptotic length L_∞ and the von Bertalanffy K were available (by Fishbase or otherwise), we calculated the natural mortality (Pauly, 1980) as:

$$M = K^{0.65} \cdot L_{\infty}^{-0.279} \cdot T^{0.463} \tag{C.3}$$

where T is the average water temperature. For Chesapeake Bay, we approximated average water temperature as 15.75 ℃ (Christensen et al., 2009).

Tmax was provided by FishBase for only two (bluefish and winter flounder) of our 41 species of fish. For the remaining species that did not already have a longevity value from Winemiller and Rose (1992), we calculated *Tmax* following Equation C.2, but now using reported M and again assuming 1% of the population should reach maximum longevity:

$$Tmax = \frac{\ln(0.01)}{-M} \tag{C.4}$$

The age class length was calculated by simply dividing the lifespan (*Tmax*) by 10, the number of age classes for all of our vertebrate groups in CAM.

Reproduction for finfish was assumed to follow Beverton-Holt dynamics; parameter estimates (unfished adult biomass [B_o], maximum reproduction of recruits [in numbers, R_o] from an unfished population, and steepness) used to calculate "BHalpha" and "BHbeta" (Table 12) came largely from the most recent available stock assessments. When no B_o values could be found, we estimated unfished biomass using a preliminary Ecopath model with no fishing. R_o values for unassessed small (forage fish, bay anchovy) and medium (panfish) forage fish were estimated based on Lubbers et al. (1990), while the value used for catfish was based on Winemiller and Rose, (1992) and Graham (2000). Steepness estimates for Atlantic menhaden, Alosines, and bottomfish came from Myers et al. (1999); weakfish, gizzard shad, bay anchovy, white perch, and panfish were from Myers et al. (2002). When no information on *Ro* or steepness was found, values were used from closely related species. If still no information was available for a particular group, overall mean values from groups with estimates were used.

Mammals

Bottlenose Dolphin (WHS)

Life history parameters for the bottlenose dolphin (*Tursiops truncatus*) are largely based on the Chesapeake Bay Program, Field Guide: bottlenose dolphin, (http://www.chesapeakebay.net/fieldguide/critter/bottlenose_dolphin; accessed May 2014). These parameters include lifespan, average adult length, average adult weight, age at maturity, recruitment age, and timing of reproduction and migration. The abundance estimate for the Chesapeake Bay came from Barco et al. (1999). The annual natural mortality rate came from Mrang et al. (1994). Our length-weight relationship parameters *a* and *b* (Equation C.1) were taken from Trites and Pauly (1998). We required weights at age for all age classes, and the length-weight relationship was used to calculate weights at age. Age at length was based on Neuenhoff et al. (2010), and growth was assumed to follow a Gompertz function. Though we assumed the productivity to biomass ratio (P/B) applied in initial Ecopath balancing is assumed to be approximately equal to the natural mortality rate, following earlier works (Field, 2004; Brand et al., 2007), balanced Ecopath estimates of initial biomass differed only slightly from our initial estimate. Therefore, our original preliminary estimate was used to initialize CAM (Table 11).

Reptiles

The length-weight relationship parameters *a* and *b* (Equation C.1) were not found in literature for the reptiles. We assumed a *b* value of 3 and estimated the value of *a* based on the average adult length and weight using Solver in Excel for each species of reptile. Following methodology described for the bottlenose dolphin (above), we assumed P/B is equal to natural annual mortality for purposes of balancing our preliminary Ecopath model, but because balanced values differed little from preliminary estimates, again applied our preliminary biomass estimate to initialize CAM (Table 11).

Diamondback Terrapin (FVV)

Life history parameters for the diamondback terrapin (*Malaclemys terrapin*) were taken from a variety of online and published sources. Average adult size (SCL), lifespan, and clutch frequency were from the online resource of the Virginia Institute of Marine Science (VIMS) (http://www.vims.edu/research/units/programs/sea_turtle/va_sea_turtles/terps.php, accessed 6-6-13). Average adult weight was taken from Brennessel (2006). Abundance was based on personal communication with R. Chambers (The College of William & Mary). Average clutch size for diamondback terrapins specific to the Chesapeake Bay area was from Roosenburg (1990). The von Bertalanffy growth parameter *k* was given by Bulté and Blouin-Demers (2009). The recruitment age was given by Burger (1976). Annual natural mortality was from Tucker et al. (2001).

Sea Turtles (REP)

The sea turtle group is an aggregate group composed of three species of sea turtle that occur in the Chesapeake: the loggerhead (*Caretta caretta*), Kemp's ridley (*Lepidochelys kempii*), and leatherback (*Dermochelys coriacea*). Life history characteristics for the *REP* group are based on a weighted average of the characteristics for these species. The relative weight attributed to each species is based on biomass estimates (reported numbers * average weight). This approach results in an aggregate group characterized mainly by the relatively common loggerhead species (94% of the total by weight). The seasonal abundance of loggerheads in the Chesapeake is based on a quote by Jack Musick (VIMS) as reported by Kobell (2010). The population estimate for Kemp's ridley comes from field observations reported by Byles (1989). Leatherbacks are known to enter the Chesapeake (Keinath, 1993), but no abundance estimate is available for the Bay. Leatherbacks are considered uncommon in the Bay (Coles, 1999), so we assume their abundance to be 10% of the Kemp's ridley population estimate. Average weight for loggerhead was from an online resource of VIMS (http://www.vims.edu/research/units/programs/sea_turtle/va_sea_turtles/loggerhead.php; accessed 6-6-13); average weight for Kemp's ridley and leatherback was given in Plotkin (1995).

Other size parameters were based on both literature and online resources. Average adult straight carapace length (SCL) for the loggerhead sea turtle was taken from an online resource provided by VIMS (http://www.vims.edu/research/units/programs/sea_turtle/va_sea_turtles/loggerhead.php; accessed 6-6-13). SCL for Kemp's ridley and leatherback were from Plotkin (1995). Size-at-age was assumed to follow the von Bertalanffy growth function; associated *k* values were taken from

Bjorndal et al. (2000) for loggerheads, Zug et al. (1997) for Kemp's ridley, and Musick (1999) for the leatherback.

The timing of critical life history events was taken from the literature. Incubation period for each species was used as indicated by Yntema and Mrosovsky (1982) for the loggerhead, Johnson et al. (1999) for Kemp's ridley, and Chan et al. (1985) for the leatherback. Age at maturity values were provided by Bjorndal et al. (2000); the National Marine Fisheries Service, U.S. Fish and Wildlife Service, and SEMARNAT (2010); and Chaloupka (2002) for the loggerhead, Kemp's ridley, and leatherback, respectively. Maximum age was based on Plotkin (1995) for loggerhead and on Zug and Parham (1996) for leatherback. We assumed maximum age for Kemp's ridley to be similar to that estimated for olive ridley sea turtles (*Lepidochelys olivacea*) reported by Zug et al. (2006).

Remigration interval (the time period between successive nesting events) and other reproductive parameters were taken from the literature. Remigration interval, clutch size, and clutch frequency was based on: Williams and Frick (2008) [remigration], and Frazer and Richardson (1985) [clutch size and frequency] for loggerheads; the National Recovery Plan (National Marine Fisheries Service et al., 2010) for Kemp's ridley; and Plotkin (1995) for leatherback.

Annual natural mortality rates were taken from Byles (1988), National Marine Fisheries Service et al. (2010), and Chaloupka (2002) for the loggerhead, Kemp's ridley, and leatherback sea turtles, respectively.

Birds

Whenever possible, we took life history parameters from Birds of North America Online (http://bna.birds.cornell.edu/bna; accessed 18 October 2010), a database maintained by the Cornell Lab of Ornithology. Parameters not included in the database were based on published literature and are listed below for each group. We assume the growth of all birds in our model follow the Gompertz growth curve. Since fledgling weight is often equal to or greater than asymptotic weight in seabirds, we assume that no additional structural growth occurs in the model beyond the rapid initial growth of young-of-the-year for all birds. The weighting of our bird species parameters within their groups was based on the annual migratory proportional biomass of each species, based on unpublished data collected by Doug Forsell (Coastal Program biologist with the U.S. Fish and Wildlife Service, Chesapeake Bay Field Office). We estimated the length-weight parameters *a* and *b* (Equation C.1) by building a power regression using as many length-weight pairs as we could find for all species within a group. As described above, the productivity to biomass ratio (P/B) applied in initial Ecopath balancing is assumed to be approximately equal to the natural mortality rate for all birds. As described above, however, the preliminary biomass estimates were used to initialize CAM (Table 11) for all bird groups, rather than the balanced estimates resulting from Ecopath.

Benthic Grazing Seabirds (FVO)

Benthic grazing seabirds is an aggregate group of five species: Atlantic Canada goose, mallard, redhead, tundra swan, and mute swan.

Life history rates for the Atlantic Canada goose (*Branta canadensis*) could not often be found on the subspecies level. In that event, we took values belonging to subspecies of *Branta canadensis*, and in the event that multiple values were available, we opted to use those belonging to subspecies of similar size and/or from similar regions whenever possible. Annual natural mortality was calculated as an average between the annual natural mortalities of two subspecies, *B. c. moffitti* and *B. c. hutchinsii*. They represented the two extremes in mortality among all the subspecies of Canada geese. Average clutch size was determined by Rohwer and Eisenhauer (1989) for *B. c. minima*. A lifespan estimate was from Krementz et al. (1989) for the species but information by subspecies was not provided. Abundance for *Branta canadensis* specific to Chesapeake Bay is from Costanzo and Hindman (2007). Age at maturity, recruitment age, natural annual mortality, and average adult length and weight were from Birds of North America Online (Mowbray et al., 2002).

The mallard duck (*Anas platyrhynchos*) annual natural mortality was taken from Kirby and Sargeant (1999). Average clutch size was from Dzubin and Gollop (1972). An estimate of maximum age came from Krementz et al. (1989). Recruitment age was found in Kirby et al. (1989). Costanzo and Hindman (2007) provided the abundance estimate specific to Chesapeake Bay. Age at maturity and average adult length and weight were from Birds of North America Online (Drilling et al., 2002).

Annual natural mortality for the redhead duck (*Aythya americana*) was found in Arnold et al. (2002). Zammuto (1987) provided the average clutch size. Lifespan estimates came from Clapp et al. (1982). Ages at maturity and recruitment were taken from Low (1945). Perry et al. (2007) provided the abundance estimate specific to Chesapeake Bay. Average adult length and weight were taken from Birds of North America Online (Woodin and Michot, 2002).

Tundra swan (*Cygnus columbianus*) annual natural mortality was taken from Nichols et al. (1992). Average clutch size was provided by Monda (1991). Average adult length was found within an online resource for the International Bird Rescue Research Center (IBRRC website: http://www.ibrrc.org/tundra_swan.html, accessed 1 October 2010). The abundance estimate for tundra swan came from a Chesapeake Bay Program report (1990). Maximum age, age at maturity, and average adult weight are from Birds of North America Online (Limpert and Earnst, 1994). We did not find a reference for age at recruitment, so we assumed the same value for mute swan, below.

Mute swan (*Cygnus olor*) abundance was taken from Costanzo and Hindman (2007). The estimate of annual natural mortality was found in Reese (1980). Average clutch size was provided by Reynolds (1972). Klimkiewicz and Fletcher (1989) estimated maximum age for this species. Age at recruitment was from Mathiasson (1980). Age at maturity and average adult length and weight were from Birds of North America Online (Ciaranca et al., 1997).

Piscivorous Seabirds (SP)

Piscivorous seabirds is an aggregate group of four species: osprey, great blue heron, brown pelican, and double-crested cormorant.

The average clutch size and ages at recruitment and maturity for the osprey (*Pandion haliaetus*) was described by Reese (1991). Annual natural mortality and lifespan were found in Henny and Wight (1969). Abundance specific to the Chesapeake Bay region was taken from Watts and Paxton (2007). Average adult length was found in Ferguson-Lees and Christie (2001), while average adult weight was found in Steidl and Griffin (1991).

Annual natural mortality for the great blue heron (*Ardea herodias*) was provided by Henny (1972). Maximum age was from Owen (1959). Abundance specifically for Chesapeake Bay was found in Williams et al. (2007). Age at maturity was found in Pratt (1973). Clutch size, recruitment age, and average adult length and weight were taken from Birds of North America Online (Butler, 1992).

The brown pelican (*Pelecanus occidentalis*) annual natural mortality was given by Schreiber and Burger (2002). Average clutch size was from Blus and Keahey (1978). Abundance specific to the Chesapeake Bay region was provided by Brinker et al. (2007). Maximum age, age at maturity, age at recruitment, and average adult length and weight were from Birds of North America Online (Shields, 2002).

Age at maturity and annual natural mortality values for the double-crested cormorant (*Phalacrocorax auritus*) were found in Van Der Veen (1973). Average clutch size was from Peck and James (1983). Lifespan estimate comes from Klimkiewicz and Futcher (1989). Average adult weight was taken from DesGrange (1982). An abundance estimate specific to Chesapeake Bay was found in Brinker et al. (2007). Recruitment age was taken from Van Tets (1959). Average adult length was taken from Birds of North America Online (Hatch and Weseloh, 1999).

Diving Ducks (SB)

Morrier et al. (1997) provided the average clutch size for surf scoters (*Melanitta perspicillata*). The recruitment age was found in Lesage et al (1996). Abundance for the Chesapeake Bay region was from Paige and Luckenbach (2008). Age at maturity and average adult length and weight were from Birds of North America Online (Savard et al., 1998). Maximum age and mortality could not be found for this species; consequently, we assumed these values were similar to those of the long-tailed duck, referenced below.

The long-tailed duck (*Clangula hyemalis*) mortality, lifespan, age at maturity, and average adult length and weight were all taken from Birds of North America Online (Robertson and Savard, 2002). The mortality rate was taken as an average of the two rates the website provided for ducks in Alaska and Iceland. Though these locations differ from the Chesapeake Bay, these were the only rates found by the authors. Clutch size and recruitment age were found in Alison (1975). An estimate of abundance specific to Chesapeake Bay was taken from Perry et al. (2007).

Bald Eagle (PIN)

For the bald eagle (*Haliaeetus leucocephalus*), annual natural mortality rate and clutch size were from Buehler et al. (1991). Our lifespan estimate came from Schempf (1997) for Alaskan bald eagles. Average adult length was taken from Palmer (1988), while average adult weight was found in Bortolotti (1986). Age at maturity was given by Gerrard et al. (1992) for eagles in Saskatchewan, and age at recruitment was provided by Kussman (1977) for eagles in Minnesota. Our abundance estimate specific to the Chesapeake Bay region was from Watts et al. (2008).

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Appendix D: Diets

Diet relationships were based primarily on published literature (both peer-reviewed and grey literature), and supplemented with information provided by FishBase.org, unpublished data, and expert opinion, in order of preference. In Atlantis, it is important to establish possible predator-prey relationships as well as known relationships, so the model will allow a predator to preferentially consume prey based on availability of all possible prey. Availability is a function of a predator's "preference" (determined by magnitude of prey availability as specified in the diet matrix; see Tables 16 and 17), its spatial and temporal overlap with the prey, and whether habitat groups (marsh grass [MA], oysters [BFF], and SAV [SG]) are available as refuge for those prey groups that use these habitats to decrease their availability to predators (Equations 17 and 18, Figure 7). Consequently, in some cases, where data were lacking but the authors believe a predator-prey relationship exists (e.g., soft-bodied invertebrate remains are not typically identifiable in vertebrate gut content studies), an arbitrary number was added to predator diet to allow such groups to be consumed by a predator if it is available. One of four values (0.001, 0.0001, 0.00001, 0.000005) was applied for each arbitrary addition to the diet matrix. Predator-prey connections believed to be important received larger values, while relatively unimportant connections (but important enough not to be excluded entirely from the matrix) were assigned small values. When literature or data were incomplete (or none were found) for the diet of a trophic group included in CAM, the authors chose the prey groups that they believed were most likely consumed by the predator, and uniform availabilities were assigned for the prey groups.

The species included in each aggregate functional group are described below and are listed in Table 11 of the main text.

Fish

Most fish species' diets were developed using a combination of diet data documented in annual reports (available online) for the ongoing ChesMMAP project (www.vims.edu/research/departments/fisheries/programs/multispecies_fisheries_research/chesmmap/), and supplemental information found in other published literature. Few diets had to be developed with supplemental information sources only.

The comprehensive list of all documented prey items was reduced to exclude any prey items that were not included in the 55 functional groups of species or aggregate groups modeled in CAM. Remaining fish diet items (i.e., those modeled in CAM) were normalized to equal 100% for each predator diet. Relevant details on the development of the diet of each CAM fish functional group are presented next.

Alosines

Alosines is an aggregate functional group. Alosines in the ChesMMAP data included alewife, American shad, blueback herring, and hickory shad. The final diets for each of these species were combined to develop one composite Alosine diet.

Atlantic Croaker

Initial diet data were derived from ChesMMAP data and supplemented with data presented on page 15 in the ASMFC benchmark stock assessment (Atlantic States Marine Fisheries Commission, 2010).

Atlantic Menhaden

Initial diets for juvenile and adult Atlantic menhaden were based on Christensen et al. (2009). As in CAM, Christensen et al. included two functional groups, or life-history "stanzas," for Atlantic menhaden. However, they assumed an ontogenetic shift from zooplanktivory to phytoplankivory (juvenile to adult stages, respectively), a shift now understood to be reversed (Lynch et al., 2010) from that assumed by Christensen et al. (2009). Consequently, juvenile and adult diets in CAM were refined based on Lynch et al. (2010).

Bay Anchovy

The most important forage fish in the Bay (Ihde et al. 2015; analysis based on ChesMMAP data), bay Anchovy are relied on as prey by most predators in the Chesapeake. The diet of this forage fish, in turn (based on Christensen et al., 2009), consists mostly of mesozooplankton, with additional important contributions from microzooplankton and lesser contributions by large phytoplankton, picophytoplankton, and dinoflagellates.

Black Drum

Initial diet data were derived from ChesMMAP data and supplemented with data presented on page 5 in Sutter et al. (1986).

Bluefish

CAM bluefish diets generally followed Christensen et al. (2009), where juveniles depend mainly on bay anchovy, pelagic forage fish, Atlantic menhaden, and panfish (in order of importance), and adult fish feed mainly on Atlantic menhaden. However, adult diets in CAM are believed to be more generalized than assumed by Christensen et al. (2009), so authors assumed adult bluefish also feed heavily on panfish, Alosines, and Atlantic croaker, and to a lesser extent on bay anchovy, weakfish, reef fish, other flatfish, and blue crab.

Bottom Fish

Bottom Fish is an aggregate group that includes spotted hake, northern searobin, and lizardfish. The ChesMMAP data set includes information only for spotted hake and northern searobin. The final diet for spotted hake was supplemented with data from table 1 in Bowman (1979), and Table 1 in Rachlin and Warkentine (1987). Northern searobin diet data from ChesMMAP was supplemented with data from Byron and Link (2010). Lizardfish diet was derived from Table 7 in Jeffers (2007). These data were combined to develop one composite diet.

Butterfish (and Harvestfish)

Diets for this aggregate group were representative of a combination of butterfish and harvestfish. Initial diet data were derived from ChesMMAP data and supplemented by data presented for butterfish on page 2 in Cross et al. (1999), and additional information on harvestfish diet from Cargo and Schultz (1966).

Catfish

The diet of this aggregate group generally follows that described by Christensen et al. (2009) but is more generalized. Catfish feed mainly on soft-bodied benthic invertebrates in CAM (i.e., benthic carnivores, benthic deposit feeders, and benthic filter feeders), and gizzard shad are an important part of their diet (following the Christensen et al. (2009) EwE model). Important dietary contributions are also made by panfish and meiobenthos. In addition, it is assumed that catfish opportunistically consume a much wider variety of additional prey in CAM (refer to Table 17) compared to the EwE model by Christensen et al. (2009). No differences in diets were modeled between juvenile and adult catfish.

Cownose Ray

Initial diet data were derived from ChesMMAP data and supplemented by data presented in Table 1 of Smith and Merriner (1985).

Gizzard Shad

The diet of gizzard shad in CAM was initially based on that of Christensen et al. (2009), but the Christensen diet was extremely limited and included only phytoplankton (75%) and mesozooplankton (25% of total diet). In CAM, the gizzard shad diet is expanded to include prey important to other *Alosa spp.* (see Alosine group diet, above), including important dietary contributions by meiobenthos, dinoflagellates, picophytoplankton, and soft-bodied benthic invertebrate groups (i.e., benthic carnivores, benthic deposit feeders, and benthic filter feeders), in order of decreasing assumed importance. No differences in diets were modeled between juvenile and adult gizzard shad.

Other Flatfish

The diet of this aggregate group represents a composite diet of hogchoker, windowpane flounder, blackcheek tonguefish, and winter flounder. The composite diet was based on ChesMMAP data supplemented by information presented in Curti (2005), Table 2 in Toepher and Fleeger (1995), page 2 in Pereira et al. (1999), and from data presented on page 9 of Link et al. (2002).

Panfish

Panfish is an aggregate group that includes silver perch, spot, yellow perch, and bluegill. Only silver perch diet data is found in the ChesMMAP data set. The final diet for silver perch in the ChesMMAP data were supplemented with information from Figure 7 of Parthree et al. (2006), and Figure 7 in Latour et al. (2006). Diet data for spot was developed from Figure 4 in Latour et al. (2006), and from data in Horvath (1997). The diet for yellow perch was taken from the Chesapeake Bay Foundation field guide (http://www.chesapeakebay.net/fieldguide/critter/yellow_perch , accessed 18 January, 2011). Diet of the bluegill was derived from the website publication by C. Parr, 2002, at http://animaldiversity.ummz.umich.edu/site/accounts/information/Lepomis_macrochirus.html, accessed 18 January 2011). These data were combined to develop one composite panfish diet.

Pelagic Forage Fish

The diet for this aggregate group, that includes both the Atlantic silverside and mummichog, is assumed to be composed mainly of mesozooplankton with important contributions of benthic filter feeders; large phytoplankton; microzooplankton; meiobenthos; other soft-bodied benthic invertebrates (i.e., benthic carnivores, benthic deposit feeders, and benthic filter feeders); dinoflagellates; and picophytoplankton.

Reef Associated Fish

Reef associated fish is an aggregate group that includes oyster toadfish, black seabass, tautog, and Atlantic spadefish. Of these, diet information was available from the ChesMMAP data for oyster toadfish, black seabass, and tautog. Final diets for each of these three species were supplemented by: oyster toadfish—Adams (1976) and Fishbase (http://www.fishbase.org/trophiceco/DietCompoSummary.php?dietcode=1817&genusname=Opsanus&speciesname=tau , accessed 18 January, 2011); black seabass—Steimle et al. (1999) and Sedberry (1988); and tautog—Steimle and Shaheen (1999). Diet data for the Atlantic spadefish was derived using information found in the web publication of the Florida Museum of Natural History, "Biological Profile, Atlantic Spadefish" available at http://www.flmnh.ufl.edu/fish/Gallery/Descript/Atlanticspadefish/Atlanticspadefish.html, accessed 18 January 2011). These data were combined to develop one composite reef associated fish diet.

Sandbar Shark

In CAM, the diet for the top carnivore in the Bay, sandbar shark, is assumed to be varied and opportunistic. We initially (pre-calibration) assumed a uniform distribution of sandbar shark prey, not dominated by any particular fish or invertebrate (see Table 16), that included blue crab and most macroscopic, pelagic prey groups available in the model (excepting bay anchovy and pelagic forage fish). No differences in diets were modeled between juvenile and adult sandbar sharks.

Smooth Dogfish

Initial diet data for smooth dogfish was derived from ChesMMAP data and supplemented based on food habits data summarized at the NMFS Apex predator website: http://na.nefsc.noaa.gov/sharks/ (accessed 18 January 2011).

Spiny Dogfish

Initial diet data for spiny dogfish was derived from ChesMMAP data and supplemented by data provided in Figure 3 of McMillan and Morse (1999).

Striped Bass

Both juvenile and adult striped bass diets were based on Christensen et al. (2009). However, "resident" and "migratory" adults of that model were combined into one adult stock in CAM, and dietary contributions for adults were expanded to reflect that published in Water and Austin (2003).

Summer Flounder

Initial diet data for summer flounder was derived from ChesMMAP data and supplemented with data presented in Figure 32 in Packer et al. (1999).

Weakfish

Initial diet data for weakfish were derived from ChesMMAP data and supplemented based on data presented in Figure C11.3-3 (page 691) of the 48th Northeast Regional Stock Assessment Workshop (Northeast Fisheries Science Center, 2009).

White Perch

Initial diet data for white perch was derived from ChesMMAP data and supplemented with data presented in Figure 5 in Neuman et al., (2004).

Mammals

The only mammal stock modeled in CAM is the bottlenose dolphin. The diet of the dolphin in CAM follows Mrang et al. (1994), which specifies that fish and squid are important in the diets of coastal bottlenose, but we assume that dolphin also consume blue crab, as reported in Lippson and Lippson (1997). Lacking specific proportions of prey from gut content analyses, we assumed that a uniform distribution of all pelagic finfishes and blue crab comprise the bottlenose dolphin diet.

Reptiles

Diamondback Terrapins

A detailed diet analysis for wild-caught diamondback terrapins was not found in the literature; consequently, a uniform distribution of probable prey was used for this group in the initial model. This was adjusted somewhat, based on spatial distribution of terrapins and their prey. Terrapins were assumed to prey mainly on fish (e.g., bay anchovy, weakfish, striped bass, white perch, pelagic forage fish, other flatfish); benthic invertebrates (e.g., benthic filter feeders, benthic deposit feeders, benthic carnivores, meiobenthos); algae (microphytobenthos); and SAV (seagrass), but feed on many additional groups as well (see Table 17). There were no differences between the prey of juvenile and adult terrapins in the model.

Sea Turtles

As specified earlier (see Appendix C), the aggregate sea turtle group consists mainly of loggerhead characteristics, while leatherback and Kemp's ridley characteristics add to the diversity of the group. The modeled sea turtle diet is consistent with this approach. Consequently, like the loggerhead diet, the sea turtle diet is characterized by crustaceans, finfish (Seney and Musick, 2007), SAV (Musick, 1988), and other benthic components. Since the leatherback and Kemp's ridley sea turtle diets (the other two common Chesapeake species included in the sea turtle group) are understood to be composed mostly of jellyfish and benthic invertebrates (mollusks and crustaceans), respectively (Musick 1988), these prey are included in the aggregate sea turtle diet as well. Because the loggerhead's preferred diet appears to vary significantly with prey availability (Seney and Musick, 2007), the aggregate sea turtle diet modeled here is assumed to be uniformly distributed among the available benthic invertebrates, finfish, and SAV and includes the detrital and bacterial components of the ecosystem.

Birds

Recent work suggests that bird population trends could be a useful indicator of forage health in the system (Piatt et al., 2006; Pikitch et al., 2012). In addition, recent trends in bird populations due to climate change could have an important effect on forage in the Chesapeake Bay (Ihde et al., 2015). Four bird groups are modeled in CAM. Three are multi-species aggregate groups (benthic grazing seabirds, piscivorous seabirds, diving ducks), and one is composed of a single species (bald eagle).

Bald Eagle

The modeled bald eagle diet consists mainly of larger species of available finfish. Lacking a regional diet study on which to base a system-wide bald eagle diet, the authors assumed a uniform distribution for the larger finfish species, blue crab, and herbivorous birds (Table 16). These assumptions were based on a general description available at the Cornell Lab of Ornithology website (https://www.allaboutbirds.org/guide/Bald_Eagle/lifehistory, last accessed 1-4-16), with assumed preferences for gizzard shad, bluefish, catfish, and weakfish.

Benthic Grazing Seabirds

Benthic grazing seabirds is an aggregate group that includes Canada goose, tundra swans, mallard ducks, mute swans, and redhead ducks. Diet of each species was based on literature summarized on Birds of North America Online (http://bna.birds.cornell.edu/bna; accessed 18 October 2010). The aggregate benthic grazing seabird diet was combined with individual species diets weighted in accordance with biomass estimates from D. Forsell (unpublished data, Coastal Program biologist with the U.S. Fish and Wildlife Service, Chesapeake Bay Field Office), with Canada goose dominating the diet characteristics of the aggregate group (0.8). Tundra swan, mallard duck, mute swan, and redhead ducks each contribute relatively small proportions to the diet (0.08, 0.063, 0.05, and 0.006, respectively). The resulting benthic grazing seabird diet is mostly herbivorous: about 45% is composed of SAV, approximately 35% marsh grass, and a small percentage of microphytobenthos. However, the diet also includes a variety of benthic invertebrates, plankton, meiobenthos, detritus, and bacteria. The modeled diet of this group pertains only to the aquatic portion of the diet of this group; i.e., diet was restricted to the model domain, and thus the contribution agricultural grains and freshwater wild rice were not included.

Diving Ducks

Diving ducks is an aggregate group. Though life history parameters are based mainly on "seaducks" (i.e., surf scoter and long-tailed ducks), detailed diet information was available for a broader group of regional diving ducks in data provided by Perry et al. (U.S.G.S. Patuxent Wildlife Research Center) in an online resource: http://www.pwrc.usgs.gov/resshow/perry/foodhabits.htm (accessed 1-4-16). Consequently, the authors decided to incorporate this detailed diet information for a more generalized predatory duck functional group. Diving duck diet, therefore, includes that of surf scoter, black scoter, long-tailed duck, ruddy duck, bufflehead, canvasback, lesser scaup, and greater scaup. Modeled diving ducks are primarily predatory birds that prey mostly on benthic invertebrates, where more than 60% of their diet consists of benthic filter feeders (BFD) and 25% of their diet is Macoma clams (BFS). They also consume submerged plant matter while foraging, and nearly 10% of their diet consists of SAV.

Piscivorous Seabirds

Piscivorous seabirds is an aggregate group consisting of brown pelican, double-crested cormorant, great blue heron, and osprey. Diet of each species was based on literature summarized on Birds of North America Online (http://bna.birds.cornell.edu/bna; last accessed 18 October 2010). The aggregate piscivorous seabird diet was combined with individual species diets weighted in accordance with biomass estimates from D. Forsell (unpublished data, Coastal Program biologist with the U.S. Fish and Wildlife Service, Chesapeake Bay Field Office), with great blue heron dominating the characteristics of the diet (0.71), double-crested cormorant contributing a relatively large proportion (0.15), and with osprey and brown pelican both contributing about (0.07). Modeled piscivorous seabirds are predators and mainly consume the wide variety of available finfish species, but this group's diet also includes terrapins, blue crab, herbivorous birds and brief squid if available.

Invertebrates

Of the 26 groups classified as "invertebrates" in CAM, 12 are heterotrophic: dinoflagellates, zooplankton (4), brief squid, blue Crab, aggregate benthic invertebrate groups (4), and oyster. See Tables 17 and 18 for additional details.

Dinoflagellates and Zooplankton

Dinoflagellates are modeled as mixotrophs in Atlantis, both producing their own nutrients through photosynthesis and acting as heterotrophs opportunistically. Though the size of dinoflagellates modeled in the Chesapeake Bay ranges widely (5 um–2 mm), a simple size-based diet was assumed to be representative for this diverse group. Dinoflagellates heterotrophy includes (in descending order of importance) picophytoplankton, microphytobenthos, bacteria, microzooplankton, and dinoflagellates.

Zooplankton are composed of four diverse and distinct groups in CAM. Ctenophores and sea nettles are modeled separately to allow for the modeling of the complex interactions with oysters currently understood to occur during different portions of the lifecycle of all three organisms (Breitburg and Fulford, 2006). In recognition of this interaction in the model, ctenophores are assumed to consume available oyster larvae, and sea nettles consume small ctenophores. Other prey for both groups are based on Christensen et al. (2009) and assumed to be mostly similar, except that a small portion of the sea nettle diet also includes fish. The two remaining zooplankton groups are size-based aggregate groups, mesozooplankton (0.2–20 mm, including copepods) and microzooplankton (0.02–0.2 mm, including rotifers, ciliates, and copepod nauplii). The largest portion of the mesozooplankton diet consists of (in order of decreasing importance) microzooplankton, cryptophyes and diatoms (one group), picophytoplankton, dinoflagellates, and microphytobenthos; and is based on the relative size of prey and Christensen et al. (2009). Likewise, the largest portion of the microzooplankton diet is picophytoplankton, cryptophyes/diatoms, and dinoflagellates.

Brief Squid

Brief squid were assumed to feed mainly on fish found in the polyhaline portions of the Chesapeake (Bartol et al., 2002). Consequently, the squid diet is modeled as that of an opportunistic piscivore, and its diet consists of bluefish, bay anchovy, pelagic forage fish, striped bass, white perch, other flatfish, brief squid, and smaller proportions of Atlantic menhaden and Alosines.

Blue Crab

Blue crabs are largely opportunistic feeders in the Chesapeake Bay (Seitz et al., 2011). Therefore, diets were assumed to be composed mostly of widely available benthic invertebrate groups (in order of decreasing importance: *Macoma sps.*, deposit feeders, and benthic filter feeders), blue crabs, and detritus. Gross diet is largely similar to that described in Christensen et al. (2009), though prey groups available were fewer and less varied in that study.

(Aggregate) Benthic Invertebrate Groups

Aggregate benthic invertebrate groups were based on species observed in the CBP Benthic Index of Biological Integrity (2002–2009, see main text for details). Groups were structured to model ecological function; e.g., "Benthic filter feeders (BFD)," "Benthic carnivores (BC)," and "Benthic deposit feeders (BD)." An additional aggregate group, "Macoma (BFS)," was included in recognition of the current understanding of the importance of clams in general (Hines et al., 1990) and of *Macoma sps.* specifically, to the blue crab diet (Seitz et al., 2005). Diets of these four groups were based mainly on Baird and Ulanowicz (1989), but were supplemented by expert knowledge (personal communication, R. Llanzo, Versar, Inc., and W. Slacum, Oyster Recovery Partnership). Information applied from Baird and Ulanowicz (1989) included Table 4 (page 344) and Figure 7 (page 347), representing the annual percent of carbon at individual nodes from donor nodes in the network flow diagram (Figure 7 on page 347).

Oyster

The diet of oyster is based largely on Baird and Ulanowicz (1989) as described previously for the aggregate benthic invertebrate groups. The largest portion of the oyster diet consists of diatoms and cryptophyes (~40%), but the diet also includes a substantial proportion of picophytoplankton, detritus, and microzooplankton.

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