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Evaluation of natural mortality rates and diet composition for gag (*Mycteroperca microlepis*) in the West Florida Shelf ecosystem using the individual-based, multi-species model OSMOSE

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Introduction

An Integrated Ecosystem Assessment (IEA) project has been initiated in the Gulf of Mexico (GOM), with the main intent to develop a framework for regularly incorporating ecosystem considerations into the SEDAR process (http://www.noaa.gov/iea/gulfofmexico.html). One of the major thrusts of the GOM IEA project is the use of ecosystem models to consider the major components of the GOM ecosystem and their interactions, and analyze the emergent properties of the ecosystem that would be missed by examining components separately (Schirripa et al. 2013).

The West Florida Shelf is one of the main subregions of the GOM ecosystem, under high and increasing anthropogenic and environmental pressures (Coleman et al. 2004, Okey et al. 2004, Walsh et al. 2011). The West Florida Shelf ecosystem is house to a very high diversity of pelagic, demersal and benthic species, of which many are of high economic importance (NOS 2008, Gentner 2009, NOAA 2010). Given the value of services provided by the West Florida Shelf ecosystem, and concerns raised regarding the sustainability of fishing activities and the impacts of environmental events such as red tides in this region, Ecopath models have been developed (Okey and Mahmoudi 2002, Okey et al. 2004, Chagaris and Mahmoudi 2013). Ecopath is a mass-balance model which explicitly considers the quasi-totality of the organisms living in a given ecosystem (fish, marine mammals, seabirds, plankton, ...), and provides a snapshot of the ecological role of functional groups, and of the effects of fishing and other pressures on the modeled food web (Pauly et al. 2000, Christensen and Walters 2004). The last Ecopath model developed for the West Florida Shelf to date has been designed to evaluate changes in biomasses, trophic interactions, and fishing pressures in time using the Ecosim module (resulting in an EwE model), and also in space using the Ecospace module (Chagaris and Mahmoudi 2013). Hereinafter, we refer to this model as to

‘WFS Ecopath’, ‘WFS EwE’ or ‘WFS Ecospace’, depending on the modules considered when mentioning parameters or variables.

WFS EwE is currently being used for multiple purposes, including policy simulations, policy optimization and management strategy evaluation (Chagaris and Mahmoudi 2013). Very recently, another ecosystem model has started being developed for the West Florida Shelf, an OSMOSE (Object-oriented Simulator of Marine biOdiverSity Exploitation) model with a monthly time step, referred to as ‘OSMOSE-WFS’. OSMOSE is a two-dimensional, individual-based and multispecies model explicitly representing major processes in the life cycle of a limited number of groups of marine species, where diet compositions emerge from simulations (Shin and Cury 2001, 2004). OSMOSE-WFS builds on WFS EwE efforts, in that the two models share a number of characteristics (e.g., the spatial domain considered, reference biomasses; Fig. 1). However, obviously, the structure and assumptions of OSMOSE and EwE models are very different. Therefore, the use of the OSMOSE-WFS and WFS EwE models is interesting to have two different perspectives on the same questions, while being able to identify where discrepancies between the two models may stem from. Using a model ensemble approach reduces our uncertainties on emergent properties of ecosystems, or at least helps identify avenues for research to that goal.

The development of the WFS EwE and OSMOSE-WFS models offers numerous perspectives to explore the trophic functioning of the West Florida Shelf ecosystem in the past, present and future; but also to provide management with ecosystem considerations, and estimates of parameters that are highly difficult to evaluate from empirical data. Currently, the primary goal of WFS EwE and OSMOSE-WFS within the GOM IEA project is to regularly provide SEDAR with parameter estimates. In 2013, simulations will be run with the two models to deliver estimates of deviations in natural mortality rates and recruitment for gag (*Mycteroperca microlepis*) to SEDAR 33 for the contemporaneous time period (the 2000s), as well as for the periods 1950-2009 (historical perspective for gag) and 2009-2029 (future perspective for gag). 2013 is seen as a pilot year, which will help define a consistent framework for the long-term.

In the present paper, we first provide an overview of the OSMOSE model, before describing the structure and assumptions of OSMOSE-WFS and detailing our parameterization choices. Next, we present the methodology we are currently implementing to calibrate OSMOSE-WFS to a reference state matching the mean conditions in the West Florida Shelf region over the period 2005-2009 predicted by WFS Ecopath. Once OSMOSE-WFS is properly calibrated, the model will be used to get first estimates of natural mortality rates, diet composition and recruitment levels for gag in the West Florida Shelf ecosystem in the 2000s. In the end of the paper, we discuss our short-term and long-term perspectives regarding the use of OSMOSE-WFS within the SEDAR process. Our objective here is to introduce OSMOSE-WFS to the SEDAR process, and open discussions on the structure, assumptions and parameterization of the model while we are attempting its first calibration.

The OSMOSE model

OSMOSE is a recently developed individual-based and multispecies model with very different hypotheses from those of Ecopath (Shin and Cury 2001, 2004). By contrast with Ecopath, OSMOSE explicitly models only a limited number of high trophic level (HTL) groups of species. Nevertheless, the other compartments of marine ecosystems (low trophic level (LTL) organisms, HTL organisms such as sharks, marine mammals, and seabirds) are somehow taken into account in OSMOSE. Food intake of modeled HTL groups partly relies on the biomass of various LTL groups (plankton, benthos). Moreover, predation of the HTL groups that are represented in OSMOSE by other HTL organisms is considered through the application of a specific mortality term.

Another difference with Ecopath is that, in OSMOSE, predation is opportunistic. In OSMOSE, a HTL group can feed on any model group (i.e., LTL or HTL group) provided: (1) the predator and its potential prey occur in the same geographical area; (2) there is size adequacy between them; and, (3) the potential prey is accessible to the predator.

In the initial version of OSMOSE, HTL groups were split into piscivorous and non-piscivorous groups according to their age and taxonomy. The total biomass of non-piscivorous groups was constrained by a carrying capacity parameter representing the maximum biomass of LTL groups, and a minimum predator/prey size ratio was defined to restrict predation (Shin and Cury 2004, Shin et al. 2004, Travers et al. 2006, Yemane et al. 2009). In recent versions of OSMOSE, the carrying capacity parameter no longer exists, and OSMOSE is either coupled to a LTL model (Travers 2009, Travers and Shin 2010, Travers et al. 2010) or forced by LTL production or biomass (Marzloff et al. 2009, Travers et al. 2009, Brochier et al. 2013). This modification in OSMOSE structure led to the definition of a maximum predator/prey size ratio in addition to the minimum predator/prey size ratio, so as to ensure that piscivorous HTL groups do not exert an unrealistically high predation pressure on LTL organisms (Travers et al. 2009, 2010).

OSMOSE applications have usually focused on pelagic and demersal marine communities, and have not explicitly represented benthic HTL groups nor considered the biomass of benthic LTL organisms to force the model (but see Brochier et al. 2013). Therefore, the accessibility of the different age classes of the HTL groups to each other has typically been set to 80%, to account for the fact that not all predator attacks are successful, and that the different age classes of HTL organisms partially overlap in the water column

(Travers 2009). On the other hand, the accessibility of HTL groups to plankton groups, which is affected by numerous processes (e.g., turbulence, stratification), and much lower and typically unknown, has usually been estimated during the calibration process of OSMOSE (Marzloff et al. 2009, Yemane et al. 2009, Travers et al. 2010).

The basic units ('super-individuals') of OSMOSE are schools, which consist in organisms belonging to the same HTL group, that have the same length, age, food requirement and, at a given time step, the same spatial coordinates. OSMOSE includes a hierarchical structure of model classes corresponding to those in a HTL community: a 'School' belongs to a 'Cohort' or age class, which itself belongs to a 'HTL group' in the community. Such a hierarchical structure allows the assessment of output variables at different levels of aggregation (e.g., size and biomass can be evaluated at the cohort, HTL group and community levels; Shin and Cury 2001, Shin et al. 2004, Travers et al. 2009).

Structure and assumptions of OSMOSE-WFS

Biomass of LTL groups

OSMOSE-WFS is forced by the biomass of nine LTL groups, consisting of four plankton groups and five benthos groups. The selection of the nine LTL groups was based on their importance in the West Florida Shelf food web (SUSFIO 1977, Phillips et al. 1990, 1991, Vargo and Hopkins 1991, Okey and Mahmoudi 2002) and, particularly, in the diet of the HTL groups that are explicitly considered in OSMOSE-WFS. Biomass of LTL groups is a local input in each model cell and each month.

We were planning to rely on a climatology, i.e., mean annual conditions for the period 2005-2009, for all plankton groups. Therefore, the biomass of the different plankton groups would have accounted for seasonality, but there would have been no consideration of the inter-annual signal in OSMOSE-WFS. The plankton groups would have included small phytoplankton (2-20 µm), diatoms (20-200 µm), microzooplankton (20-200 µm), and mesozooplankton (200-3000 µm). To estimate monthly values of plankton biomasses for OSMOSE-WFS, we were planning to use mean predictions of plankton concentrations over the period 2005-2009 from the LTL model COSINE-13 (Chai et al. 2002, 2003, 2007, Fujii et al. 2007) adapted to the Gulf of Mexico (De Rada et al. 2009). Since COSINE-13 and OSMOSE-WFS have different dimensions (3D versus 2D) and currencies (µmolN/m^{-3} versus wet weight), COSINE-13 outputs would have had to be vertically integrated and transformed into biomasses using specific conversion factors (Table 1).

The COSINE-13 model is currently being improved, such that we were not able to estimate mean plankton biomasses in the West Florida Shelf from simulations of the COSINE-13 model. Therefore, to be able to calibrate and test a first OSMOSE model for the West Florida Shelf ecosystem, we presently consider the following four plankton groups: (1) small phytoplankton (2-20 µm); (2) diatoms (20-200 µm); (3) small copepods (100-1300 µm); and (4) large mesozooplankton (1000-3000 µm). We used estimates of chlorophyll a concentration in the West Florida Shelf as a proxy of phytoplankton biomass in the region. We produced a climatology of chlorophyll a concentration in the West Florida Shelf region from SeaWiFS data, downloaded from http://oceancolor.gsfc.nasa.gov/SeaWiFS/ (Hooker 1992, McClain et al. 2004; Fig. 2). From the climatology of chlorophyll a concentration and the total biomass of the phytoplankton group in the WFS Ecopath model (Table 2), we generated a climatology of biomass for the small phytoplankton and diatoms groups, under the assumption that these two groups are equally abundant in biomass in the West Florida Shelf. Moreover, we assumed that small copepods and large mesozooplankton occur over the whole West Florida Shelf ecosystem. We estimated the total biomass of each of these two zooplankton groups in the West Florida Shelf region from WFS Ecopath (Table 2), that we distributed uniformly over our study system. Here, the biomass values of small copepods and large mesozooplankton do not vary from one month to the next.

LTL benthos groups in OSMOSE-WFS consist of meiofauna, small infauna, small mobile epifauna, bivalves, and echinoderms and large gastropods (Table 2). In the absence of detailed spatial information for these five groups, we made the assumption that they all occur over the whole West Florida Shelf. We evaluated the total biomass of each of these groups in the West Florida Shelf region from WFS Ecopath, which we distributed uniformly over our study system. The biomass values of the LTL benthos groups do not vary from one month to the next.

The estimates of LTL biomasses used here are provisional, and we are planning to update these estimates in the near future, once new simulations of the COSINE-13 model have been run (see the Discussion and perspectives section).

Life cycle of HTL groups

Twelve groups of HTL species are explicitly considered in OSMOSE-WFS. These 12 groups were selected for their contribution to total biomass and economic value in the West Florida Shelf region during the 2000s, and/or because they are key to the West Florida Shelf food web and, particularly, to the diet of gag. The selection of 12 HTL groups was also based on data availability. Hence, for example, we do not explicitly consider here stomatopods and different groups of small coastal carnivores, which sometimes have a non-negligible importance in the diet of gag (Florida Fish and Wildlife Research Institute, unpub. data). The explicit representation of a limited number of HTL groups in OSMOSE allows disentangling the complexity of interactions within marine ecosystems (Travers et al. 2010). More HTL groups may be added in future versions of OSMOSE-WFS if more data and information become available and if it is relevant regarding the questions that need to be addressed.

Species of a given HTL group exhibit similar life history traits, size ranges, diets and exploitation patterns. Some species constitute their own group, as they are emblematic to the West Florida Shelf ecosystem and of high economic importance. HTL groups include 10 fish species/groups of fish species and two crustacean groups: (1) king mackerel (*Scomberomorus cavalla*); (2) amberjacks; (3) red grouper (*Epinephelus morio*); (4) gag; (5) red snapper (*Lutjanus campechanus*); (6) the sardine-herring-scad complex; (7) anchovies and silversides; (8) coastal omnivores; (9) reef carnivores; (10) reef omnivores; (11) shrimps; and (12) large crabs. A reference species was identified for each of the HTL groups (Table 3). Growth, reproduction, mortality and diet parameters of each group are those of the reference species of the group.

Within a monthly time step, the following succession of events occurs in OSMOSE-WFS: Schools are distributed on a two-dimensional grid → Mortalities (fishing mortality, predation and starvation mortalities, and natural mortality from other sources) are applied to schools → The growth in size and weight of schools is evaluated based on their predation success → Reproduction takes place.

Spatial distribution of schools

The spatial distribution of a school at each time step is driven by specific maps that depend on the HTL group and cohort to which the school belongs and to the season. The great majority of these distribution maps were generated for each reference species of the HTL groups using a generalized additive modeling (GAM) approach developed by Drexler and Ainsworth (in revision) (Box 1). For some age groups of the reference species, we did not have enough data to implement the GAM approach. In this case, we resorted to information from the literature and to experts' opinion to produce distribution maps (Box 1).

When the distribution of schools remains static (within a season or if the distribution is identical, throughout the year), these schools move to immediately adjacent cells within their distribution area following a random walk. Random walk movements are meant to represent small-scale foraging movements and/or to account for uncertainties on the distribution patterns predicted by the maps we produced.

The GAM approach we used predicts spatial patterns of abundance of age groups in the West Florida Shelf region over the period 2000-2010 from large research survey datasets and local environmental features (chlorophyll A, dissolved oxygen, temperature and sediment type). The research survey datasets we used include the SEAMAP (Southeast Area Monitoring and Assessment Program) groundfish dataset (Rester 2011), the National Marine Fisheries Service (NMFS) bottom longline (BLL) survey dataset (Ingram et al. 2005), and the SEAMAP reef fish dataset (Gledhill et al. 2005). The GAM approach combines a GAM model describing the probability of occurrence of age groups at survey sampling stations and another one describing abundance at non-zero locations, using a delta method (see Box 1 for more details).

Mortalities

Previously, in OSMOSE, within a time step, natural mortality due to causes other than starvation and predation was applied to schools, then predation mortality, then starvation mortality, and finally fishing mortality. One major flaw of this order of succession of mortality events is that fishing mortality was applied to schools that were already depleted by predation. As a result, the effective fishing mortality rates exerted on HTL groups were often lower than the fishing mortality rates specified as inputs (Y.-J. Shin & P. Verley, pers. obs.).

Here, we take a different approach and consider that all types of mortalities are continuous processes that occur simultaneously, and that there is neither competition nor stochasticity in the predation process. Within each time step, the total mortality of a given school i (Z_i) comprises fishing mortality (F_i), starvation mortality (S_i), predation mortality caused by various schools j ($P_{i,j}$), and natural mortality rate due to causes other than starvation and predation ($M_{diverse\ i}$).

Natural mortality $M_{diverse}$

We distinguish between two sources of natural mortality other than predation and starvation: the mortality due to marine organisms that are not considered in OSMOSE-WFS, *D*; and the mortality of larval schools due to different causes (e.g., non-fertilization of eggs, advection away from suitable habitat, sinking), *M0*. For each HTL group, the *D* parameter was estimated from evaluating the natural mortality rate of these groups due to predation of marine organisms that are considered in WFS Ecopath but not in OSMOSE-WFS (Chagaris and Mahmoudi 2013). *M0* is unknown for the quasi-totality of our HTL groups. Therefore, this parameter will be estimated during the calibration process of OSMOSE-WFS (see below).

Fishing mortality

Fishing is here assumed to be uniform over space. Fishing reduces school abundance through the application of a month- and group-specific fishing mortality rate to any school whose body length is larger than the recruitment size specified for each HTL group. Monthly fishing mortality rates for each HTL group are estimated from a group-specific annual fishing mortality rate F_{annual} (Table 4) and the seasonality of F_{annual}. Discards were explicitly taken into account in the calculation of F_{annual} for king mackerel (SEDAR 16 2009), amberjacks (SEDAR 2011), red grouper (SEDAR 2009a), gag (SEDAR 33, in prep.) and red snapper (SEDAR 2009b). Bycatch in the shrimp trawl fishery was also explicitly taken into account in the calculation of F_{annual} for king mackerel (SEDAR 16 2009) and red snapper (SEDAR 2009b).

In the absence of data, we assumed no seasonality of F_{annual} for the sardine-herring-scad complex, the anchovies and silversides group and reef carnivores. The seasonality of F_{annual} of all other HTL groups – except reef omnivores that are not targeted by fishing – was estimated from the monthly total catches of their reference species over the period 2005-2009. Monthly total catches were calculated from NMFS statistics for the commercial and recreational fisheries of the west coast of Florida (Box 2).

Predation and starvation

Due to our assumption that all types of mortalities are concomitant and that there is neither competition nor stochasticity in the predation process, predation and starvation mortality rates at each time step are relatively complex to estimate.

In OSMOSE, each school *i* has a maximum ration in biomass at each time step, Y_i^*, determined the maximum annual ingestion rate of the HTL group to which it belongs. To reach this maximum ration, the school *i* should consume a quantity $C_{j,i}^*$ of a given prey *j* (*j* belonging either to a HTL or to a LTL group) falling in the feeding size range of school *i*.

Provided that only a fraction $\delta_{j,i}$ of prey *j* is accessible to school *i*, the potential maximum number of prey *j* that could be predated by school *i* at time *t* ($C_{j,i,t}^{\max}$) is given by:

$$C_{j,i,t}^{\max} = \min\left(C_{j,i}^{*}, \delta_{j,i} N_{j,t}\right) \tag{1}$$

where $N_{j,t}$ is the abundance of school *j* at *t*. Then, the potential maximum predation mortality rate of prey *j* caused by school *i* at *t* ($P_{j,i,t}^{\max}$) can be evaluated as:

$$P_{j,i,t}^{\max} = \ln\left({N_{j,t}} \big/ {N_{j,t} - C_{j,i,t}^{\max}} \right) \tag{2}$$

The fact that $\delta_{j,i} < 1$ ensures that $P_{j,i,t}^{\max} < \infty$. Given that the prey *j* is exposed to sources of mortality other than the predation of school *i*, the effective maximum number of individuals of school *j* consumed by predator *i* at time *t* ($P_{j,i,t}^{eff\,\max}$) is:

$$P_{j,i,t}^{eff\,\max} = P_{j,i,t}^{\max}\left[\left(1 - e^{-Z_{j,t}}\right)/ Z_{j,t}\right] N_{j,t} \tag{3}$$

Then, in the situation where predator *i* could maximize its predation on all potential prey items, its ration in biomass at time *t* would be equal to:

$$Y_{i,t} = \sum_{j} W_j P_{j,i,t}^{eff\,\max} \tag{4}$$

where W_j is the average weight of individuals of prey *j*. The ration estimated in Eq. 4 may be greater than Y_i^{*} and, in this case, may need to be adjusted to ensure that the predation pressure exerted by school *i* is not overestimated.

The ratio between $Y_{i,t}$ and Y_i^{*} determines the predation efficiency of school *i* at time *t*, $\xi_{i,t}$. If $\xi_{i,t}$ is less than the predation efficiency ensuring the maintenance of school *i*, ζ_i^{crit}, then school *i* undergoes a starvation mortality $S_{i,t}$, increasing linearly with the decrease of $\xi_{i,t}$ (Shin and Cury 2001, 2004):

$$S_{i,t} = S_i^{\max} - \frac{S_i^{\max}}{\xi_i^{crit}} \xi_{i,t} \tag{5}$$

where $S_i^{\max}$ is the maximum starvation mortality rate of school *i* at any time step, determined from the maximum annual starvation mortality rate of the HTL group to which it belongs.

As mentioned above, the ration in biomass of school *i* at time *t* could be greater than Y_i^*. To correct this, we implemented an algorithm consisting in: (1) calculating a correction factor so as to adjust the effective number of individuals of each prey item consumed by each predator at *t*; (2) reevaluating the total mortality rate of each prey item and the effective number of individuals of each prey item consumed by each predator; (3) reevaluating the ration in biomass of each school at *t*; (4) repeating previous steps until the ration in biomass of all the schools present in the different cells of the model is equal to or less than its maximum value. The correction factor for a given school *i* at time *t* ($cf_{i,t}$) mentioned in step (1) is given by:

$$cf_{i,t} = \min\left(Y_i^* / Y_{i,t}, 1 \right) \tag{6}$$

Under numerical experiments conducted with 2000 to 10000 schools per annual annum, the iteration of the algorithm stopped after 6 to 11 iterations (R. Oliveros-Ramos, pers. com.).

Estimation of instantaneous mortality rates

The instantaneous mortality rates of eggs and larvae (0-1 month old individuals), pre-recruits (individuals older than 1 month whose length is smaller than the recruitment size) and recruits (individuals whose length is larger than the recruitment size) of HTL groups can be evaluated for each time step. For each HTL group, the instantaneous mortality rate of life stage *s* due to cause *k* at time *t*, $\mu_{s,t}^{k}$, is given by:

$$\mu_{s,t}^{k} = Z_{s,t} \frac{N_{s,t}^{Dead\ k}}{\left(1-e^{-Z_{s,t}}\right)N_{s,t}} \tag{7}$$

with *k* being (i) larval mortality due to various causes or predation mortality for eggs and larvae; (ii) predation mortality, starvation mortality, or natural mortality from other sources for pre-recruits; (iii) predation mortality, starvation mortality, natural mortality from other sources, or fishing mortality for recruits; $N_{s,t}$ is here the abundance of life stage *s* at the start of time *t*; $N_{s,t}^{Dead\ k}$ is the total number of individuals of life stage *s* undergoing mortality due to cause *k* at time *t*; and $Z_{s,t}$ is here the total mortality rate of life stage *s* at time *t*, given by:

$$Z_{s,t} = \ln\left(\frac{N_{s,t}}{N_{s,t} - N_{s,t}^{Dead\ k}}\right) \tag{8}$$

Growth

Individuals of a given school *i* are assumed to grow in size and weight at time *t* only when the amount of food they ingested fulfill maintenance, i.e., only when their predation efficiency at *t* is at or greater than ζ_{i}^{crit}. In such as case, the growth in size of school *i* at time *t* ($\Delta L_{i,t}$) varies between 0 and twice the mean length increase *ΔL* calculated from either a linear or a von Bertalanffy model, depending on $\xi_{i,t}$ (Shin and Cury 2001, 2004):

$$\Delta L_{i,t} = \frac{2\Delta L}{1-\zeta_i^{crit}}\left(\xi_{i,t} - \zeta_i^{crit}\right) \tag{9}$$

A von Bertalanffy model is used to calculate mean length increase only above a threshold age A_{thres} determined for each HTL group from the literature. Below A_{thres}, a simple linear model is used. The rationale behind this is that von Bertalanffy models are usually estimated from data excluding youngs of the year or including only very few of them. Assuming a linear growth between age 0 day and A_{thres} ensures a more realistic calculation of mean length increases for early ages of HTL groups (Travers 2009).

The weight of school i at time t is evaluated from the allometric relationship:

$$W_{i,t} = cL_{i,t}{}^{b} \tag{10}$$

where b and c are allometric parameters for the HTL group to which school i belongs.

Reproduction

Any school whose age is greater than the age of sexual maturity A_{mat} reproduces at the end of each time step, allowing for the generation of new schools at the larval stage for the next time step. At the scale of the HTL group, the number of eggs produced at time t ($N_{0,t}$) is calculated as:

$$N_{0,t} = SR.\Phi^{Month}\Theta\sum_{a=A_{mat}}^{A_{\max}} B_{a,t} \quad if\ t = Month \tag{11}$$

where SR is the female: male sex ratio of the HTL group; Θ the relative annual fecundity of the group (number of eggs spawned per gram of mature female per year); Φ^{Month} the probability for the HTL group to spawn a given month relatively to the other months of the year; $B_{a,t}$ the biomass of the group at age a and time t; and A_{max} the maximum age of the group. In the absence of information, we assumed no seasonality of reproduction for reef omnivores. The Φ^{Month} parameters of all other HTL groups were estimated from the literature (Box 3). The eggs of all HTL groups are allocated a size of 1 mm, which appears to be a representative mean for marine fish species regardless of the size of the adults (Cury and Pauly 2000), and a weight of 0.0005386 g, considering eggs as spheres with water density.

It can be noted that, since the growth of schools is evaluated in relation to their predation efficiency, the number of eggs produced at each time step, which depends on biomass (Eq. 11), also depends implicitly on the food intake of schools (Shin and Cury 2001, 2004).

Parameterization of OSMOSE-WFS

The geographical area considered in OSMOSE-WFS is identical to that modeled in WFS Ecospace. The spatial domain of OSMOSE-WFS extends from approximately 25.2° N to 31°N in latitude and from approximately 80.2°W to 87°W in longitude, and it comprises 465 square cells with closed boundaries (Fig. 1).

The growth and reproduction parameters of the HTL groups and their mortality parameters other than those related to predation and starvation processes are detailed in Table 4, along with their sources. Of all OSMOSE parameters, relative annual fecundity is the most difficult to obtain (Shin et al. 2004, Plagányi 2007) so that, for a few reference species, the value of this parameter had to be estimated from information on related species living in other geographical areas (Table 4). Note that two HTL groups considered in OSMOSE-WFS, red grouper and gag, are protogynous, i.e., mature first as females and then change sex to males (Coleman et al. 1996a, Koenig and Coleman 2011). Explicitly considering sex change in

OSMOSE would necessitate differentiating between female and male grouper schools. Furthermore, egg fertilization and, therefore, recruitment success of protogynous species may decrease when fishing increases female: male sex ratio above a certain threshold, although solid empirical evidence of this phenomenon is lacking (Coleman et al. 1996a, Koenig et al. 1996a, Fitzhugh et al. 2006a). For simplicity, we chose to not represent sex change in OSMOSE-WFS, though we accounted for species-wide sex ratios biased towards females in red grouper and gag (Table 4). Moreover, the estimation of larval mortalities, *M0*, through model calibration compensates for not explicitly representing the numerous processes influencing larval survival including egg fertilization.

As to the parameterization of predation and starvation processes, we set some parameters at a default value for all HTL groups due to a lack of information. Thus, for all HTL groups, we set maximum ingestion rate to 3.5 g of food per g of individual and per year, critical predation efficiency to 0.57, and maximum starvation mortality to 0.3 year^{-1} (Shin and Cury 2001, 2004). Moreover, we estimated values for the minimum and maximum predator/prey size ratios of our HTL groups from queries in a large trophic database that is being compiled for the Gulf of Mexico trophic ecosystem, the Gulf of Mexico Species Interaction (GoMexSI) database (Simons et al. 2013). The estimation of these feeding size ranges was carried out in two steps. Firstly, all entries in the GoMexSI database containing prey length data along with predator length data were extracted; and first estimates of minimum and maximum predator/prey size ratios were calculated. Secondly, publications, reports, theses and dissertations and government reports about the diet composition of the reference species of HTL groups were identified from the GoMexSI database; and estimates of minimum and maximum predator/prey size ratios were refined based on information from this literature, and estimates of the mean, minimum and maximum lengths of the different predators and prey considered (Table 5).

Finally, we had to determine accessibility coefficients for HTL groups once predator/prey size ratios were defined. Here, we did not set the accessibility coefficients of the different age classes of the HTL groups to a default value of 80% since our model groups occupy diverse positions in the water column (consider, e.g., king mackerel which is pelagic, gag which is demersal and bivalves which are benthic). Instead, we defined several of the accessibility coefficients of the HTL groups to each other and to benthic low trophic level groups from the literature and expert opinion (J. Simons, Center for Coastal Studies, Texas A&M University-Corpus Christi). The values attributed to accessibility coefficients given in Box 4 are meant to reflect the degree of overlap of model groups in the water column and, to a lesser extent, some factors limiting prey handling (e.g., swimming capabilities), and strong diet preferences. Intentionally, these values differ from the default value of 80% only if it is completely unrealistic to assume something else than low (10% or 40%) or no accessibility (0%), so as to let the diet compositions of the HTL groups emerge primarily from spatial co-occurrence and size adequacy between predators and prey.

The accessibility of each HTL group *i* to a given plankton group *j* (in %) is evaluated as:

$$\delta_{j,i} = \rho_i . \alpha_j \tag{12}$$

where ρ_i is a boolean variable which indicates whether HTL group i feeds on plankton groups (1) or not (0); and α_j the availability coefficient of all HTL groups to plankton group *j* (in %). The ρ parameter was set 1 to 1 for all HTL groups here, based on the literature and expert opinion (J. Simons, Center for Coastal Studies, Texas A&M University-Corpus Christi), while the α parameters will be estimated during the calibration process of OSMOSE-WFS (see next subsection).

Calibration of OSMOSE-WFS

OSMOSE-WFS is currently being calibrated so that the biomasses of HTL groups match the mean values of biomasses predicted by WFS Ecopath for the period 2005-2009 (hereafter referred to as ‘reference biomasses’; Table 6; Chagaris and Mahmoudi 2013). Because OSMOSE is an individual-based model, is stochastic and simulates non-linear processes, classical minimization methods cannot be used for model calibration. Therefore, to calibrate OSMOSE-WFS, we used an improved version of the genetic algorithm method developed by Duboz et al. (2010). The genetic algorithm method was applied to a set of 16 unknown parameters, comprising the larval mortalities (*M0* parameters) of the 12 HTL groups considered in OSMOSE-WFS and the availability coefficient of all HTL groups to the 4 plankton groups forcing the model (α parameters). Reference biomasses were associated with coefficients of variation (Table 6) and, therefore, valid intervals. These coefficients of variation were defined to reflect the uncertainty of WFS Ecopath biomass estimates, according to the criteria specified in Okey and Mahmoudi (2002). So as to justify future comparisons between OSMOSE-WFS and WFS Ecopath, we considered similar individuals to those modeled by means of functional groups in WFS Ecopath for evaluating biomasses in OSMOSE-WFS during the calibration process. Thus, to calculate biomasses in OSMOSE-WFS during calibration, we only took into account individuals older than 1 month for all HTL groups, except for the shrimps group for which we only took into account individuals older than 4 months. For all HTL groups except the shrimps group, individuals younger than 1 month belong to the ‘ichthyoplankton’ group in WFS Ecopath. Shrimps younger than 4 months, i.e., juvenile shrimps (Hart and Nance 2010) belong to the ‘small mobile epifauna’ group in WFS Ecopath.

The genetic algorithm method aims at selecting the best set of unknown parameters based on the Darwinian theory of evolution, which makes the assumption that only the best-adapted genotypes survive and reproduce. The calibration process begins with 200 sets of unknown parameters, constituting the ‘genotype’, set randomly inside their search space ([0; 14 month^{-1}] for larval mortalities and [0; 100%] for availability coefficients). These genotypes are evaluated by running OSMOSE simulations for 50 years: the closer the biomasses of the HTL groups produced by OSMOSE-WFS to reference biomasses, the higher the fitness of the genotypes tested. This fitness results from a combination of 12 pre-fitness functions (one per HTL group), each of which increases with decreasing distance between the biomass simulated by OSMOSE-WFS and the reference biomass. Only the best 50 genotypes are selected and cross-combined to determine a distribution law for the different parameters. These distribution laws are employed to produce 100 new genotypes, replacing half of the parameters population, to be evaluated at the next generation. Using distribution laws allows the introduction of new values of parameters (‘mutations’). Mutations have been shown to improve the convergence of genetic algorithms. Avoidance of local minima is implemented every generation through a naïve strategy exploring step by step the entire search space of the different parameters. The genetic algorithm does not stop running until parameter estimation converges on an optimal genotype. Further details of the genetic algorithm method are provided in Travers (2009), Marzloff et al. (2009) and Duboz et al. (2010).

A first application of OSMOSE-WFS: Evaluation of natural mortality rates and diet composition for gag in the 2000s

Once OSMOSE-WFS is properly calibrated, we will use the model to evaluate first estimates of natural mortality rates and diet composition for gag in the West Florida Shelf ecosystem in the reference situation, i.e., in the 2000s. The ‘reference scenario’ we will consider will consist simply in setting the annual fishing mortality rates of HTL groups to the F_{annual} values specified in Table 4, and evaluate long-term annual mortality rates and diet composition (expressed as percentage of prey groups in mass) for gag; The mortality rates we will evaluate will comprise: (1) total instantaneous natural mortality rate (M); and (2) total instantaneous predation mortality rate, and the instantaneous natural mortality rate due to all other causes (M_{others}), which is the sum of $M_{diverse}$ and the instantaneous starvation mortality rate, S.

In OSMOSE-WFS, the diet composition of each HTL group emerges from encounters at the different time steps with prey of suitable size that are accessible. By contrast, the diet composition of the HTL groups in WFS Ecopath was defined *a priori*, primarily from data of stomach contents collated by the Florida Fish and Wildlife Research Institute (FWRI) and information in FishBase (Froese and Pauly 2010) (Fig. 3). We will only take into account gag individuals older than 1 month to estimate the diet composition of the species in OSMOSE-WFS. To calculate the diet composition of the other HTL groups represented in OSMOSE-WFS, we will also only take into account individuals older than 1 month, except for the shrimps group for which we will only take into account individuals older than 4 months. The rationale behind that is to facilitate future comparisons between the outcomes of the OSMOSE-WFS and those of WFS Ecopath.

OSMOSE-WFS will be run for 50 years. The outputs of the model will be saved for the last 20 years of simulation. Since OSMOSE model is a stochastic model, 10 simulations will be considered for analyzing the outcomes of the reference scenario. The maximum number of schools per annual annum will be set to 240, so as to ensure long-term system stability while allowing for reasonable computation time.

Discussion and perspectives

In the present paper, we introduced the OSMOSE model we are currently developing for the West Florida Shelf, OSMOSE-WFS. A first calibration of OSMOSE-WFS is presently performed, with the main objective to evaluate first estimates of natural mortality rates and diet composition for gag in the 2000s for SEDAR 33. The calibration of OSMOSE models is a relatively long process, which is useful to detect errors and inconsistencies in the model code or in the configuration, as well as to understand the sensitivity of the dynamics of the modeled system to inputs. After ten days of calibration, the genetic algorithm method still has not converged to an optimal genotype and made it possible to reproduce the biomasses predicted by WFS Ecopath over the period 2005-2009 for the all of the 12 HTL groups considered in OSMOSE-WFS. However, the last results of the calibration process we obtained are encouraging.

Our main intent this year is to introduce OSMOSE-WFS to the SEDAR process and not to provide definitive parameter estimates. Currently, we are using OSMOSE version 2 (released in August 2012) to build a first OSMOSE-WFS model, and we are going to then start using OSMOSE version 3 (released in March 2013) to assess in-depth the trophic functioning of the West Florida shelf ecosystem as well as deviations in natural mortality rates and recruitment for gag under different exploitation and environmental scenarios. The major difference between OSMOSE version 3 and OSMOSE version 2 is that the latest version of the model allows for calibration using time series of biomasses and landings. This will give us the opportunity to evaluate past (over the period 1950-2009) and future deviations (over the period 2009-2009) in natural mortality rates and recruitment for gag.

We see the OSMOSE-WFS model as an ongoing process, i.e., as a model that is regularly evolving depending the questions that need to be addressed for resource management in the West Florida Shelf region. In other words, the structure, assumptions and parameterization of OSMOSE-WFS described in the present paper are not fixed, but simply based on the best data and knowledge that have been made available to us so far; and will be updated as new information becomes available and new important questions arise. Two types of changes are going to be performed in the OSMOSE-WFS model: (i) changes in the short-term, essentially due to the use of OSMOSE version 3 rather than OSMOSE version 2; and (ii) changes in the longer-term so as to assess in-depth the trophic functioning of the West Florida Shelf ecosystem under different exploitation and environmental scenarios.

Potential changes in OSMOSE-WFS in the short term include - but are not limited to:

(1) The definition of maps of biomass distribution for the plankton groups we were initially planning to consider in the present paper (i.e., small phytoplankton, diatoms, microzooplankton, and mesozooplankton), from simulations of the LTL model COSINE-13 over the period 2005-2009 (De Rada et al. 2009).

(2) The definition of new maps of biomass distribution for LTL benthos groups (meiofauna, small infauna, small mobile epifauna, bivalves, and echinoderms and large gastropods) in case detailed spatial information for these groups is made available to us.

(3) The improvement of some of the distribution maps of HTL groups. In particular, we are planning to produce distribution maps for 0-1 year old red grouper and 0-1 year old gag from simulations with the Connectivity Modeling System, an individual-based model evaluating the movement of particles in a 3-D velocity field, which has the ability to reproduce complex behaviors displayed by fish larvae (Paris et al. 2013).

(4) The decomposition of the total mortality of HTL groups into more components, and evaluation of each of these components at age rather than for three different life stages (larvae, juveniles and adults). Components of total mortality in future versions of OSMOSE-WFS map include in addition to natural mortality due to various causes ($M_{diverse}$), starvation mortality and predation mortalities: fishing mortality due to landings, fishing mortality due to discards, mortality due to by-catch by the shrimp fishery, and natural mortality due to red tide outbreaks.

(5) The consideration of sex change in the OSMOSE model for red grouper and gag so as to differentiate between male and female schools for these species, along with the evaluation of female: male sex ratio and the impacts of this sex ratio on egg fertilization when calculating the number of eggs produced by red grouper and gag at the end of each time step (Eq. 11; Coleman et al. 1996b, Koenig et al. 1996b, Fitzhugh et al. 2006a).

(6) The update of the minimum and maximum predator/prey size ratios defined for each HTL group, based on new entries in the GoMexSI database (Simons et al. 2013).

Plans for the longer-term include:

(1) The consideration of additional LTL and HTL groups of species if this is relevant regarding the questions that need to be addressed and if enough data and information are available to that goal. However, as mentioned earlier, we are willing to consider a limited number of model groups in OSMOSE-WFS so as to be able to disentangle relatively easily the complexity of interactions within the West Florida Shelf ecosystem.

(2) Analyzes to explore in depth the trophic functioning of the West Florida Shelf ecosystem, comprising an evaluation of: (i) the diet composition of the different HTL groups explicitly considered in OSMOSE-WFS, (ii) the number and strength of trophic links between model groups; and (iii) the trophic levels (TLs) of HTL groups and the mean TL of the HTL

community. The diets and TLs estimated by OSMOSE-WFS will be compared to those estimated by WFS Ecopath (Chagaris and Mahmoudi 2013). TLs provided by Ecopath rely on predetermined dietary linkages and the relative abundance of each of the functional groups. By contrast, the TLs predicted by OSMOSE-WFS are estimated from the diet composition of the HTL groups which emerge from model simulations.

(3) The consideration of alternative exploitation scenarios when evaluating recruitment levels, natural mortality rates, and the trophic functioning of the West Florida Shelf ecosystem. The exploitation scenarios we are planning to consider include, but are not limited to: (i) an increase or a decrease of F_{annual} for all HTL groups (‘HTL community scenarios’); (ii) an increase or a decrease of F_{annual} for gag only (‘gag scenarios’); (iii) an increase of F_{annual} for forage fish groups only (i.e., for the sardine-herring-scad complex and the anchovies and silversides group only; ‘forage fish scenarios’); and (iv) the implementation of harvest control rules (HCRs) for gag (‘HCR scenarios’). The gag scenario aims at complementing SEDAR 33 assessments by assessing the ecosystem consequences of rebuilding or further overfishing the gag stock. The forage fish scenario aims at examining the impacts of increasing the importance of small pelagic fisheries in the West Florida Shelf ecosystem. Such a situation is likely to occur as in many other ecosystems, so as to try to satisfy the increasing demand for forage fish as feed for aquaculture (Walters et al. 2008, Smith et al. 2011). The HCR scenarios will necessitate the coupling of OSMOSE-WFS with a regulatory submodel. This regulatory submodel must be designed so as to enable comparisons between OSMOSE-WFS, WFS EwE (Chagaris and Mahmoudi 2013) and Atlantis-GOM (an Atlantis model developed for the entire Gulf of Mexico; Ainsworth et al., in prep.) on the impacts of HCRs. The biomass of the different HTL groups, mean TL of the HTL community, landings of the different HTL groups, and mean TL in catches, as well as the annual mortality rates and recruitment levels of gag will be evaluated for all exploitation

scenarios. These variables and patterns will be given relative to their value in the reference situation (i.e., the situation considered in the present paper).

(4) The consideration of alternative environmental scenarios when evaluating recruitment levels, natural mortality rates, and the trophic functioning of the West Florida Shelf ecosystem. We are planning to consider two alternative environmental scenarios: (i) a ‘status-quo environmental scenario’; and (ii) a ‘changing environmental scenario’. The ‘status-quo environmental scenario’ consists in simply using the climatology of plankton biomasses estimated for the present study to predict monthly values of plankton biomasses in the West Florida Shelf region each year over the period 2009-2029. The ‘changing environmental scenario’ will take into account monthly trends in plankton biomasses over the period 2009-2029. These future trends in plankton biomasses for the different months of the year will be estimated from forecast simulations with the LTL model COSINE-13 (De Rada et al. 2009).

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Table 1. Parameters of the low trophic level (LTL) groups we initially planned to consider in OSMOSE-WFS.

LTL group	**Size range (mm)**	**Trophic level**	**Conversion factor (mm ww.µmol N^{-1})**
Small phytoplankton	0.002-0.02	1 *	0.72 [e]
Diatoms	0.02-0.2	1 *	0.72 [e]
Microzooplankton	0.02-0.2	2 *	0.65 [e]
Mesozooplankton	0.2-3	2.25 *	1 [e]
Meiofauna	0.065-0.5 [a]	2.13 *	N/A
Small infauna	0.5-20 [a]	2.25 *	N/A
Small mobile epifauna	0.5-20 [b]	2.25 *	N/A
Bivalves	0.2-95 [b,c]	2 *	N/A
Echinoderms and large gastropods	20-450 [b,d]	2.5 *	N/A

[a] SUSFIO (1977) - [b] Okey and Mahmoudi (2002) - [c] Rosenberg (2009) - [d] Miller and Pawson (1984) - [e] Travers (2009) - * Arbitrarily set - N/A = Not applicable.

Table 2. Parameters of the low trophic level (LTL) groups that are currently considered in OSMOSE-WFS, and their mean biomass in the West Florida Shelf over the period 2005-2009 according to WFS Ecopath.

LTL group	Size range (mm)	Trophic level	Biomass in WFS Ecopath (tons)
Small phytoplankton	0.002-0.02	1 *	2 309 400
Diatoms	0.02-0.2	1 *	2 309 400
Small copepods	0.2-1.3 [a,b,c]	2.09 *	1 550 700
Large mesozooplankton	1-3 [d]	2.28 *	1 148 400
Meiofauna	0.065-0.5 [e]	2.13 *	2 315 800
Small infauna	0.5-20 [e]	2.25 *	3 283 800
Small mobile epifauna	0.5-20 [f]	2.25 *	1 979 600
Bivalves	0.2-95 [f,g]	2 *	8 508 800
Echinoderms and large gastropods	20-450 [f,h]	2.5 *	3 085 908

[a] Grice (1960) - [b] Ferrari (1975)- [c] Turner (2004)- [d] Kimmel et al. (2010) - [e] SUSFIO (1977) – [f] Okey and Mahmoudi (2002) - [g] Rosenberg (2009) - [h] Miller and Pawson (1984) - * Arbitrarily set

Table 3. High trophic level (HTL) groups represented in OSMOSE-WFS. The reference species of each group is indicated in bold.

HTL group	Species
King mackerel	**King mackerel (*Scomberomorus cavalla*)**
Amberjacks	**Greater amberjack (*Seriola dumerili*)** , banded rudderfish (*Seriola zonata*), lesser amberjack (*Seriola fasciata*)
Red grouper	**Red grouper (*Epinephelus morio*)**
Gag	**Gag (*Mycteroperca microlepis*)**
Red snapper	**Red snapper (*Lutjanus campechanus*)**
Sardine-herring-scad complex	**Scaled sardine (*Harengula jaguana*)**, Spanish sardine (*Sardinella aurita*), Atlantic thread herring (*Opisthonema oglinum*), round scat (*Decapterus punctatus*)
Anchovies and silversides	**Bay anchovy (*Anchoa mitchilli*)**, striped anchovy (*Anchoa hepsetus*), silversides (Atherinidae spp.), alewife (*Alosa* sp.)
Coastal omnivores	**Pinfish (*Lagodon rhomboides*)**, spottail pinfish (*Diplodus holbrooki*), orange filefish (*Aluterus schoepfii*), fringed filefish (*Monacanthus ciliatus*), planehead filefish (*Monacanthus hispidus*), orangespotted filefish (*Cantherhines pullus*), honeycomb filefish (*Acanthostracion polygonius*), Atlantic spadefish (*Chaetodipterus faber*), scrawled cowfish (*Lactophrys quadricornis*), pufferfish (Tetraodontidae spp.)
Reef carnivores	**White grunt (*Haemulon plumieri*)**, black sea bass (*Centropristis striata*), rock sea bass (*Centropristis philadelphica*), belted sandfish (*Serranus subligarius*), longtail bass (*Hemanthias leptus*), butter hamlet (*Hypoplectus unicolor*), creole fish (*Paranthias furcifer*), splippery dick (*Halichoeres bivittatus*), painted wrasse (*Halichoeres caudalis*), yellowhead wrasse (*Halichoeres garnoti*), bluehead (*Thalassoma bifasciatum*), reef croaker (*Odontoscion dentex*), jackknife-fish (*Equetus lanceatus*), leopard toadfish (*Opsanus pardus*), scopian fish (Scorpaenidae spp.), bigeyes (Priacanthidae spp.), littlehead porgy (*Calamus proridens*), jolthead porgy (*Calamus bajonado*), saucereye progy (*Calamus calamus*), whitebone progy (*Calamus leucosteus*), knobbed progy (*Calamus nodosus*), French grunt (*Haemulon flavolineatum*), Spanish grunt (*Haemulon macrostomum*), margate (*Haemulon album*), bluestriped grunt (*Haemulon sciurus*), striped grunt (*Haemulon striatum*), sailor's grunt (*Haemulon parra*), porkfish (*Anisotremus virginicus*), neon goby (*Gobiosoma oceanops*)
Reef omnivores	**Doctorfish (*Acanthurus chirurgus*)**, other surgeons (Acanthuridae spp.), blue angelfish (*Holacanthus bermudensis*), gray angelfish (*Pomacanthus arcuatus*), cherubfish (*Cantropyge argi*), rock beauty (*Holacanthus tricolor*), cocoa damselfish (*Pomacentrus variabilis*), bicolor damselfish (*Pomacentrus partitus*), beau gregory (*Pomacentrus leocostictus*), yellowtail damselfish (*Microspathodon chrysurus*), seaweed blenny (*Parablennius marmoreus*), striped parrotfish (*Scarus croicensis*), bibled goby (*Coryphopterus glaucofraenum*), Bermuda chub (*Kyphossus sectarix*)
Shrimps	**Pink shrimp (*Farfantepenaeus duorarum*)**, brown shrimp (*Farfantepenaeus aztecus*), white shrimp (*Litopenaeus setiferus*), other shrimp species
Large crabs	**Blue crab (*Callinectes sapidus*)**, stone crabs (*Menippe mercenaria* and *Menippe adina*), horseshoe crab (*Limulus polyphemus*), hermits crab (e.g., *Pylopagurus operculatus* and *Clibanaris vittatus*), spider crabs (e.g., *Stenocionops furcatus*), arrow crabs (e.g., *Stenorynchus seticornis*)

Table 4. (a) Growth, reproduction and mortality parameters of the 12 high trophic level groups explicitly considered in OSMOSE-WFS, and (b) sources used to estimate these parameters. L_∞: maximum size – K: instantaneous growth rate at small size- t_0: theoretical age of zero length - A_{max}: threshold age below which a linear growth model is used to calculate mean length increase – c: constant of proportionality of the allometric length-weight relationship - b: exponent of the allometric length-weight relationship - Θ: annual number of eggs per gram of mature female – SR: female:male sex ratio – *Maturity*: age or size of sexual maturity – A_{max}: longevity – D: mortality rate due to the predation of marine organisms not represented in OSMOSE-WFS – L_{rec}: size of recruitment into fisheries – F_{annual}: annual fishing mortality rate - N/A: not applicable. All the parameters related to body size in this table are for sizes in cm TL unless otherwise specified. TL: total length – FL: fork length – CW: carapace width. We highlighted in grey parameter estimates imported from studies conducted on species related to the reference species of the HTL group elsewhere than in Southeastern US.

a) Parameter values	**Growth**						**Reproduction**				**Mortality**		
	L_∞ *(cm)*	***K*** *(yr^{-1})*	***t_0*** *(yr)*	***A_{thres}*** *(yrs)*	***c*** *($g.cm^{-3}$)*	***b***	***Θ*** *($eggs.g^{-1}$)*	***SR***	***Maturity***	***A_{max}*** *(yrs)*	***D*** *(yr^{-1})*	***L_{rec}*** *(cm)*	***F_{annual}*** *(yr^{-1})*
King mackerel	152.2	0.17	-1.83	1	$8.5.10^{-3}$ (FL)	2.98	1904	0.5	2 yrs	27	0.28	32.5	0.16
Amberjacks	164.5	0.14	-2.53	1	$3.25.10^{-2}$ (FL)	2.87	1208	0.55	3 yrs	15	0.01	14.8	0.61
Red grouper	85.4	0.16	-0.19	1	$8.3.10^{-3}$	3.14	1419	0.78	3 yrs	29	0.02	25.2	0.22
Gag	130	0.14	-0.19	1	$1.07.10^{-2}$	3.03	1068	0.92	58.5 cm	31	0.01	34.3	0.53
Red snapper	94.1	0.18	-0.55	1	$1.67.10^{-2}$	3.06	3477	0.5	2 yrs	57	0.19	22.9	0.55
Sardine-herring-scad complex	19.4	0.6	-0.25	0.5	$1.06.10^{-2}$ (FL)	3.25	2640	0.5	9.3 cm	3	1.43	8.5	0.2
Anchovies and silversides	11.1	0.36	-0.81	0.5	$1.71.10^{-2}$	2.81	3313	0.5	4.6 cm	3	2.29	2.4	0.17
Coastal omnivores	25.7	0.33	-1.1	0.5	$1.04.10^{-2}$ (FL)	3.25	1234	0.5	15.3 cm	7	1.1	16.5	0.12
Reef carnivores	32.7	0.19	-4.21	2	$7.8.10^{-2}$	2.75	1925	0.5	17.4 cm	18	0.35	19	0.28
Reef omnivores	33.4	0.086	-5.76	2	$4.1.10^{-3}$ (FL)	3.53	17739	0.5	15.5cm	17	0.55	N/A	0
Shrimps	19.9	2.87	0	0	$7.5.10^{-3}$	3.06	83161	0.5	8 cm	2	1.58	7.6	0.36
Large crabs	17.6	1.45	0.13	0.5	0.2275 (CW)	2.44	17802	0.5	1.25 yrs	3	0.74	12.7	0.57

b) Sources	**Growth**	**Reproduction**	**Mortality**
King mackerel	Godcharles and Murphy 1986, Devries and Grimes 1997	SEDAR 5 2004, Fitzhugh et al. 2008	Trent et al. 1983, SEDAR 16 2009, WFS Ecopath
Amberjacks	Murie and Parkyn 2008, Froese and Pauly 2010	Harris 2004, SEDAR 9 2006	Diaz et al. 2005, SEDAR 2011, WFS Ecopath
Red grouper	SEDAR 12 2006, SEDAR 2009a	Coleman et al. 1996, Fitzhugh et al. 2006b, SEDAR 2009a	Rothschild et al. 1997, SEDAR 2009a, WFS Ecopath
Gag	SEDAR 2009b	Fitzhugh et al. 2006a, SEDAR 2009b	SEDAR 10 2006, SEDAR 2009b, SEDAR 33 in prep., WFS Ecopath
Red snapper	Schirripa and Legault 1999, Wilson and Nieland 2001	Woods et al. 2003, Fitzhugh et al. 2004, White and Palmer 2004, SEDAR 7 2005	Allman et al. 2002, SEDAR 2009c, WFS Ecopath
Sardine-herring-scad complex	Froese and Pauly 2010	Martinez and Houde 1975, Houde 1977, Carpenter 2002, B. Mahmoudi, FMRI St. Petersburg, pers. comm.	B. Mahmoudi, FMRI St. Petersburg, pers. comm., WFS Ecopath
Anchovies and silversides	Froese and Pauly 2010	Robinette 1983, Wang and Houde 1995, Froese and Pauly 2010	Acosta 2000, B. Mahmoudi, FMRI St. Petersburg, pers. comm., WFS Ecopath
Coastal omnivores	Nelson 2002, Froese and Pauly 2010	Caldwell 1957, Nelson 2002	Nelson 2002, WFS Ecopath
Reef carnivores	Potts and Manooch III 2001, Murie and Parkyn 2005	De Silva and Murphy 2001, Murie and Parkyn 2005, Palazón-Fernández 2007, Froese and Pauly 2010	de Silva and Murphy 2001, WFS Ecopath
Reef omnivores	Kishore and Chin 2001, Froese and Pauly 2010	Bushnell et al. 2010, Froese and Pauly 2010	WFS Ecopath
Shrimps	Bielsa et al. 1983, Palomares and Pauly 2010	Eldred et al. 1961, Martosubroto 1974, Palacios and Racotta 2003	Nance 2009, Hart and Nance 2010, WFS Ecopath
Large crabs	Smith 1997, Guillory et al. 2001	Tagatz 1968, Millikin and Williams 1984, Guillory et al. 2001	Murphy et al. 2007, WFS Ecopath

Table 5. (a) Feeding size ranges of the high trophic level (HTL) groups explicitly considered in OSMOSE-WFS expressed as predator/prey size ratios, and (b) sources used to estimate these parameters. L_{thres} is here the size threshold that separates two sets of predator/prey size ratios for some HTL groups, one set for the juvenile individuals and one set for adult individuals - $(L_{pred}/L_{prey})_{min}$: minimum predator to prey body size ratio - $(L_{pred}/L_{prey})_{max}$: maximum predator to prey body size ratio.

a) Parameter values	L_{thres} *(cm TL)*	$(L_{pred}/L_{prey})_{min}$		$(L_{pred}/L_{prey})_{max}$	
		Juveniles	*Adults*	*Juveniles*	*Adults*
King mackerel	97.5	2.9	4.5	18	2000
Amberjacks	-	3.2	3.2	60	60
Red grouper	34.1	1.5	3	50	100
Gag	46.8	1.5	3.9	200	23
Red snapper	34.6	1.2	2.6	626	100
Sardine-herring-scad complex	-	1.5	1.5	10000	10000
Anchovies and silversides	4.6	1.5	1.5	1409	1000
Coastal omnivores	-	1.5	1.5	500	500
Reef carnivores	-	1.5	1.5	50	50
Reef omnivores	-	5	5	1000	1000
Shrimps	8	3	5	10000	242
Large crabs	-	1.1	1.1	50	50

b) Sources	
King mackerel	Naughton and Saloman (1981), Salomon and Naughton (1983), Godcharles and Murphy (1986), Finucane et al. (1990), Bowman et al. (2000), Link and Almeida (2000), Peláez-Rodríguez et al. (2005)
Amberjacks	Manooch and Haimovici (1983), Nelson and Bortone (1996), Bowman et al. (2000), Link and Almeida (2000)
Red grouper	Gudger (1929), Brule and Canche (1993), Nelson and Bortone (1996), Weaver (1996)
Gag	Gudger (1929), Mullaney Jr (1994), Naughton and Saloman (1985), Mullaney Jr and Gale (1996), Link and Almeida (2000), Lindberg et al. (2002)
Red snapper	Baughman (1943), Miles (1949), Bradley and Bryan (1975), Futch and Bruger (1976), Nelson (1988), Prerost (2004), Szedlmayer and Lee (2004), McCawley et al. (2006), Sheridan (2008)
Sardine-herring-scad complex	Springer and Woodburn (1960), Starck and Davis (1966), Odum and Heald (1972), Carr and Adams (1973), Vega-Cendejas et al. (1994)
Anchovies and silversides	Odum and Heald (1972), Carr and Adams (1973), Sheridan (1978), Din (1981), Peebles and Hopkins (1993)
Coastal omnivores	Hansen (1969), Carr and Adams (1973), Stoner (1980), Stoner and Livingston (1984), Czapla (1991), Schmidt (1993), Vega-Cendejas et al. (1994), Bowman et al. (2000), Link and Almeida (2000), Russell (2005), Canto-Maza and Vega-Cendejas (2008), Wrast (2008)
Reef carnivores	Randall (1967), Carr and Adams (1973), Vega-Cendejas et al. (1994), Bowman et al. (2000), Link and Almeida (2000)
Reef omnivores	Starck and Davis (1966), Randall (1967), Hernández et al. (2008)
Shrimps	Williams (1955, 1958), Eldred et al. (1961), Odum and Heald (1972)
Large crabs	Darnell (1958), Tagatz (1968), Jaworski (1972), Krantz and Chamberlin (1978), Laughlin (1979, 1982), Blundon and Kennedy (1982a, 1982b), Alexander (1986), Stoner and Buchanan (1990), Hsueh et al. (1992)

Table 6. Target biomass of the 12 high trophic level (HTL) groups considered in OSMOSE-WFS, and associated pedigree and coefficient of variation. Biomass values come from the calibration of the WFS Ecopath model. Coefficients of variations were set from biomass pedigree categories according to the criteria specified in Okey and Mahmoudi (2002).

HTL group	**Target biomass (tons)**	**Pedigree category of the biomass estimate**	**Associated coefficient of variation**
King mackerel	9 703	Approximate or indirect method	0.25
Amberjacks	1 328	Approximate or indirect method	0.25
Red grouper	19 759	Approximate or indirect method	0.25
Gag	9 189	Approximate or indirect method	0.25
Red snapper	8 786	Approximate or indirect method	0.25
Sardine-herring-scad complex	289 000	From other model	0.4
Anchovies and silversides	162 120	From other model	0.4
Coastal omnivores	303 450	From other model	0.4
Reef carnivores	276 980	From other model	0.4
Reef omnivores	78 862	From other model	0.4
Shrimps	154 710	Approximate or indirect method	0.25
Large crabs	109 640	From other model	0.4

Figure 1. Map of the West Florida Shelf in the Gulf of Mexico showing the spatial cells of OSMOSE-WFS (filled in dark grey).

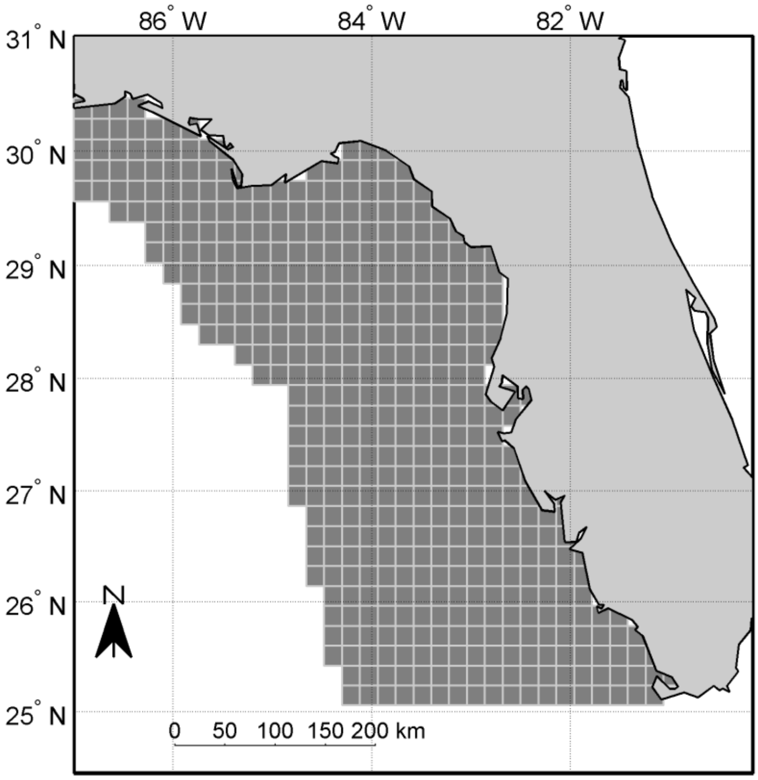


Figure 2. Monthly maps of total phytoplankton biomass in the West Florida Shelf (in tons), produced from chlorophyll a SeaWiFS data downloaded from http://oceancolor.gsfc.nasa.gov/SeaWiFS/.

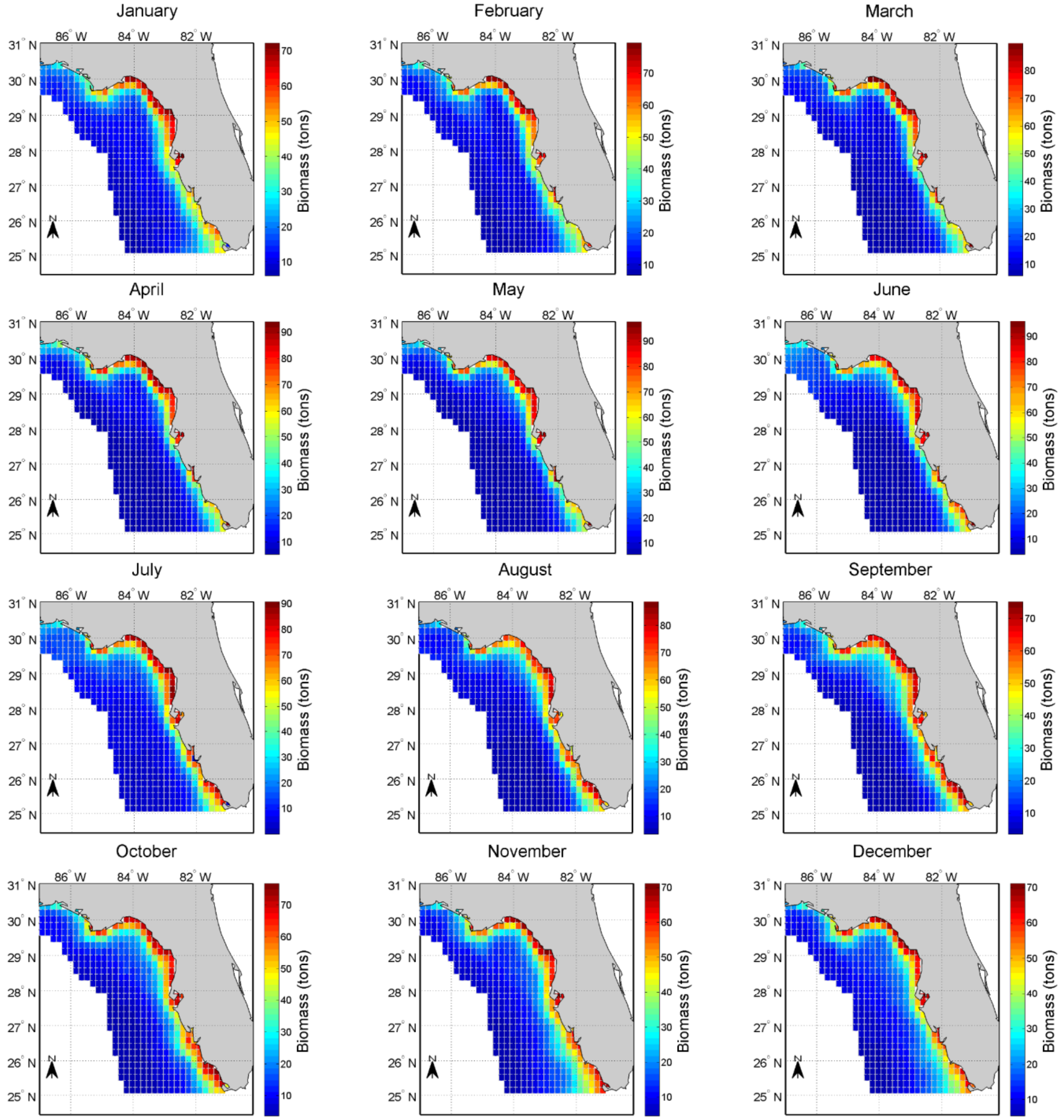
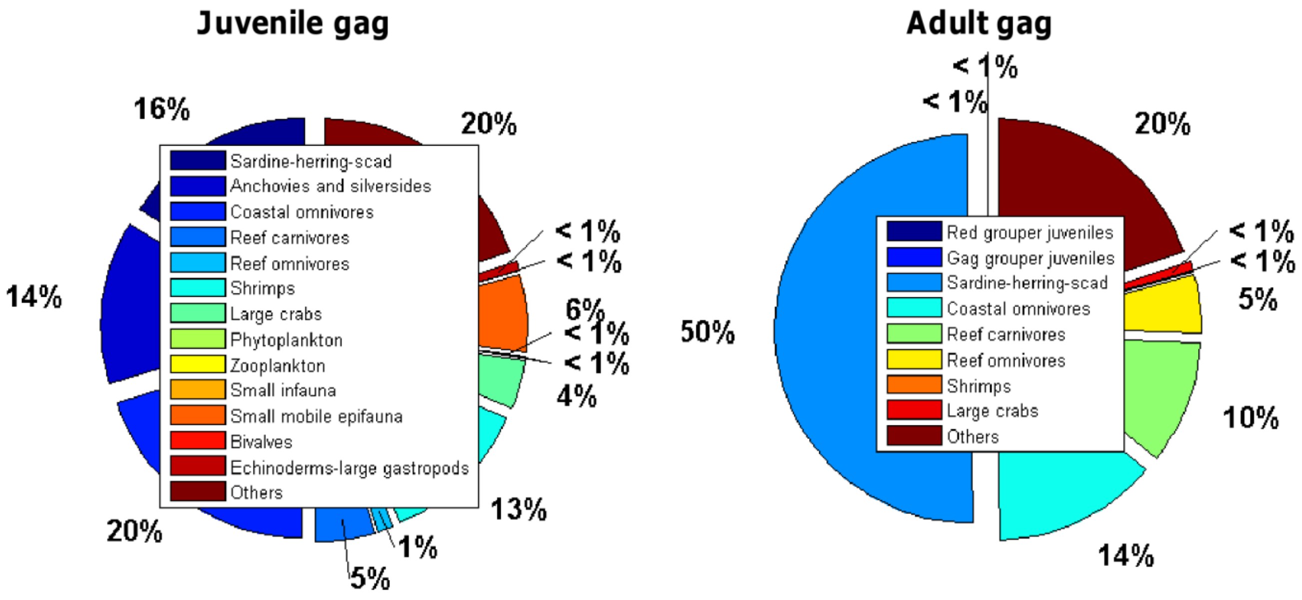


Figure 3. Diet composition of (a,b) juvenile and (c,d) adult gag (*Mycteroperca microlepis*), predicted by WFS Ecopath, expressed as percentage of prey in mass.



Box 1. Distribution maps of the high trophic level (HTL) groups represented in OSMOSE-WFS.

To produce distribution maps for OSMOSE-WFS, we mostly relied on a GAM approach developed by Drexler and Ainsworth (in revision). In their publication, Drexler and Ainsworth (in revision) use a negative binomial GAM approach to generate distribution maps for an Atlantis model (Fulton et al. 2004, 2007) designed for the entire Gulf of Mexico, Atlantis-GOM (Ainsworth et al., in prep.). OSMOSE-WFS has a finer spatial resolution than Atlantis-GOM, and the use of a delta GAM approach rather than a negative binomial GAM approach appeared more appropriate to allow for smoother spatial distributions and enough spatial overlap between the different model groups that are considered in OSMOSE-WFS.

A delta GAM approach was initially employed to produce distribution maps for Atlantis-GOM, using local environmental predictors (chlorophyll A, dissolved oxygen, temperature, depth and sediment type) and SEAMAP groundfish survey data (Rester 2011). More precisely, two GAM models were developed, one describing the probability of occurrence of fish at survey sampling stations using a binomial response, and another one describing abundance at non-zero locations using a Poisson response. These two GAM models were then combined employing the delta method to yield abundance estimates throughout the Gulf of Mexico. Finally, the delta GAM model was validated by using 2/3 of the SEAMAP groundfish data as training, and 1/3 of these data as validation (Drexler and Ainsworth, unpub. data).

Here we employ the delta GAM approach described in the previous paragraph to generate distribution maps for different age groups of the reference species of the HTL groups that are explicitly considered in OSMOSE-WFS, using different research survey datasets and the local environmental predictors mentioned earlier (see Drexler and Ainsworth (in revision) for more information on these predictors). Research survey datasets comprise the SEAMAP groundfish dataset, the National Marine Fisheries Service (NMFS) bottom longline (BLL) survey dataset (Ingram et al. 2005), and the SEAMAP reef fish (video) dataset (Gledhill et al. 2005).

Distribution maps drive the probability of presence of specific cohorts in OSMOSE-WFS, which consist of organisms belonging to the same HTL group that have the same length and weight. Therefore, distribution maps can be produced for OSMOSE-WFS from catches per unit effort data estimated from either abundance or biomass survey data. To map the distribution of most of the reference species of HTL groups in Spring-Summer and Fall-Winter, we used estimates of the number of individuals caught per square kilometer from data recorded in the SEAMAP groundfish dataset for Summer months and Fall months, respectively. NMFS BLL biomass data are collected each year during the Summer season (Ingram et al. 2005), and were used to estimate the biomass of fish caught per 100 hook hour so as to generate yearly maps for 1-3 and 3+ years old red grouper, as well as for 1-3 years old gag. Finally, SEAMAP reef fish 'mincount' data, which are collected in Spring-Summer each year, were useful to map the mean yearly distribution of 3+ years old gag; mincount is defined for the SEAMAP reef fish database as the greatest number of fish that appears on screen at one time for a given 20-minutes video record (Gledhill et al. 2005). For some age groups of the reference species, we did not have enough data to implement the GAM approach. In this case, we resorted to information from the literature and to experts' opinion to create distribution maps.

GAM models were fit using the 'mgcv' package in the R version 2.15.3 environment (Wood 2006). Smoothers were limited to 5 knots in the Poisson GAM model and 3 knots in the binomial GAM model, which control the 'wiggleness' of the fit (Wood 2006). The number of knots was determined by Drexler and Ainsworth (unpub. data) through an iterative process to minimize the variability of the predicted response over ecologically meaningful intervals of the predictive variables.

Distribution maps were produced for OSMOSE-WFS from implementation of the GAM models in two steps (Figs. I to XII and Table I). Firstly, the binomial and Poisson GAM models were fitted using all the aforementioned predictors (chlorophyll A, dissolved oxygen, temperature, depth and sediment type). Predictions of the resulting delta GAM models over a 0.1° x 0.1° spatial grid covering the entire Gulf of Mexico for depths up to 300 m with R version 2.15.3 (Wood 2006) were used to map the distribution of age groups in the West Florida Shelf region through 2D interpolation using MATLAB version 7.8.0 and the 'inpolygon' function (Hanselman and Littlefield 2005). The predictions of the delta GAM model were gauged based on: (1) examinations of smoothed curves of the additive effect to the estimated abundance of the individual predictors; and (2) comparisons of the maps we generated with MATLAB to the maps created for WFS Ecospace from the literature and experts' opinion (Chagaris and Mahmoudi 2013).

Secondly, based on diagnoses from examinations of smoothed curves and maps created for WFS Ecospace, we refitted the binomial and Poisson GAM models until making sure that (1) none of the additive terms in the binomial and Poisson GAM models leads to run-away predictions; and that (2) the distribution maps we produced for OSMOSE-WFS are relatively consistent with those produced for WFS Ecospace. Here, we consider that an additive term leads to run-away predictions and, therefore, must be dropped from a GAM model when its scale does not range between -10 and +10 (Wood 2006).

Figure I. Distribution maps of king mackerel (Scomberomorus cavalla)

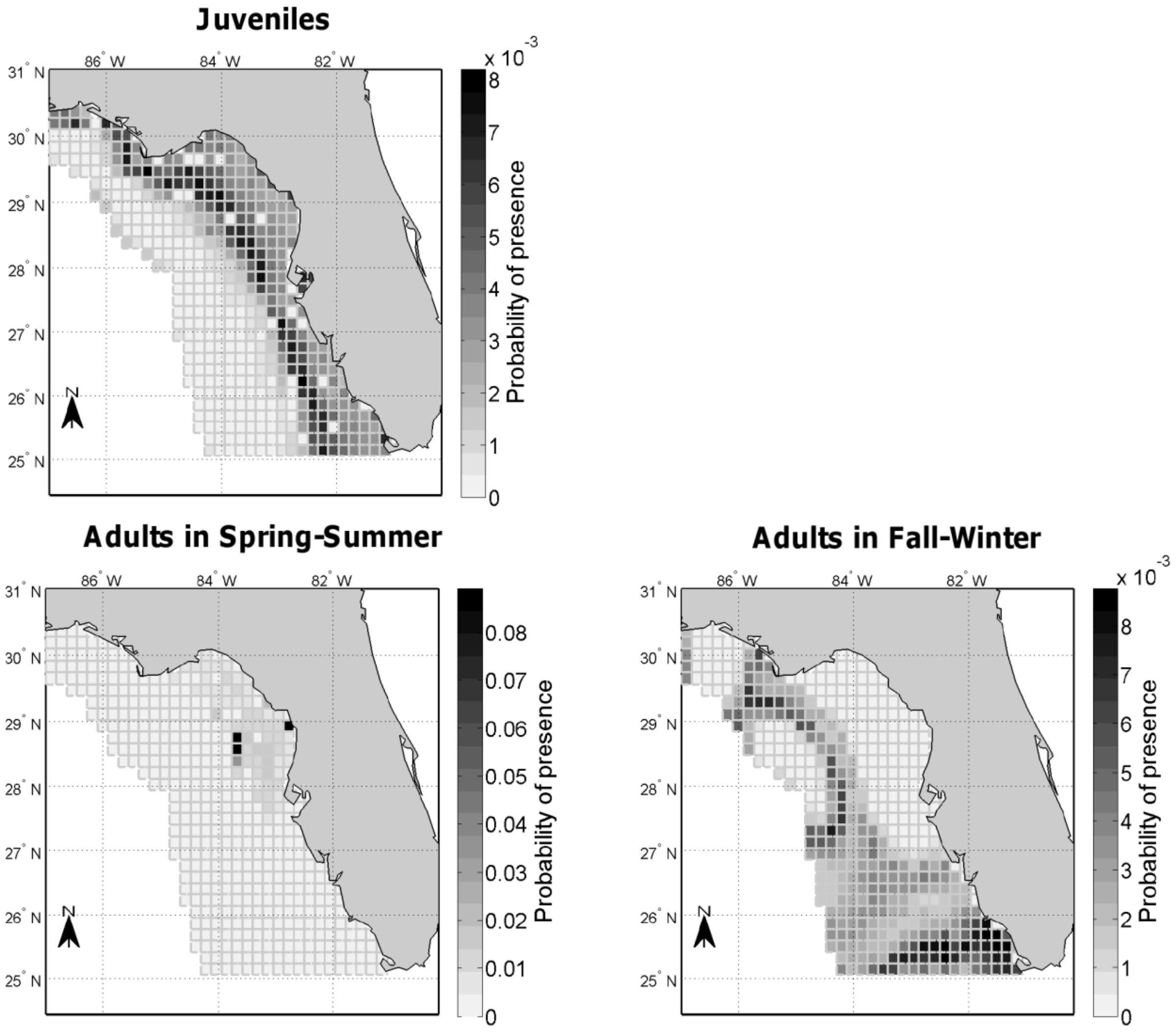


Figure II. Distribution maps of amberjacks (Reference species: Greater amberjack, Seriola dumerili)

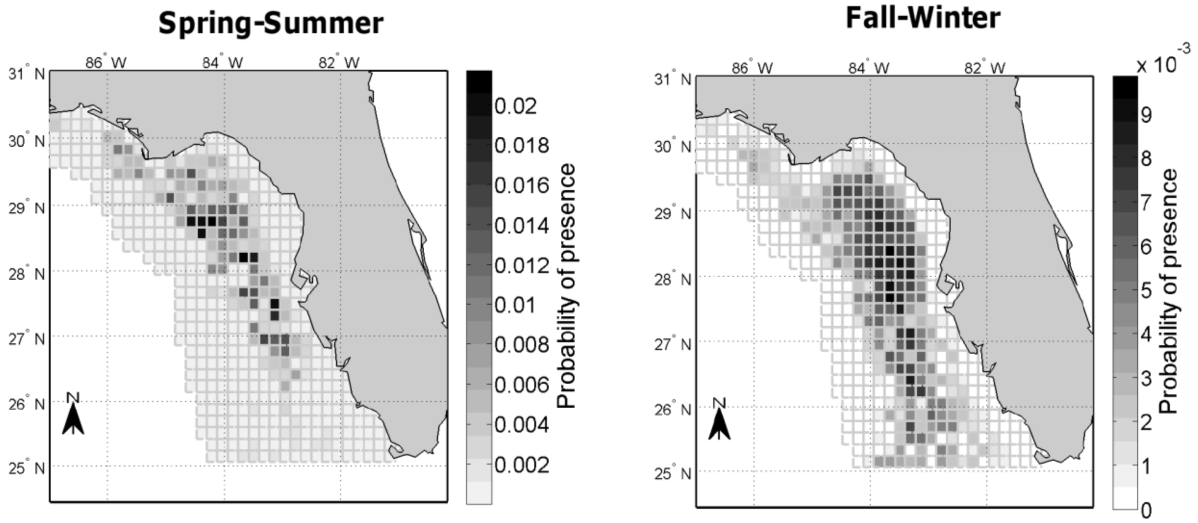


Figure III. Distribution maps of red grouper (Epinephelus morio)

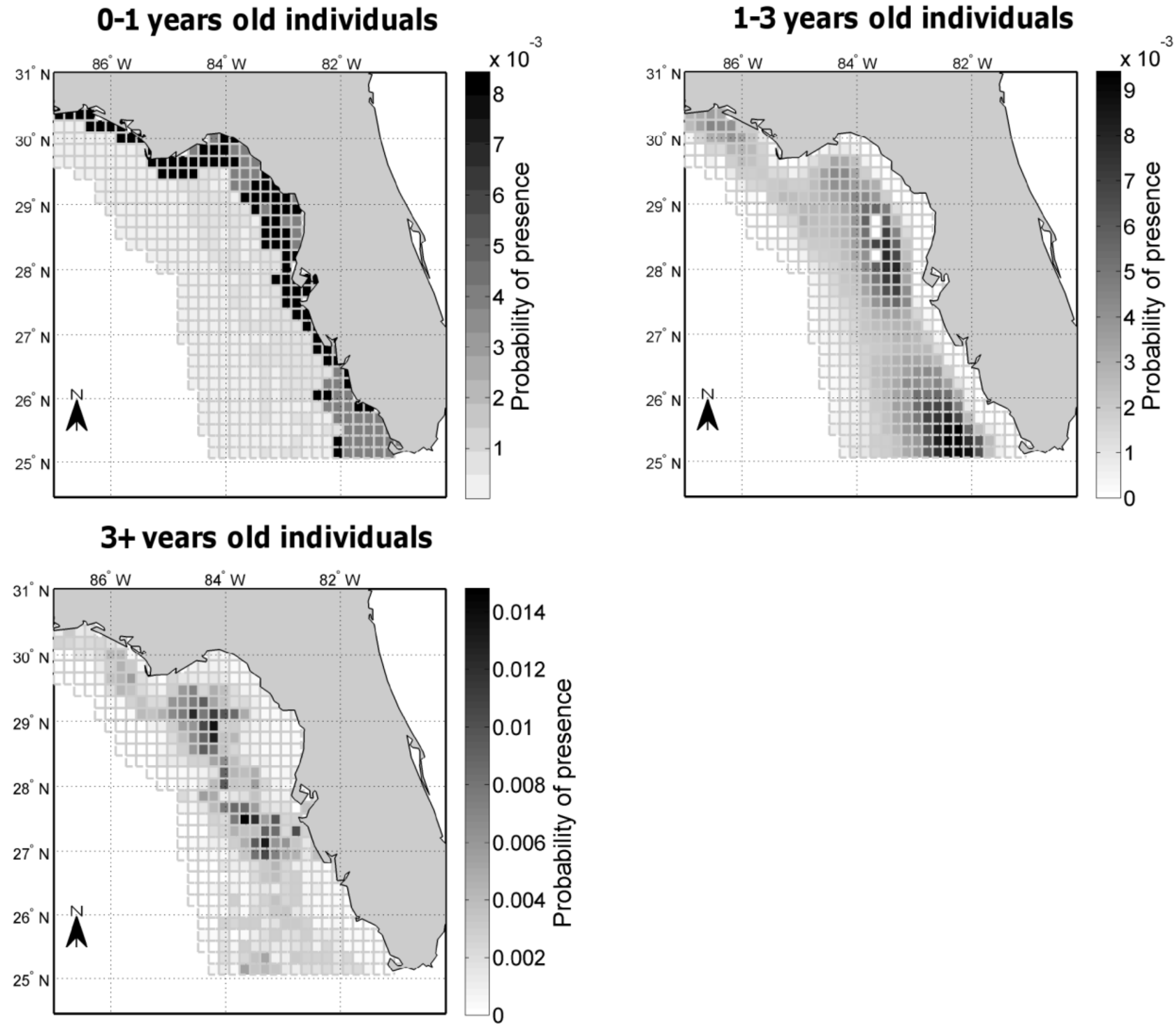


Figure IV. Distribution maps of gag (Mycteroperca microlepis)

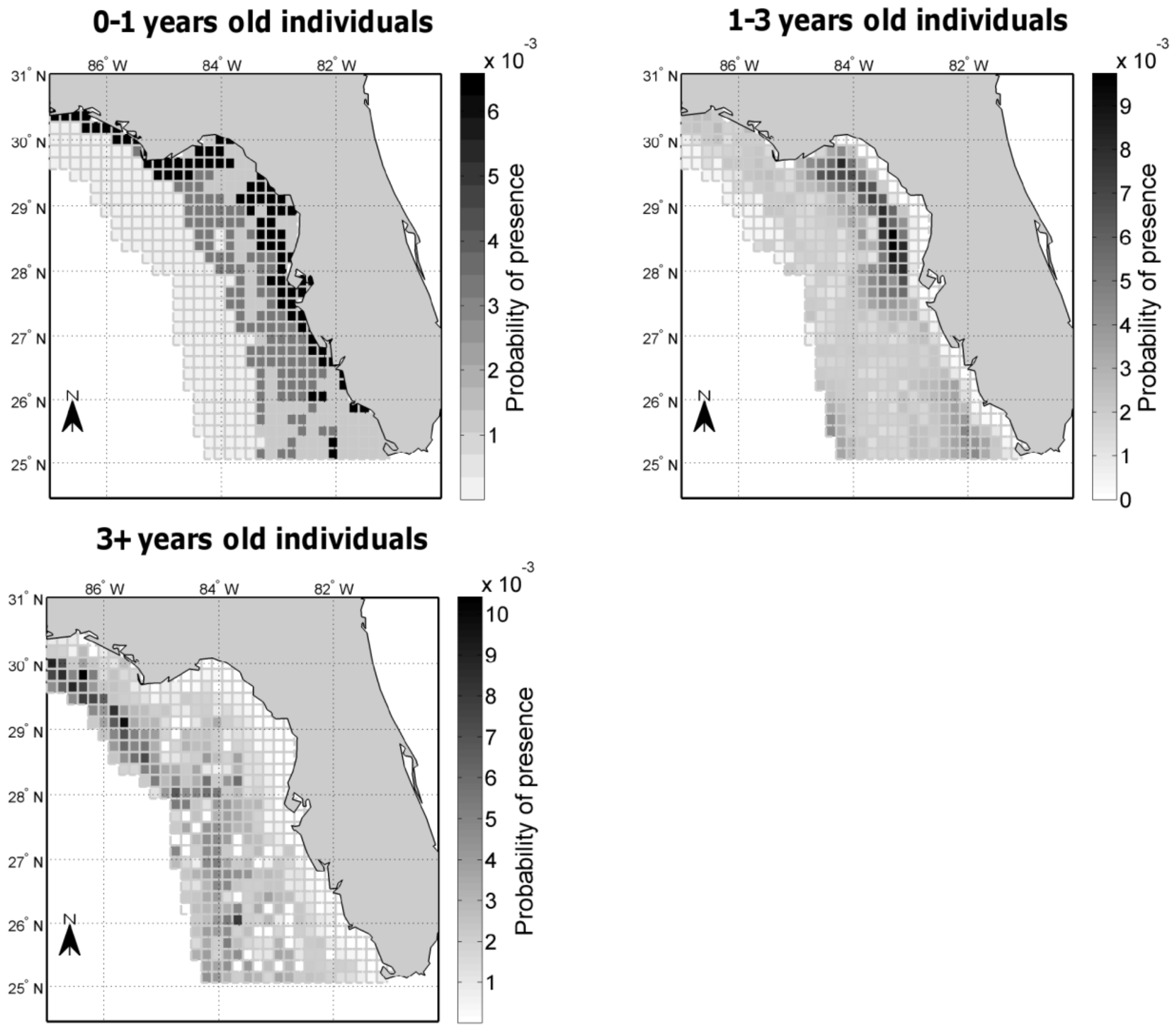


Figure V. Distribution maps of red snapper (Lutjanus campechanus)

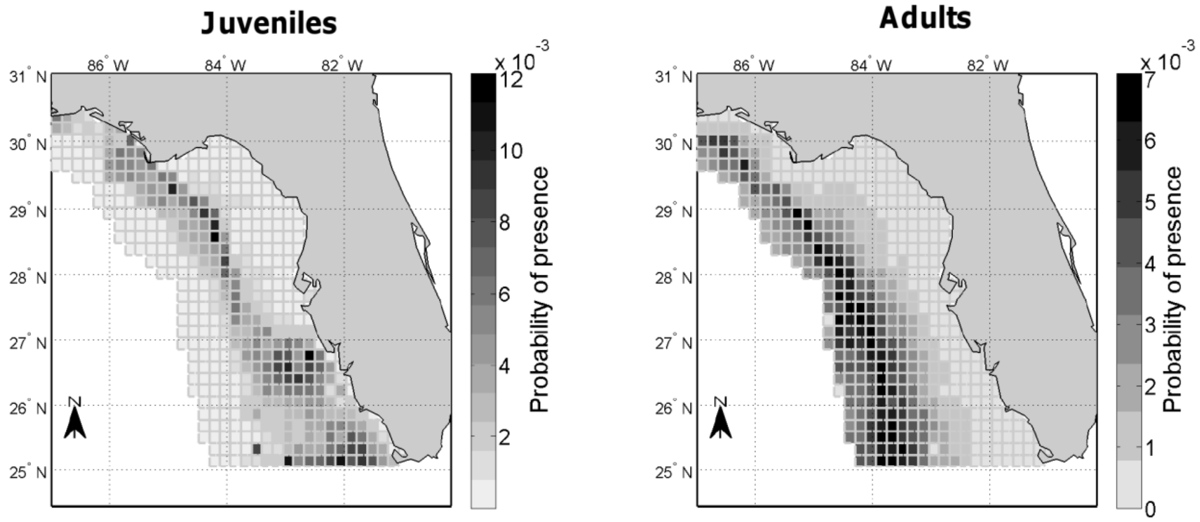


Figure VI. Distribution maps of the sardine-herring-scad complex (Reference species: Scaled sardine, Harengula jaguana)

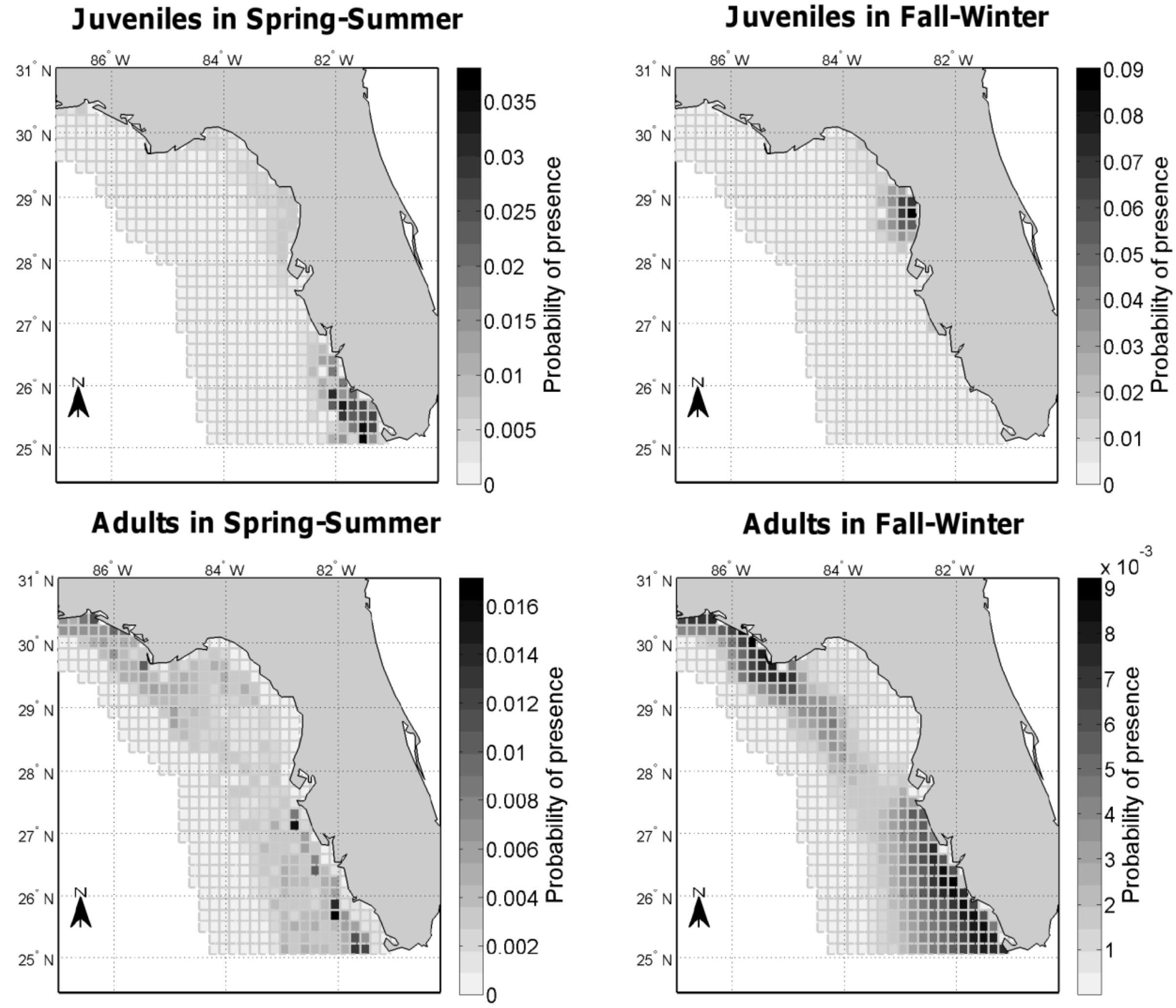


Figure VII. Distribution maps of anchovies and silversides (Reference species: Bay anchovy, Anchoa mitchili, Anchoa mitchili)

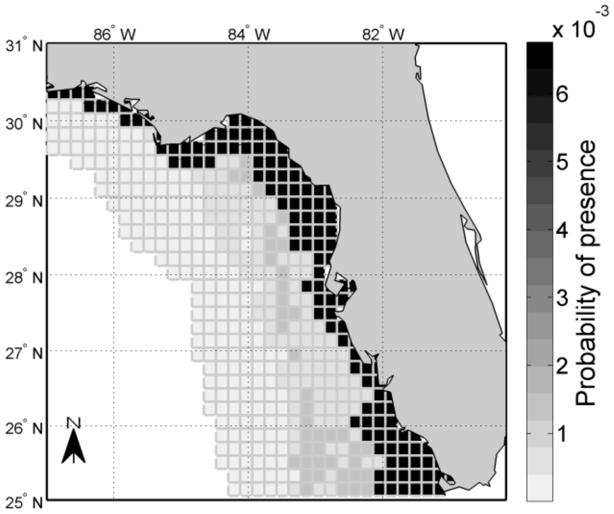


Figure VIII. Distribution maps of coastal omnivores (Reference species: Pinfish, Lagodon rhomboides)

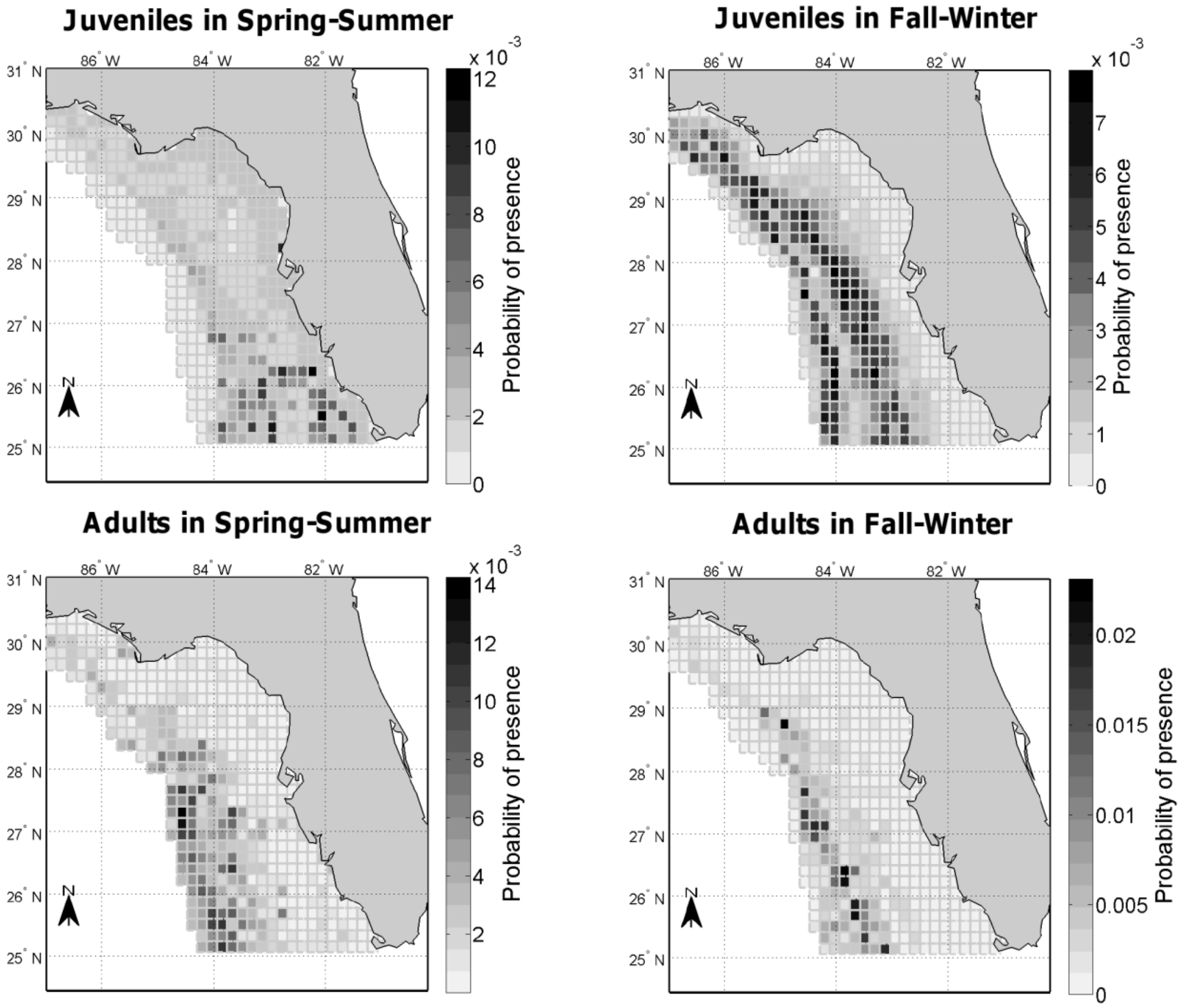


Figure IX. Distribution map of reef carnivores (Reference species: White grunt, Haemulon plumieri)

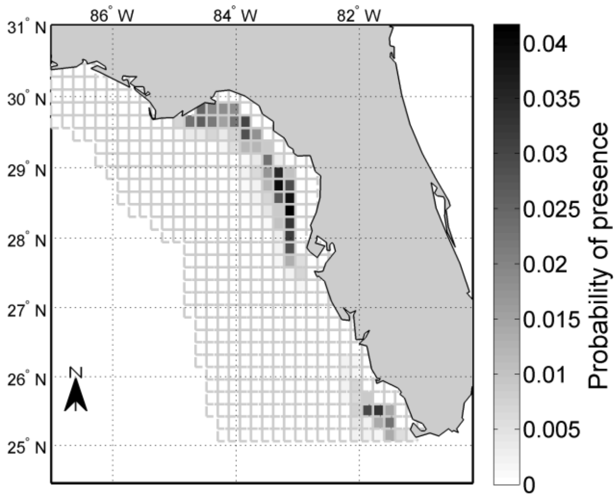


Figure X. Distribution map of reef omnivores (Reference species: Doctorfish, Acanthurus chirurgus)

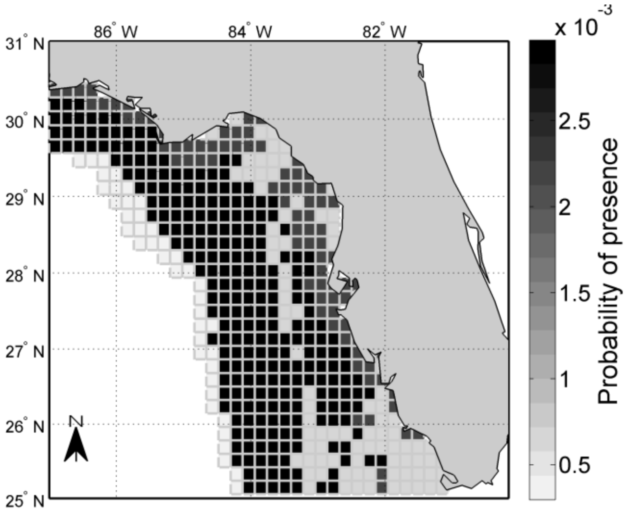


Figure XI. Distribution maps of shrimps (Reference species: Pink shrimp, Farfantepenaeus duorarum)

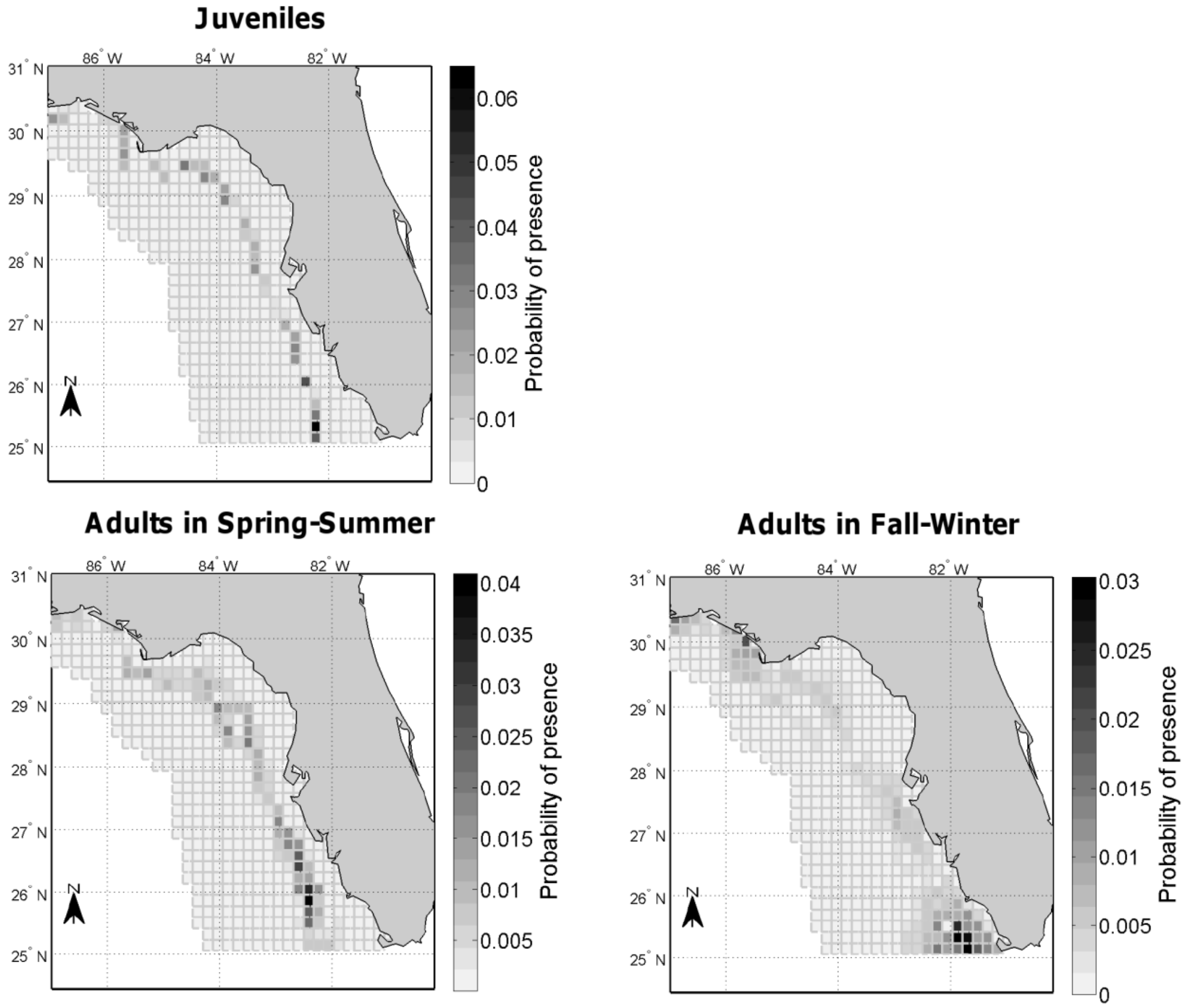


Figure XII. Distribution maps of maps of large crabs (Reference species: Blue crab, Callinectes sapidus)

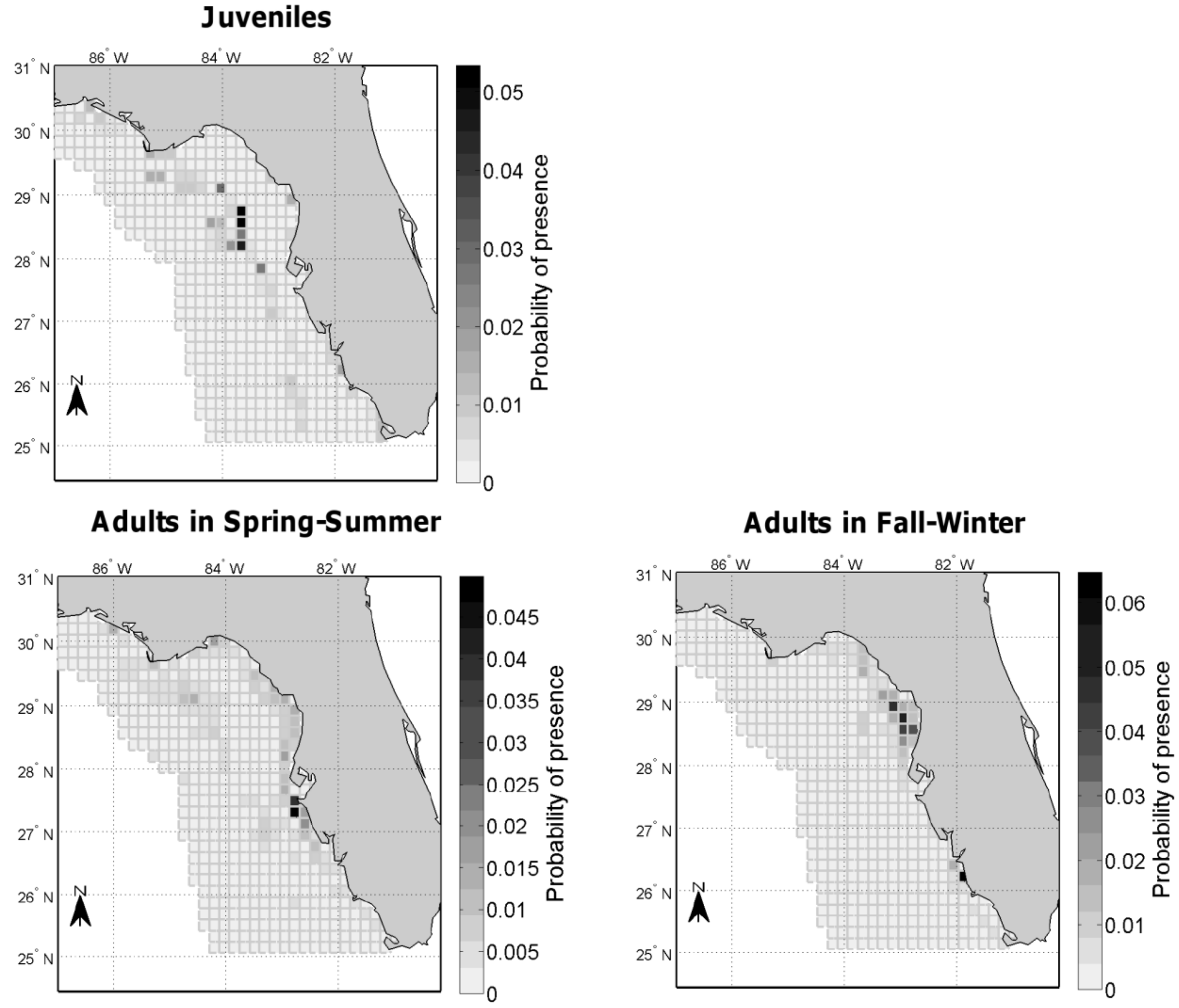


Table I. Summary of the distribution maps created for OSMOSE-WFS, and of the modifications introduced in the GAM models that were used to produce the great majority of the maps. N/A: not applicable.

Age group	Maps that should be ideally produced according to the literature	Map produced for this age group due to data availability	Dataset used to produce distribution maps	Modifications in the GAM models for Spring-Summer	Modifications in the GAM models for Fall-Winter
Juvenile king mackerel (*Scomberomorus cavalla*)	1 yearly map (Godcharles and Murphy 1986, SEDAR 16 2009).	1 yearly map	SEAMAP groundfish	Predictors 'Depth', 'Chlorophyll a' and 'Sediments' dropped from both the binomial and Poisson GAM models.	Predictors 'Oxygen', 'Chorophyll a' and 'Sediments' dropped from both the binomial and Poisson GAM models.
Adult king mackerel (*Scomberomorus cavalla*)	4 maps, 1 for each season of the year. Adult king mackerels undertake migrations over large distances in Fall and Spring (Godcharles and Murphy 1986, SEDAR 16 2009).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	Predictor 'Chlorophyll a' dropped from the Poisson GAM model.	Predictors 'Depth', 'Chlorophyll a' and 'Sediments' dropped from both the binomial and Poisson GAM models.
Amberjacks (Reference species: Greater amberjack, *Seriola dumerili*)	1 yearly map for 0-6 months old individuals and 4 maps for 6+ months old individuals, 1 for each season. Evidence suggests that greater amberjack shifts habitat (pelagic to demersal) at 6 months of age (SEDAR 9 2006). Moreover, sub-adult and adult greater amberjacks utilize a variety of habitats and/or areas each year (SEDAR 9 2006).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	Predictor 'Sediments' dropped from the binomial GAM model; and predictors 'Depth', 'Oxygen' and 'Sediments' dropped from the Poisson GAM model.	Predictor 'Sediments' dropped from the binomial GAM model; and predictors 'Oxygen' and 'Chlorophyll a' dropped from the Poisson GAM model.
0-1 year old red grouper (*Epinephelus morio*)	1 yearly map. Habitat and diet preferences of red grouper reported in SEDAR 12 (2006) suggest differentiating at least between 0-1 year old individuals, 1-3 year olds individuals and 3+ year olds individuals. Red grouper does not form spawning aggregations (Coleman et al. 1996, 2011). Moreover, evidence of movements in red grouper that are not related to ontogeny is not conclusive (SEDAR 12 2006).	1 yearly map	None. In the absence of significant data, we use here the map produced for 0-1 year old red grouper in WFS Ecospace from information in the literature. 0-1 year old red groupers, like 0-1 year old gags, live inshore and prefer areas with a relatively steep slope. However, 0-1 year old red grouper have a little more preference for shallow flat areas, where they are found in potholes more often than 0-1 year old gag (Moe 1969, Coleman et al. 2010).	N/A	N/A
1-3 years old red grouper (*Epinephelus morio*)	1 yearly map (Coleman et al. 1996, SEDAR 12 2006).	1 yearly map	NMFS BLL	No modification.	N/A
3+ years old red grouper (*Epinephelus morio*)	1 yearly map (Coleman et al. 1996, SEDAR 12 2006).	1 yearly map	NMFS BLL	Predictor 'Depth' dropped from the binomial GAM model; and predictors 'Depth' and 'Chlorophyll a' dropped from the Poisson GAM model.	N/A
0-1 year old gag	1 yearly map. Habitat and diet preferences of	1 yearly map	None. In the absence of	N/A	N/A

(*Mycteroperca microlepis*)	gag reported in SEDAR 10 (2006) and Coleman et al. (2011) suggest differentiating between 0-1 year old individuals, 1-3 year olds individuals, 3+ year olds female individuals and 3+ years old male individuals; as well as to generate 2 maps for 3+ year olds female individuals, 1 for the non-reproductive season and 1 for the reproductive season.		significant data, we use here the map produced for 0-1 year old gag in WFS Ecospace from information in the literature. 0-1 year old gag live inshore and prefer areas with a relatively steep slope (Switzer et al. 2012).		
1-3 years old gag (*Mycteroperca microlepis*)	1 yearly map (SEDAR 10 2006, Coleman et al. 2011).	1 yearly map	NMFS BLL	No modification.	N/A
3+ years old gag (*Mycteroperca microlepis*)	1 yearly map for male gag, and 2 maps for mature female gag, 1 for the Winter months, and 1 for all the other months of the year. Gag forms spawning aggregations. Gags are protogynous and relatively unusual in that males stay year-round in spawning sites, whereas mature females migrate to these sites in Winter and stay the rest of the year in nearshore habitats that they share with juveniles (Coleman et al. 1996).	1 yearly map	SEAMAP reef fish	Predictor 'Sediments' dropped from the binomial GAM model; and predictors 'Depth', 'Chlorophyll a' and 'Oxygen' dropped from the Poisson GAM model.	N/A
Juvenile red snapper (*Lutjanus campechanus*)	1 yearly map. Habitat and diet preferences of red snapper reported in Workman et al. (2002) and SEDAR 7 (2005) suggest differentiating between juvenile and adult red snappers.	1 yearly map	SEAMAP groundfish	No modification.	Predictor 'Depth' dropped from the binomial GAM model.
Adult red snapper (*Lutjanus campechanus*)	1 yearly map. Adult red snappers undertake migrations to form spawning aggregations. Evidence suggests that these migrations occur over relatively small distances (Szedlmayer 1997, Patterson III et al. 2001).	1 yearly map	SEAMAP groundfish	Predictors 'Chlorophyll a', 'Temperature' and 'Oxygen' dropped from both the binomial and Poisson GAM models.	Predictors 'Chlorophyll a', 'Temperature' and 'Oxygen' dropped from both the binomial and Poisson GAM models.
Juveniles of the sardine-herring-scad complex (Reference species: Scaled sardine, *Harengula jaguana*)	4 maps, 1 for each season of the year. Scaled sardines undertake seasonal migrations (Houde 1976).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	Predictors 'Sediments' and 'Temperature' dropped from the binomial GAM model; and predictors 'Sediments' and 'Depth' dropped from the Poisson GAM model.	Predictors 'Sediments' and 'Oxygen' dropped from the binomial GAM model; and predictors 'Sediments', 'Depth' and 'Temperature' dropped from the Poisson GAM model.
Adult of the sardine-herring-scad complex (Reference species: Scaled sardine, *Harengula jaguana*)	4 maps, 1 for each season of the year (Houde 1976).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	Predictors 'Sediments' and 'Depth' dropped from the binomial GAM model; and predictors 'Sediments' and 'Oxygen' dropped from the Poisson GAM model.	Predictor 'Sediments' dropped from both the binomial and Poisson GAM models.
Anchovies and	4 maps for juveniles, 1 for each season of the	1 map for Spring-	None. In the absence of	N/A	N/A

silversides (Reference species: Bay anchovy, *Anchoa mitchili*)	year, and 4 maps for adults, 1 for each season of the year. Bay anchovies undertake seasonal migrations (Robinette 1983).	Summer and 1 map for Fall-Winter	significant data, we use here the map produced for anchovies and silversides in WFS Ecospace from information in the literature. Bay anchovy and striped anchovy (*Anchoa hepsetus*) live inshore, mostly in estuaries, and have a very high preference for no-relief areas and a low preference for low relief areas (Robinette 1983).		
Juvenile of the coastal omnivores group (Reference species: Pinfish, *Lagodon rhomboides*)	4 maps, 1 for each season of the year Pinfish undertake seasonal feeding and spawning migrations. In particular, they move to offshore waters during the late Fall and spawn there from late Fall through early Spring (Hansen 1969, Darcy 1985).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	Predictors 'Temperature', 'Oxygen' and 'Chlorophyll a' dropped from both the binomial and the Poisson GAM models.	The predictors 'Temperature', 'Oxygen' and 'Chlorophyll a' dropped from both the binomial and the Poisson GAM models.
Adults of the coastal omnivores group (Reference species: Pinfish, *Lagodon rhomboides*)	4 maps, 1 for each season of the year (Hansen 1969, Darcy 1985).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	Predictors 'Depth' and 'Chlorophyll a' dropped from both the binomial and Poisson GAM models.	No modification.
Reef carnivores (Reference species: White grunt, *Haemulon plumieri*)	1 yearly map for all cohorts. White grunts of the west coast of Florida reside in one general area and do not undertake substantial movements or seasonal migrations. They also undertake ontogenetic migrations over small distances (de Silva and Murphy 2001).	1 yearly map	SEAMAP groundfish	Predictors 'Sediments' and 'Depth' and 'Chlorophyll a' dropped from the binomial GAM model; and predictor 'Sediments' dropped from the Poisson GAM model.	N/A
Reef omnivores (Reference species: Docrofish, *Acanthurus chirurgus*)	1 yearly map for all cohorts. Doctorfish, like the other species of the reef omnivores group, undertake movements only over very small spatial scales (Froese and Pauly 2010).	1 yearly map	None. In the absence of significant data and of information in the literature, we use here the map produced for the reef omnivores group in WFS Ecospace from expert opinion (B. Mahmoudi, FMRI St. Petersburg). This map is based on the simple assumption that reef omnivores have full preference for any reef habitat and only a small preference for all the other habitats considered	N/A	N/A

			in WFS Ecospace.		
Juvenile shrimps (Reference species: Pink shrimp, *Farfantepenaeus duorarum*)	1 yearly map. Pink shrimp emigrate from shallow coastal nursery grounds to deeper offshore waters in the late juvenile or early adult stage (Bielsa et al. 1983).	1 yearly map	SEAMAP groundfish	Predictors 'Sediments' and 'Oxygen and 'Chlorophyll a' dropped from both the binomial and Poisson GAM models.	Predictors 'Depth' and 'Chlorophyll a' dropped from both the binomial and Poisson GAM models.
Adult shrimps (Reference species: Pink shrimp, *Farfantepenaeus duorarum*)	2 maps, 1 for Spring-Summer and 1 for Fall-Winter. In late Fall and Winter, pink shrimp spawning activity shifts from shallow to deep water; this shift may be due to movement of adults to deep waters when temperature of shallow waters decrease (Bielsa et al. 1983).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	No modification.	No modification.
Juvenile large crabs (Reference species: Blue crab, *Callinectes sapidus*)	4 maps, 1 for each season of the year. Blue crab undertakes seasonal migrations that are different for juveniles and adults (Guillory et al. 2001).	1 yearly map	SEAMAP groundfish	Predictors 'Chlorophyll a', 'Temperature' and 'Oxygen' dropped from both the binomial and Poisson GAM models.	Predictors 'Chlorophyll a', 'Temperature' and 'Oxygen' dropped from both the binomial and Poisson GAM models.
Adult large crabs (Reference species: Blue crab, *Callinectes sapidus*)	4 maps, 1 for each season of the year (Guillory et al. 2001).	1 map for Spring-Summer and 1 map for Fall-Winter	SEAMAP groundfish	Predictor 'Depth' dropped from the binomial GAM model.	Predictors 'Depth' and 'Oxygen' dropped from the binomial GAM model.

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Box 2. Fishing seasonality of the high trophic level (HTL) groups represented in OSMOSE-WFS. In the absence of data, we assumed no seasonality of fishing mortality (F) for the sardine-herring-scad complex, the anchovies and silversides group and reef carnivores. The seasonality of F of all other HTL groups – except reef omnivores that are not targeted by fishing – was estimated from the monthly total catches of their reference species over the period 2005-2009 (Figs. I and II). Monthly total catches were estimated from National Marine Fisheries Service (NMFS) statistics for the commercial and recreational fisheries of the West coast of Florida.

Figure I. Fishing seasonality of some HTL groups estimated from NMFS statistics.

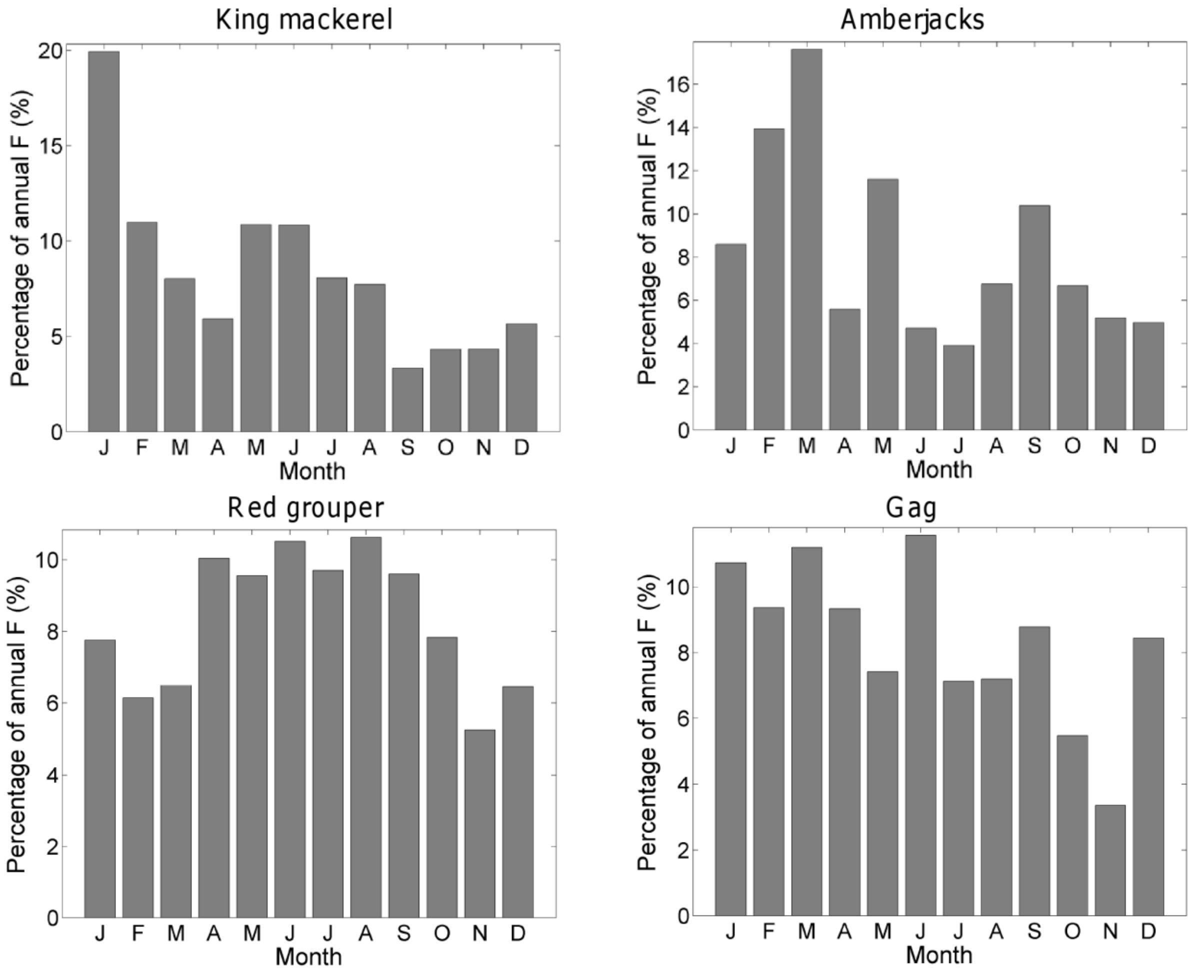
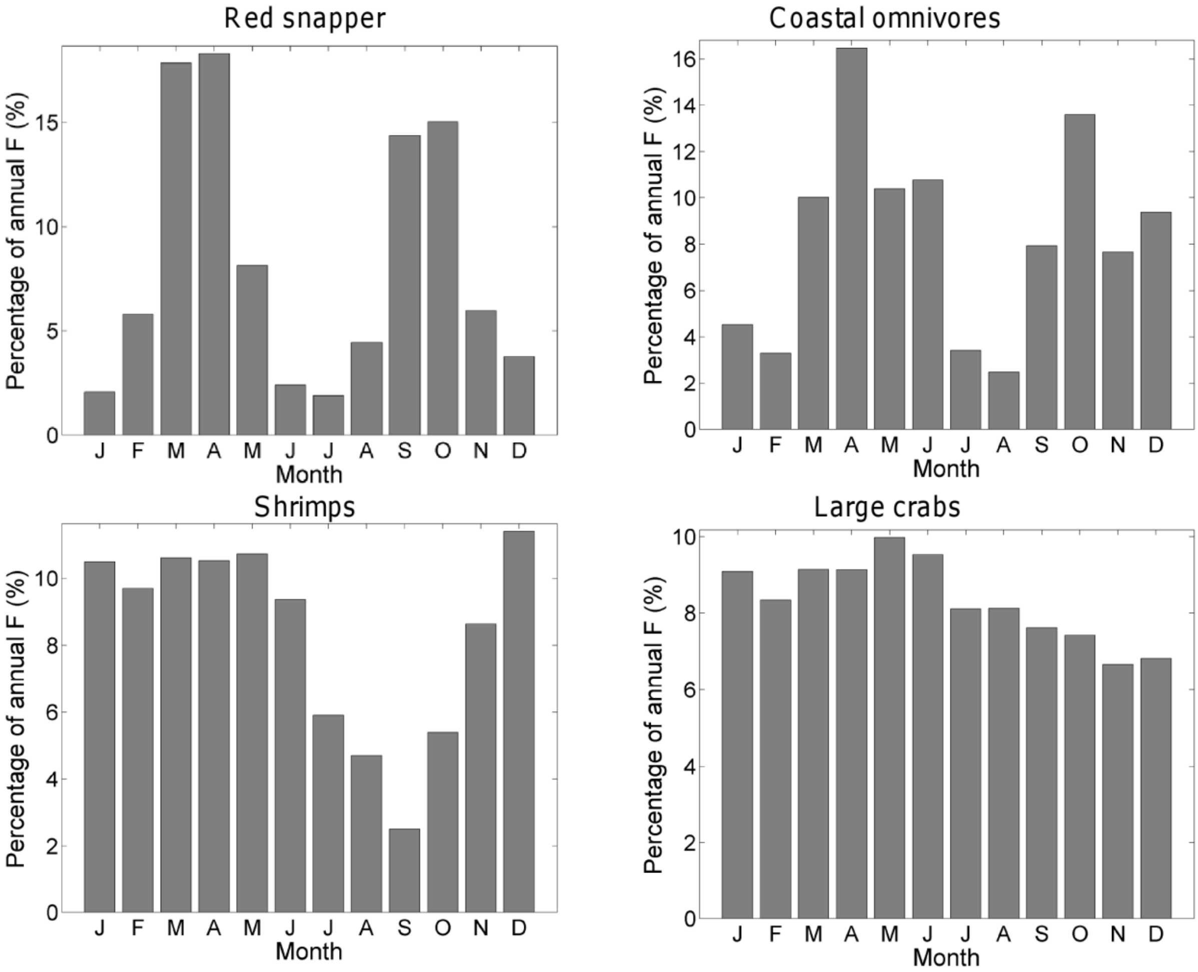


Figure II. Fishing seasonality of some HTL groups estimated from NMFS statistics.



Red snapper

Coastal omnivores

Shrimps

Large crabs

Box 3. Seasonality of reproduction of the high trophic level (HTL) groups represented in OSMOSE-WFS. In the absence of information, we assumed no seasonality of reproduction for reef omnivores. The seasonality of reproduction of all other HTL groups was estimated from the literature (Figs. I and II and Table I).

Figure I. Seasonality of reproduction of some of the HTL groups estimated from the literature.

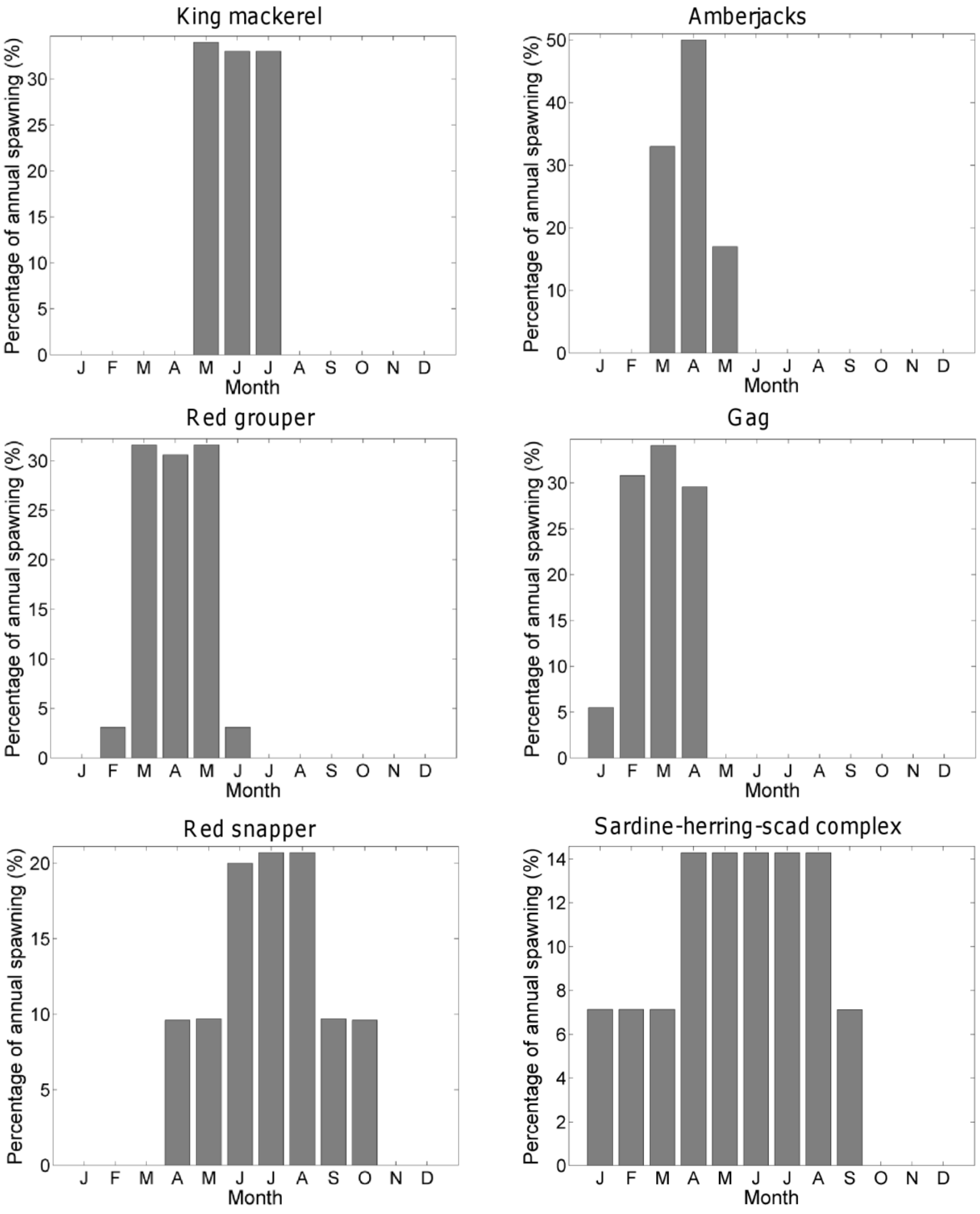


Figure II. Seasonality of reproduction of some of the HTL groups estimated from the literature.

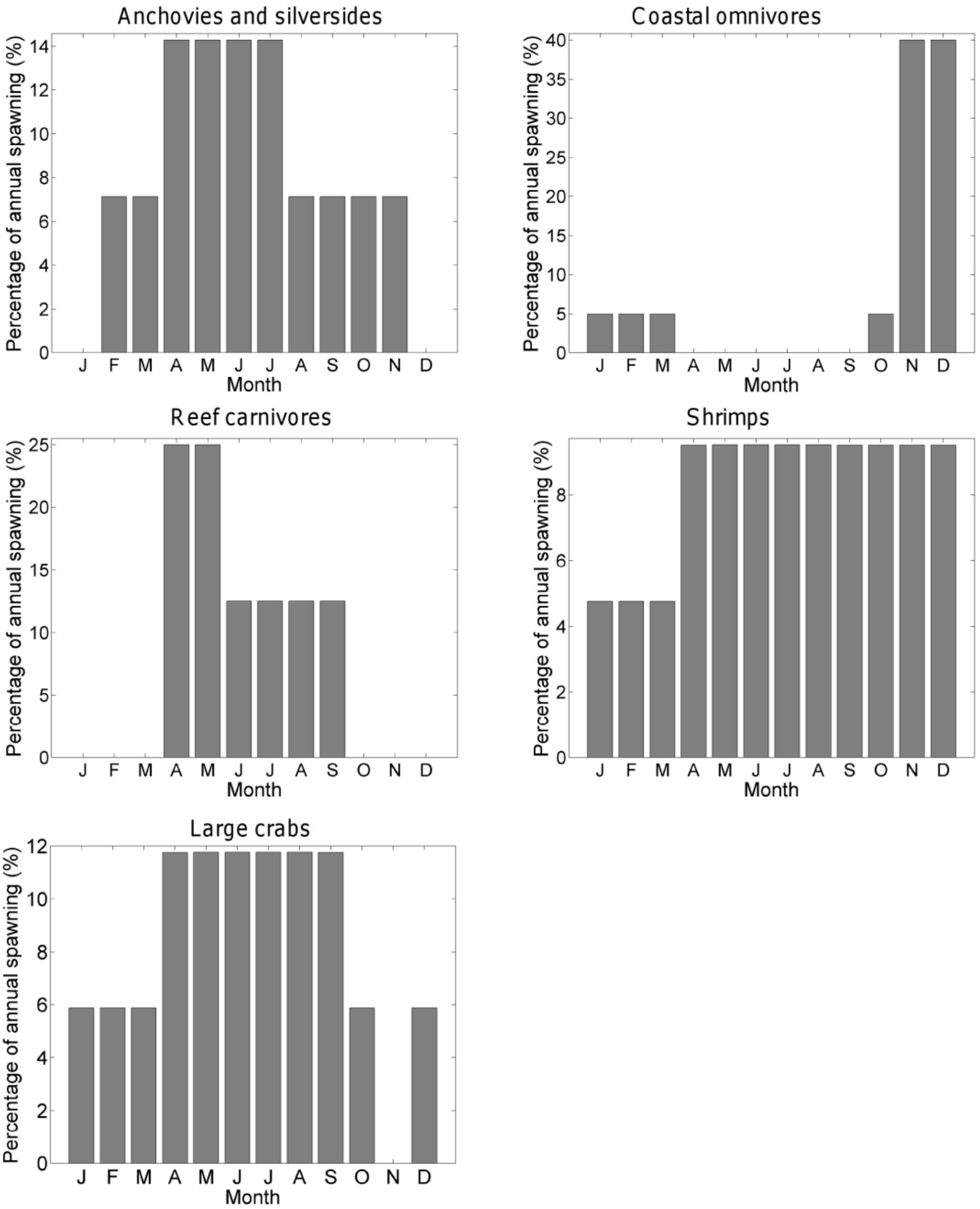


Table I. Sources used to estimate the seasonality of reproduction of the high trophic level (HTL) groups represented in OSMOSE-WFS.

HTL group	**Reference species**	**Source**
King mackerel	King mackerel (*Scomberomorus cavalla*)	Fitzhugh et al. (2008)
Amberjacks	Greater amberjack (*Seriola dumerili*)	Harris (2004)
Red grouper	Red grouper (*Epinephelus morio*)	Fitzhugh et al. (2006a)
Gag	Gag grouper (*Mycteroperca microlepis*)	Fitzhugh et al. (2006b)
Red snapper	Red snapper (*Lutjanus campechanus*)	Fitzhugh et al. (2004)
Sardine-herring-scad complex	Scaled sardine (*Harengula jaguana*)	Carpenter (2004)
Anchovies and silversides	Bay anchovy (*Anchoa mitchilli*)	Robinette (1983)
Coastal omnivores	Pinfish (*Lagodon rhomboides*)	Nelson (2002)
Reef carnivores	White grunt (*Haemulon plumieri*)	Murie and Parkyn (1999)
Shrimps	Pink shrimp (*Farfantepenaeus duorarum*)	Bielsa et al. (1983)
Large crabs	Blue crab (*Callinectes sapidus*)	Millikin and Williams (1984)

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Box 4. Accessibility of the different age classes of the HTL groups to each other and to benthic LTL groups (Table I), and comments on the value of some accessibility coefficients (Table II).

Table I. Accessibility of the different age classes of the HTL groups (in columns) to each other and to benthic LTL groups (in rows), determined from the literature and expert opinion (J. Simons, Center for Coastal Studies, Texas A&M University-Corpus Christi).

	Juvenile king mackerel	**Adult king mackerel**	**Amberjacks**	**Juvenile red grouper**	**Adult red grouper**	**Juvenile gag**	**Adult gag**	**Juvenile red snapper**	**Adult red snapper**	**Sardine-herring-scad complex**
Juvenile king mackerel	80%	80%	0%	0%	0%	0%	0%	80%	80%	80%
Adult king mackerel	80%	80%	0%	0%	0%	0%	0%	80%	80%	80%
Amberjacks	80%	80%	0%	0%	0%	0%	0%	80%	80%	80%
Juvenile red grouper	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Adult red grouper	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Juvenile gag	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Adult gag	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Juvenile red snapper	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Adult red snapper	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Sardine-herring-scad complex	80%	80%	80%	80%	80%	80%	80%	80%	80%	80%
Anchovies and silversides	80%	80%	80%	80%	80%	80%	80%	80%	80%	80%
Coastal omnivores	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Reef carnivores	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Reef omnivores	80%	80%	80%	80%	80%	80%	80%	80%	80%	40%
Shrimps	40%	40%	40%	80%	80%	80%	40%	80%	80%	10%
Large crabs	0%	0%	10%	80%	80%	80%	40%	80%	40%	10%
Meiofauna	40%	10%	10%	80%	80%	80%	40%	40%	40%	10%
Small infauna	40%	10%	10%	80%	80%	80%	40%	40%	40%	10%
Small mobile epifauna	40%	10%	10%	80%	80%	80%	40%	40%	40%	10%
Bivalves	40%	10%	10%	10%	0%	80%	40%	10%	10%	10%
Echinoderms and large gastropods	40%	10%	10%	10%	0%	80%	40%	10%	10%	10%

Table I (continued).

	Anchovies and silversides	**Costal omnivores**	**Reef carnivores**	**Reef omnivores**	**Shrimps**	**Large crabs**
Juvenile king mackerel	80%	40%	80%	80%	0%	0%
Adult king mackerel	80%	40%	80%	80%	0%	0%
Amberjacks	80%	40%	80%	80%	0%	0%
Juvenile red grouper	40%	80%	80%	80%	0%	0%
Adult red grouper	40%	80%	80%	80%	0%	0%
Juvenile gag	40%	80%	80%	80%	0%	0%
Adult gag	40%	80%	80%	80%	0%	0%
Juvenile red snapper	40%	80%	80%	80%	0%	0%
Adult red snapper	40%	80%	80%	80%	0%	0%
Sardine-herring-scad complex	80%	40%	80%	80%	0%	10%
Anchovies and silversides	80%	40%	80%	80%	0%	10%
Coastal omnivores	40%	80%	80%	80%	0%	10%
Reef carnivores	40%	80%	80%	80%	0%	0%
Reef omnivores	40%	80%	80%	80%	0%	0%
Shrimps	10%	40%	80%	80%	0%	80%
Large crabs	10%	0%	80%	80%	0%	80%
Meiofauna	40%	80%	80%	80%	80%	80%
Small infauna	40%	80%	80%	80%	80%	80%
Small mobile epifauna	40%	80%	80%	80%	80%	80%
Bivalves	10%	80%	80%	80%	80%	80%
Echinoderms and large gastropods	10%	80%	80%	80%	80%	80%

Table II. Comments on the value of some accessibility coefficients.

	Comments
Juvenile king mackerel	Accessibility to shrimps and to the different LTL benthic groups set to 40% to account for little overlap in the vertical dimension. Accessibility to large crabs set to 0% to account for very little overlap in the vertical dimension, and the very weak preference for large crabs; according to FWRI (unpub. data), juvenile king mackerel feeds on zoeae and megalopae of large crabs, though in little quantities.
Adult king mackerel	Accessibility to shrimps set to 40% to account for little overlap in the vertical dimension. Accessibility to the different LTL benthic groups set to 10% to account for very little overlap in the vertical dimension. Accessibility to large crabs set to 0% to account for very little overlap in the vertical dimension, and the very weak preference for large crabs; according to FWRI (unpub. data), adult king mackerel feeds on zoeae and megalopae of large crabs, though in little quantities.
Amberjacks	Accessibility to shrimps set to 40% to account for little overlap in the vertical dimension. Accessibility to large crabs and to the different LTL benthic groups set to 10% to account for very little overlap in the vertical dimension. Accessibility to amberjacks set to 0% to account for the fact that amberjacks are not cannibalistic according to available evidence (Froese and Pauly 2010; FWRI, unpub. data). Accessibility to juvenile and adult king mackerels set to 0% to account for the fact that amberjacks cannot predate on king mackerels which have high swimming capabilities.
Juvenile red grouper	Accessibility to juvenile and adult king mackerels and to amberjacks set to 0%, to account for the fact that red grouper is primarily a benthic dweller around hard bottoms and reefs, while king mackerel and amberjacks are pelagic and also fleet swimmers. Accessibility to bivalves and to echinoderms and large gastropods set to 10% to account for very small overlap in the vertical dimension and for the fact that the morphology of red grouper is not well suited to feeding on the two mentioned LTL benthic groups.
Adult red grouper	Accessibility to juvenile and adult king mackerels and to amberjacks set to 0%, to account for the fact that red grouper is primarily a benthic dweller around hard bottoms and reefs, while king mackerel and amberjacks are pelagic and also fleet swimmers. Accessibility to bivalves and to echinoderms and large gastropods set to 0% to account for very small overlap in the vertical dimension and for the fact that the morphology of red grouper is not well suited to feeding on the two mentioned LTL benthic groups.
Juvenile gag	Accessibility to juvenile and adult king mackerels and to amberjacks set to 0%, to account for the fact that gag is primarily a benthic dweller around hard bottoms and reefs, while king mackerel and amberjacks are pelagic and also fleet swimmers.
Adult gag	Accessibility to shrimps, large crabs and to the different LTL benthic groups set to 40% to account for little overlap in the vertical dimension. Accessibility to juvenile and adult king mackerels and to amberjacks set to 0%, to account for the fact that gag is primarily a benthic dweller around hard bottoms and reefs, while king mackerel and amberjacks are pelagic and also fleet swimmers.
Juvenile red snapper	Accessibility to large crabs and to the different LTL benthic groups set to 40% to account for little overlap in the vertical dimension. Accessibility to bivalves and to echinoderms and large gastropods set to 10% to account for very small overlap in the vertical dimension and for the fact that the morphology of red snapper is not well suited to feeding on the two mentioned LTL benthic groups.
Adult red snapper	Accessibility to large crabs, meiofauna, small infauna and small mobile epifauna set to 40% to account for little overlap in the vertical dimension. Accessibility to bivalves and to echinoderms and large gastropods set to 10% to account for very small overlap in the vertical dimension and for the fact that the morphology of red snapper is not well suited to feeding on the two mentioned LTL benthic groups.
Sardine-herring-scad complex	Accessibility to red grouper, gag, red snapper, coastal omnivores, reef carnivores and reef omnivores set to 40% to account for little overlap in the vertical dimension. Accessibility to shrimps, large crabs and to the different LTL benthic groups set to 10% to account for very little

	overlap in the vertical dimension.
Anchovies and silversides	Accessibility to red grouper, gag, red snapper, coastal omnivores, reef carnivores, reef omnivores, meifauna, small infauna and small mobile epifauna set to 40% to account for little overlap in the vertical dimension. Accessibility to shrimps, large crabs, bivalves, and echinoderms and large gastropods set to 10% to account for very little overlap in the vertical dimension.
Coastal omnivores	Accessibility to king mackerel, amberjacks, the sardine-herring-scad complex, anchovies and silversides and shrimps set to 40% to account for little overlap in the vertical dimension. Accessibility to large crabs set to 0% to account for little overlap in the vertical dimension and for the fact that the morphology of coastal omnivores is not well suited to feeding on large crabs.
Reef carnivores	-
Reef omnivores	-
Shrimps	Accessibility to all HTL groups set to 0% to account for the fact that shrimps only feed on very small items, mostly very small benthic organisms, detritus and benthic algae (Eldred et al. 1961, Odum and Heald 1972).
Large crabs	Accessibility to the sardine-herring-scad complex, anchovies and silversides and coastal omnivores set to 10% to account for very little overlap in the vertical dimension. Accessibility to all other HTL groups set to 0% to account for the fact that large crabs can certainly capture small fish on occasion along with many other small invertebrates, and detritus, but not large fish (Darnell 1958, Tagatz 1968, Laughlin 1982, Alexander 1986, Stoner and Buchanan 1990).

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