

1 **Building bridges between global information systems on marine organisms and**
2 **ecosystem models**

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57 **ABSTRACT**

58 To facilitate the wider implementation of ecosystem modeling platforms and, thereby, to help
59 advance ecosystem-based fisheries management (EBFM) worldwide, tools delivering a large
60 quantity of inputs to ecosystem models are needed. We developed a web application
61 providing OSMOSE ecosystem models with values for trophic, growth and reproduction
62 parameters derived from data from two global information systems (FishBase and
63 SeaLifeBase). Our web application guides the user through simple queries to extract
64 information from FishBase and SeaLifeBase data archives, and it delivers all the
65 configuration files necessary for running an OSMOSE model. Here, we present our web
66 application and demonstrate it for the West Florida Shelf ecosystem. Our software
67 architecture can serve as a basis for designing other advanced web applications using
68 FishBase and SeaLifeBase data in support of EBFM.

69

70 **Keywords:**

71 Web application
72 FishBase
73 SeaLifeBase
74 Ecosystem model
75 OSMOSE
76 Web application programming interface

77 **1. Introduction**

78 Ecosystem-based fisheries management (EBFM), which recognizes the importance of
79 non-target marine organisms, trophic dynamics, the abiotic environment and socio-economic
80 factors in fisheries systems, has emerged as a key concept (Pikitch et al., 2004; Link, 2010;
81 Harvey et al., 2016). Because they can simulate the effects of fishing, environmental stressors
82 and management measures at multiple spatial and temporal scales, ecosystem models have
83 become central tools for informing EBFM (Christensen and Walters, 2011; Collie et al., 2016;
84 Grüss et al., 2017a). Major breakthroughs have been achieved in the field of ecosystem
85 modeling over the past 25 years, resulting in the emergence of a diversity of modeling
86 platforms, which allow tackling the numerous questions associated with EBFM (Plagányi,
87 2007; Fulton, 2010; Espinoza-Tenorio et al., 2012). O’Farrell et al. (2017) updated Plagányi
88 (2007)’s seminal terminology and distinguished between six types of ecosystem models,
89 based on their structure. These six types of ecosystem models are, in order of complexity:
90 conceptual and qualitative models, extensions of single-species models, dynamic multispecies
91 models, aggregated (or whole ecosystem) models, biogeochemical-based end-to-end models,
92 and coupled and hybrid model platforms (O’Farrell et al., 2017).

93 Three of the most commonly used ecosystem modeling platforms belong to the most
94 sophisticated types of ecosystem models: the aggregated (or whole ecosystem) modeling
95 platform Ecopath with Ecosim (EwE) (Walters et al., 1997; Pauly et al., 2000; Christensen
96 and Walters, 2004), the biogeochemical-based end-to-end modeling platform Atlantis (Fulton
97 et al., 2004, 2007, 2011), and the individual-based, multispecies modeling platform
98 OSMOSE, which belongs to the coupled and hybrid model platforms’ type (Shin and Cury,
99 2001a, 2004; Grüss et al., 2016c). During the last decade, the trio EwE-Atlantis-OSMOSE has
100 been increasingly employed to address EBFM questions such as the impacts of exploiting low
101 trophic level species on marine ecosystems (Smith et al., 2011), the consequences of fishing
102 scenarios on the structure of the Southern Benguela ecosystem (Smith et al., 2015), the
103 performance of trophic level-based indicators for tracking fishing effects (Reed et al., 2017),
104 the specificity of ecological indicators to fishing (Shin et al., 2018), and the synergistic
105 impacts of fishing and environmental changes on marine ecosystems (Fu et al., 2018).

106 Despite the broad interest in EwE, Atlantis and OSMOSE for assisting EBFM,
107 progress towards the wide use of these ecosystem modeling platforms (particularly Atlantis
108 and OSMOSE) has been impeded by their large data requirements. Because they represent
109 many of the components of marine ecosystems, from primary producers to large marine

110 predators and humans, EwE, Atlantis and OSMOSE require an extremely large number of
111 inputs (Fulton et al., 2007; Steele et al., 2013; Grüss et al., 2016a). As a result, the
112 parameterization of EwE, Atlantis and OSMOSE models takes a relatively long time, while
113 their calibration, which comes next before ecosystem models can be employed for
114 simulations, is even more time-demanding (Oliveros Ramos, 2014; Ainsworth et al., 2015;
115 Oliveros-Ramos et al., 2017). Therefore, to facilitate the wider implementation of
116 sophisticated ecosystem modeling platforms such as EwE, Atlantis and OSMOSE and,
117 thereby, to help advancing EBFM worldwide, there is a need for tools providing ecosystem
118 models with a large quantity of inputs of reasonable quality (Grüss et al., 2016a; Coll and
119 Steenbeek, 2017). Recent years have seen the creation of such tools. For example,
120 probabilistic methods using maximum likelihood estimation have been developed for
121 generating diet matrices for EwE and Atlantis models in a robust and relatively rapid manner
122 (Ainsworth et al., 2010; Masi et al., 2014; Sagarese et al., 2016; Tarnecki et al., 2016;
123 Morzaria-Luna et al., 2018). Another example are the statistical habitat methods that were
124 designed for producing annual and seasonal distribution maps in bulk for Atlantis and
125 OSMOSE models (Grüss et al., 2017b, 2018a, 2018b, 2018c, 2019). However, none of these
126 recently-created tools are user-friendly, and they do not cover many of the important trophic
127 (e.g., Ecopath's consumption rates, OSMOSE's predator/prey size ratios), growth and
128 reproduction parameters required by EwE, Atlantis and OSMOSE.

129 The most efficient way to provide the largest possible number of inputs of reasonable
130 quality to EwE, Atlantis and OSMOSE models would be to create a tool for querying large
131 global information systems on marine organisms, namely FishBase (<http://www.fishbase.org>;
132 Froese and Pauly, 2018) and SeaLifeBase (<http://www.sealifebase.org/>; Palomares and Pauly,
133 2018). FishBase is the world's largest database on fish on the web; it supplies taxonomic,
134 ecological, morphological and metabolic information on 34,000 species and subspecies as of
135 June 2018 (Froese and Pauly, 2018). SeaLifeBase is a large global information system similar
136 to FishBase, which covers all types of marine organisms apart from fish; as of June 2018, it
137 includes information for 75,100 non-fish species (Palomares and Pauly, 2018). In the "Tools"
138 section of FishBase, a routine provides some EwE parameters for aquatic ecosystems and
139 national waters within Food and Agriculture Organization (FAO) areas. However, this routine
140 is basic and supplies only a couple of inputs for the Ecopath component of EwE (e.g., trophic
141 levels (TLs), consumption rates) on a webpage. Also, this routine assigns species to functional
142 groups (i.e., groups of species sharing similar life history traits and ecological niches), based

143 on their maximum body length, habitat and depth range, but also based on their family, which
144 results in the definition of many more functional groups than usually defined in EwE models.
145 Lastly, this routine focuses on fish, while many other types of marine organisms, including
146 invertebrates, marine mammals, sea turtles and seabirds, are usually represented in EwE
147 models. Therefore, it would be advantageous to develop more sophisticated tools establishing
148 bridges between both FishBase and SeaLifeBase and ecosystem modeling platforms like
149 EwE, Atlantis and OSMOSE, so as to provide the largest possible number of trophic, growth
150 and reproduction parameters of reasonable quality to these ecosystem modeling platforms.

151 In this study, we present the web application we developed for providing OSMOSE
152 models with values for trophic, growth and reproduction parameters derived from FishBase
153 and SeaLifeBase data. Our web application combines a web user interface (web UI)¹ guiding
154 the user through simple queries with a web application programming interface (web API)²
155 and data archives for retrieving and managing FishBase and SeaLifeBase data, and it
156 ultimately delivers a zip file containing all the information necessary for running an OSMOSE
157 model. Although our initial intent was to create a web application for helping the
158 parameterization of OSMOSE models, we developed a framework that is as generic as
159 possible, so as to enable its future use for designing web applications capable of processing
160 FishBase/SeaLifeBase data to produce parameter values for other sophisticated ecosystem
161 models (e.g., Atlantis applications). In the following, we first describe the OSMOSE
162 modeling platform, its inputs, and its requirements. Then, we provide an overview of our web
163 application, before presenting the different steps that are followed to ultimately deliver
164 OSMOSE inputs to the user. Next, we demonstrate our web application for the West Florida
165 Shelf, an ecosystem located within the Gulf of Mexico. Finally, we discuss the strengths and
166 limitations of our web application in its current form and provide avenues for future research.

167

168 **2. Material and methods**

169 ***2.1. The OSMOSE modeling platform***

¹ A web user interface (web UI) is a shared boundary between a web application and humans, designed to facilitate the exchange of information between the two entities.

² A web application programming interface (web API) is an ensemble of routine definitions, protocols and tools for implementing a web application.

170 OSMOSE (Object-oriented Simulator of Marine ecOSystEms) is a two-dimensional,
171 individual-based, multi-species modeling platform created around 20 years ago (Shin, 2000;
172 Shin and Cury, 2001a, 2004; <http://www.osmose-model.org>). OSMOSE models simulate the
173 entire life cycle of (typically 10 to 15) “focal functional groups” and their trophic interactions.
174 In addition, OSMOSE models are forced by the biomass of a second type of functional groups
175 called “biotic resources” (usually plankton and benthos groups), which only serve to provide
176 extra food to the modeled system (Grüss et al., 2016b, 2016c). OSMOSE was initially
177 developed for simulating the life cycle of individual focal species rather than that of focal
178 functional groups (Shin, 2000; Shin and Cury, 2001a, 2004). Existing OSMOSE applications
179 represent focal species (e.g., Marzloff et al., 2009; Halouani et al., 2016), focal functional
180 groups (e.g., Brochier et al., 2013; Grüss et al., 2015), or a mix of the two (e.g., Oliveros-
181 Ramos et al., 2017; Xing et al., 2017). Our web application initially defines focal functional
182 groups for the user, but let the user the possibility to define only focal species for their
183 OSMOSE model if they wish (see Subsection 2.3.2).

184 The focal functional groups and biotic resources considered in OSMOSE models are
185 usually only fish and invertebrate groups. An exception to this usual pattern is the focal
186 marine mammal group (harbor seal, *Phoca vitulina*) represented in the OSMOSE model of the
187 Strait of Georgia in British Columbia, Canada (Fu et al., 2012, 2013). However, the processes
188 currently represented in OSMOSE are not well suited for simulating the biology and ecology
189 of marine mammals and other organisms such as sea turtles and seabirds, which are, in many
190 aspects, different from the biology and ecology of fish and invertebrates. Therefore, it is
191 recommended to focus on fish and invertebrates in OSMOSE applications, and those are the
192 two types of marine organisms for which our web application currently provides input
193 parameters.

194 The key difference between OSMOSE and EwE and Atlantis is that OSMOSE does
195 not use a diet matrix as input, but rather relies on the tenet that predation is an opportunistic
196 and size-based process. Thus, OSMOSE lets diet compositions emerge from simulated trophic
197 interactions (Shin and Cury, 2001a, 2004; Grüss et al., 2016c). In OSMOSE, the predation
198 process is conditioned by three types of input: (1) spatial distribution maps, which, along with
199 the random walk movements simulated for focal functional groups, define the annual or
200 seasonal spatial distributions of marine organisms and, consequently, patterns of spatial
201 overlap between predators and their potential prey; (2) minimum and maximum predator prey
202 size ratios, which govern size adequacy between predators and their potential prey; and (3)

203 accessibility coefficients, which determine if potential prey items are accessible to the
204 predators, because of implicit, underlying factors such as distribution in the water column and
205 animal morphology (e.g., presence of spikes) (Grüss et al., 2016c).

206 The basic units of OSMOSE models are “schools”, namely individuals of a given focal
207 functional group, which have the same age, body size, body weight, and, at a given time step,
208 the same geographical location (Shin and Cury, 2001a, 2004). At each time step, schools
209 undergo a series of processes: spatial distribution and random walk movement, then mortality
210 processes (predation, starvation and fishing mortalities, and other mortality due to causes not
211 explicitly modeled in OSMOSE), then growth in size and weight, and, finally, reproduction,
212 which results in the production of age-0 schools for the next time step (Appendix A; Grüss et
213 al., 2016c). The individual-based structure of OSMOSE allows one to track ecological
214 information at different hierarchical levels: school, cohort (age class), focal functional group,
215 and ecological community (Shin et al., 2004; Grüss et al., 2015; Travers-Trolet et al., 2014a).

216 OSMOSE has gone through three versions, and the last version itself has gone through
217 two updates (“OSMOSE v3u1” and “OSMOSE v3u2”) (Table 1). OSMOSE has served to
218 address various EBFM questions, including the consequences of fishing scenarios on the
219 structure and functioning of marine ecosystems (Shin et al., 2004; Marzloff et al., 2009;
220 Travers et al., 2010; Smith et al., 2011, 2015), the effects of marine protected areas (MPAs)
221 (Shin and Cury, 2001b; Yemane et al., 2009; Brochier et al., 2013), the impacts of
222 environmental changes in fisheries systems (Fu et al., 2012, 2013; Travers-Trolet et al.,
223 2014b), the sensitivity of ecological indicators and their specificity to fishing (Reed et al.,
224 2017; Fu et al., 2018; Shin et al., 2018; Halouani et al., 2019), the estimation of predation
225 mortality rates (Travers and Shin, 2010; Travers et al., 2009; Grüss et al., 2015, 2016c; Fu et
226 al., 2017; Xing et al., 2017), and management strategy evaluation (MSE) in an ecosystem
227 context (Grüss et al., 2016b).

228

229 **Table 1**

230 Versions of the OSMOSE modeling platform and their applications.

OSMOSE version	Applications
OSMOSE v1	Theoretical ecosystems (Shin and Cury, 2001a, 2001b; Vergnon et al., 2008), Southern Benguela ecosystem for the 1980s period (Shin et al., 2004; Travers et al., 2006; Yemane et al., 2009)

OSMOSE v2	Southern Benguela ecosystem for the 1990s period (Travers and Shin, 2010; Travers et al., 2009, 2010; Travers-Trolet et al., 2014a, 2014b), Humboldt for the period 2000-2006 (Marzloff et al., 2009), Bamboung Bolong in Senegal for the 2000s period (Brochier et al., 2013), Strait of Georgia in Canada for the 2000s period (Fu et al., 2012, 2013)
OSMOSE v3	West Florida Shelf ecosystem for the 2000s period (Grüss et al., 2015)
OSMOSE v3u1	West Florida Shelf ecosystem for the 2000s period (Grüss et al., 2016c)
OSMOSE v3u2	West Florida Shelf ecosystem for the 2000s period (Grüss et al., 2016b), Gulf of Gabes in Tunisia for the 2000s period (Halouani et al., 2016, 2019), Humboldt for the period 1992-2008 (Oliveros-Ramos et al., 2017), west coast of Canada for the period 1950-2014 (Fu et al., 2017), Jiaozhou Bay in China for the 2000s period (Xing et al., 2017)

231

232 The version of OSMOSE considered in the present study is the latest one, i.e.
233 OSMOSE v3u2, which is available for download from [http://www.osmose-](http://www.osmose-model.org/downloads)
234 [model.org/downloads](http://www.osmose-model.org/downloads). The two main characteristics of OSMOSE v3u2 are that: (1) it employs
235 a “stochastic mortality algorithm” to compute mortality rates, which assumes that all types of
236 mortalities are simultaneous processes and that there is competition and stochasticity in the
237 predation process; and (2) it implements a “seeding process”, which helps guarantee
238 population persistence at the initialization of the modeled system (Appendix A; Grüss et al.,
239 2016b). A user guide (<https://documentation.osmose-model.org/>) and GitHub repositories
240 (<https://github.com/osmose-model>) are currently being developed for OSMOSE. The
241 programming language used for implementing OSMOSE is Java (Gosling, 2000). An
242 Integrated Development Environment (IDE) such as the free, open-source IDE NetBeans
243 (<https://netbeans.org/>) can be utilized to compile OSMOSE models. OSMOSE models can
244 also be run within the R environment with R package “osmose”, which is now available on
245 CRAN.

246 Two types of input files (“configuration files”) are fed into OSMOSE: CSV (comma-
247 separated value) and netCDF files (<http://www.osmose-model.org>). The CSV and netCDF
248 files provided to the template version of OSMOSE v3u2 (i.e., the version that can be
249 downloaded from <http://www.osmose-model.org/downloads>) are detailed in Table 2 and
250 Appendix B. The template version of OSMOSE v3u2 is based on the OSMOSE model for the
251 Southern Benguela ecosystem for the 1990s period (Travers and Shin, 2010; Travers et al.,
252 2009, 2010; Travers-Trolet et al., 2014a, 2014b). The great majority of OSMOSE
253 configuration files use the key-value system to inform OSMOSE parameterization (e.g.,
254 “simulation.nspecies” is the key for the number of focal functional groups represented, and
255 “15” is a potential value for this parameter; Appendix B). Numerous inputs are needed for
256 focal functional groups, because their entire life cycle is modeled explicitly. In contrast, since
257 biotic resources only serve to provide additional food to the modeled system, only a limited

258 number of inputs are required for them, *viz*: biomass fields for the different time steps within a
 259 year considered in the OSMOSE model, minimum and maximum body sizes, TL, and
 260 availability and theoretical accessibility coefficients (Table 2 and Appendix B). Usually, two
 261 types of OSMOSE inputs are estimated during the calibration process of OSMOSE: the larval
 262 mortality rates of focal functional groups, and the availability coefficients of biotic resources
 263 (Travers-Trolet et al., 2014a; Grüss et al., 2015).

264

265 **Table 2**

266 Details about the CSV (.csv) and netCDF (.nc) configuration files supplied to the template version of OSMOSE
 267 v3u2. Details about the parameters provided by these CSV and netCDF files are given in Appendix B. $n =$
 268 number of focal functional groups represented in the OSMOSE model.

Configuration file name	Description
osm_all-parameters.csv	Main OSMOSE configuration file, where general OSMOSE parameters, such as the number of time steps per year and the number of focal functional groups and biotic resources considered, are provided
osm_param-species.csv	File defining the basic parameters (e.g., growth parameters, longevity) of focal functional groups
osm_param-ntl.csv	File defining the parameters of biotic resources (e.g. minimum and maximum body sizes)
osm_param-grid.csv	File providing information about the spatial grid of the OSMOSE model
grid-mask.csv	Spatial grid of the OSMOSE model
osm_ltlbiomass.nc	File providing biomass fields for biotic resources for the different annual time steps represented in the OSMOSE model
osm_param-fishing.csv	File defining the exploitation patterns of focal functional groups
osm_param-init-pop.csv	File providing the initial biomasses (i.e., the biomasses at time step 0) of focal functional groups
osm_param-movement.csv	File defining the spatial distribution and movement patterns of focal functional groups
osm_param-natural-mortality.csv	File defining the larval mortality rate of focal functional groups and their non-larval mortality due to causes unrepresented in OSMOSE
osm_param-predation.csv	File defining the trophic parameters of focal functional groups (e.g., their minimum and maximum predator/prey size ratios)
osm_param-reproduction.csv	File providing the names of the CSV files defining the seasonal patterns of reproduction of focal functional groups
osm_param-starvation.csv	File defining the maximum annual starvation mortality rate of focal functional groups
predation-accessibility.csv	File providing the accessibility coefficients of focal functional groups and the theoretical accessibility of biotic resources; all these coefficients define the accessibility of potential prey items to individual predators
reproductionseasonality-sp _{<i>i</i>} .csv, with $i = 0, 1, \dots, n-1$	Files defining the seasonal patterns of reproduction of focal functional groups
fishing/fishing-seasonality-name _{<i>i</i>} .csv, with $i = 0, 1, \dots, n-1$	Files (located within a “fishing” folder) that define the seasonal patterns of exploitation of focal functional groups
maps/name _{<i>i</i>} _j.csv, with $i = 0, 1, \dots, n-1$ and where j is an integer	Files (located within a “maps” folder) that define the spatial distribution patterns of focal functional groups, possibly at different seasons (if $j > 1$)

269

270 Due to its ability to track ecological information at different hierarchical levels,
271 OSMOSE can deliver a large number of outputs, at different levels of aggregation. Thus, for
272 example, OSMOSE models can inform one about biomasses and body sizes at the cohort,
273 focal functional group and ecological community levels (Shin et al., 2004; Marzloff et al.,
274 2009; Grüss et al., 2015; Travers-Trolet et al., 2014a). The template version of OSMOSE
275 v3u2 can provide up to 31 different types of basic outputs, such as biomasses, mean body
276 sizes in the catch or TLs (Appendix B). However, a diversity of more complex outputs (e.g.,
277 Shannon-Wiener index, Fishing-in-Balance index, net present value of discounted fisheries
278 revenues) can be obtained from OSMOSE, either by modifying OSMOSE Java code or
279 through a post-processing of OSMOSE basic outputs (e.g., Travers et al., 2006; Grüss et al.,
280 2016b; Reed et al., 2017).

281 OSMOSE models are stochastic, because they: (1) distribute limited numbers of
282 schools over space based on the distribution maps provided as input; (2) employ random walk
283 movement to simulate the movements of schools within their distribution areas; and (3) use a
284 “stochastic mortality algorithm” to compute mortality rates (Grüss et al., 2016b, 2016c).
285 Consequently, OSMOSE outputs are analyzed on the basis of several OSMOSE replicates
286 (generally 10 or 20; Marzloff et al., 2009; Travers et al., 2010; Grüss et al., 2015; Halouani et
287 al., 2016).

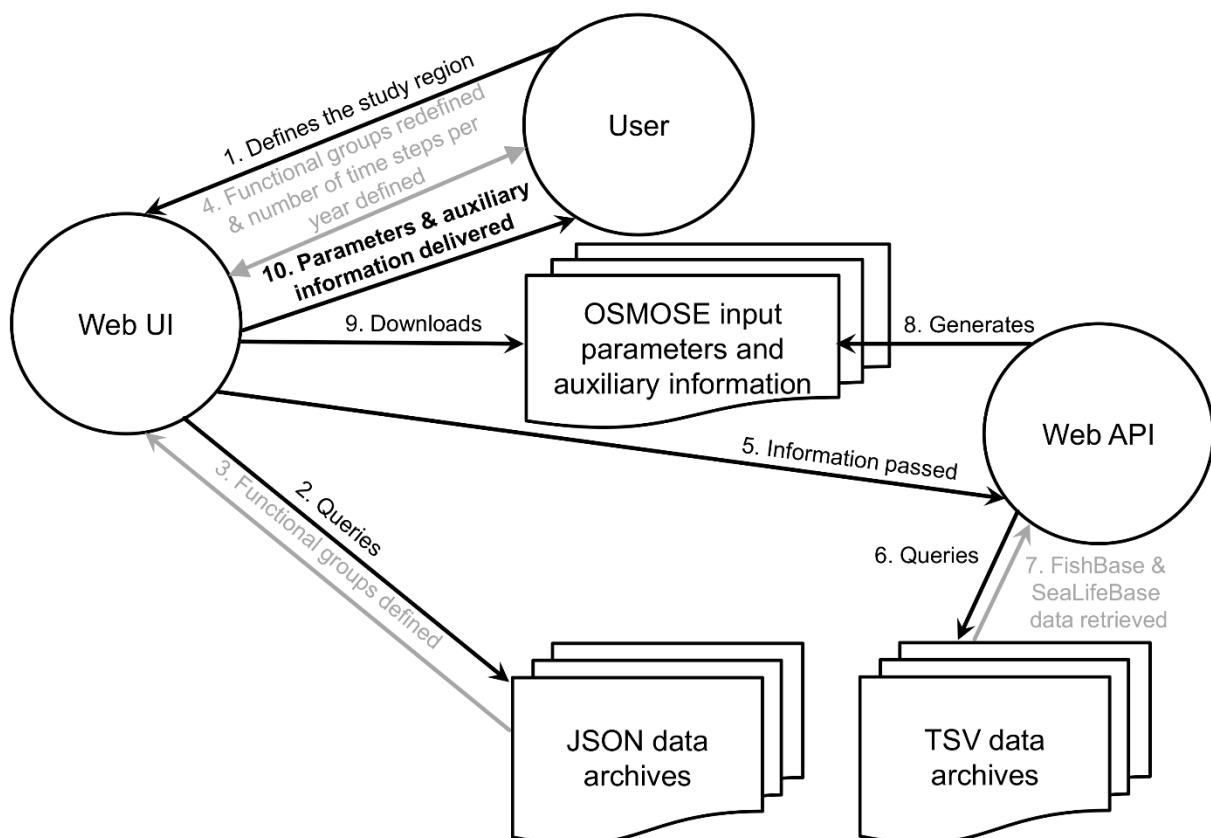
288

289 ***2.2. Overview of the web application***

290 Our web application relies on interactions between a web UI
291 (<https://doi.org/10.5281/zenodo.1418543>) and a web API
292 (<https://doi.org/10.5281/zenodo.1411483>) (Fig. 1). The user starts interacting with the web
293 application by querying the web UI, which utilizes JavaScript and the JQuery library
294 (Osmani, 2012). After the user has defined the study region, the web UI queries information
295 stored in JavaScript Object Notation (JSON) data archives to define functional groups for the
296 OSMOSE model. Then, the web UI offers the possibility to the user to redefine functional
297 groups and the user is also requested to indicate the number of time steps per year of their
298 OSMOSE model. Next, the information resulting from the interactions between the user and
299 the web UI is passed to the web API. The web API queries the required FishBase and

300 SeaLifeBase data (Table 3 and Appendix C) from TSV (tab-separated value) data archives
 301 and processes these data to generate OSMOSE input parameters, which are communicated to
 302 the web UI. The web API is coded in the Java programming language (Gosling, 2000) and is
 303 deployed on the Heroku platform (<https://www.heroku.com/>). Finally, the web UI delivers a
 304 zip file (“osmose_config.zip”) to the user, which contains OSMOSE configuration files filled
 305 with information, as well as a “README” file and a CSV file listing the species making up
 306 the focal functional groups and biotic resources defined for the OSMOSE model. We employ
 307 GitHub to share, document and discuss our web application and the tools on which our web
 308 application relies (see <https://github.com/osmose-model/osmose-model.github.io>,
 309 <https://github.com/osmose-model/osmose-web-api>, and [https://github.com/osmose-](https://github.com/osmose-model/osmose-web-api-js)
 310 [model/osmose-web-api-js](https://github.com/osmose-model/osmose-web-api-js)). The second of three aforementioned GitHub repositories archives
 311 all of the Java code of the web API, and it keeps track of the issues faced during the
 312 development and use of our web API, as well as reflections on future improvements or
 313 developments. The repository <https://github.com/osmose-model/osmose-web-api-js> provides
 314 the JavaScript library necessary for running our web API
 315 (<https://doi.org/10.5281/zenodo.1411481>).

316



317

318 **Fig. 1.** Schematic of the different steps followed to obtain OSMOSE configuration files via the web application
319 presented in this study. (1) The user starts interacting with the web user interface (web UI) and defines the study
320 region. (2) The web UI queries data from JavaScript Object Notation (JSON) data archives to define functional
321 groups and their species breakdown. (3) The defined functional groups are communicated to the web UI. (4) The
322 user interacts with the web UI to redefine functional groups and to define the number of time steps per year in
323 the OSMOSE model. (5) All the information resulting from the interactions between the user and the web UI is
324 passed to the web application programming interface (web API). (6) The web API queries FishBase/SeaLifeBase
325 data from TSV (tab-separated value) data archives. (7) The web API retrieves FishBase/SeaLifeBase data. (8)
326 The web API processes the FishBase/SeaLifeBase data to generate OSMOSE input parameters. (9) The
327 OSMOSE input parameters and auxiliary information are passed to the web UI. (10) The web UI communicates
328 OSMOSE input parameters and auxiliary information to the user.

329 **Table 3**

330 FishBase/SeaLifeBase's data used to derive OSMOSE parameters. Further details are provided in Appendix C. $X = 0, 1, \dots, n_X-1$, where n_X is the number of focal functional
 331 groups represented in the OSMOSE model. $Y = 0, 1, \dots, n_Y-1$, where n_Y is the number of biotic resources represented in the OSMOSE model. * = FishBase/SeaLifeBase
 332 parameter used for calculating the "data richness" metric (see the main text for details on this metric).

OSMOSE parameter	OSMOSE parameter key	FishBase/ SeaLifeBase table(s) to screen	FishBase/ SeaLifeBase column(s) to use
Longevity (years)	species.lifespan.spX	species	LongevityWild*
Instantaneous growth rate at small size (year ⁻¹)	species.K.spX	popgrowth	K*
Maximum size (cm)	species.lInf.spX	popgrowth	Loo*
Theoretical age of zero length (years)	species.t0.spX	popgrowth	to*
Constant of proportionality of the allometric length-weight relationship	species.length2weight.condition.factor.spX	poplw	a*
Exponent of the allometric length-weight relationship	species.length2weight.allometric.power.spX	poplw	b*
Body size at sexual maturity (cm)	species.maturity.size.spX	maturity	Lm*
Age at sexual maturity (years)	species.maturity.age.spX	maturity	tm*
Threshold age below which a linear growth model is used to calculate mean length increase (years)	species.vonbertalanffy.threshold.age.spX	poplw popgrowth estimate	LengthMin* to*, Loo*, K* AgeMin, AgeMax
Annual number of eggs per g of mature female	species.relativefecundity.spX	species fecundity	LongevityWild* SpawningCycles*, RelFecundityMean*
Sex ratio, defined as the proportion of females in the population	species.sexratio.spX	spawning	SexRatiomid*
Egg size (cm)	species.egg.size.spX	eggs	Eggsdiammod*
Egg weight (g)	species.egg.weight.spX	eggs	Eggsdiammod*
Trophic level	plankton.TL.plkY	estimate	Troph*
Minimum body size (cm)	plankton.size.min.plkY	popll	LengthMin*
Maximum body size (cm)	plankton.size.max.plkY	popll	LengthMax*
Natural mortality rate due to causes unrepresented in OSMOSE	mortality.natural.rate.spX	popqb	mortality*
Maximum annual ingestion rate (g of food per g of individual and per year)	predation.ingestion.rate.max.spX	popqb	PopQB*
Critical predation efficiency	predation.ingestion.rate.max.spX	popqb	MaintQB*, PopQB*
Minimum predator/prey size ratios	predation.predPrey.sizeRatio.max.spX	popqb estimate	PredPreyRatioMin

Maximum predator/prey size ratios	predation.predPrey.sizeRatio.min.spX	estimate	PredPreyRatioMax
Body size threshold that separates the predator/prey size ratios for juvenile individuals from those for adult individuals (cm)	predation.predPrey.stage.threshold.spX	maturity	Lm*
Accessibility coefficients and theoretical accessibility coefficients	Content of the “predation-accessibility.csv” file	ecology	Benthic
Age threshold that separates the accessibility coefficients of the juvenile and adult stages of focal functional groups (years)	predation.accessibility.stage.threshold.spX	maturity	tm*
Reproduction seasonality	Content of the “reproduction-seasonality-spX” files	spawning	Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec

333 **2.3. Steps followed to provide OSMOSE inputs to the user**

334 **2.3.1. Definition of the study region**

335 To access the web UI, the user needs to go to the FishBase (<http://www.fishbase.org>)
336 or SeaLifeBase website (<http://www.sealifebase.org/>), and to select the “OSMOSE
337 parameters” radio button in the “Tools” section (Step 1 in Fig. 1). Then, the user reaches a
338 first webpage, requesting them to select a marine ecosystem or a combination of a country
339 and FAO area (Fig. 2). For some countries, it is also possible to select a given state (e.g.,
340 Louisiana in the U.S.) or province (e.g., Queensland in Australia). Once the study region has
341 been defined, the user can press the “Proceed” button. Note that the web UI is also available
342 at the following address: <http://config.osmose-model.org>.

343

Getting parameter estimates for your OSMOSE model

You are about to query parameter estimates for your OSMOSE model.
To get started, please select an ecosystem or a combination of a country and FAO area.

Ecosystem * Required

Country * Required

State/Province

FAO Area * Required

344

345 **Fig. 2.** Snapshot of the first page of the web user interface.

346

347 **2.3.2. Definition of functional groups and of the number of time steps per year**

348 To work on a first definition of functional groups and their species breakdown for the
349 marine region defined by the user, the web UI queries information stored in JSON data
350 archives we compiled (located in [https://github.com/osmose-model/osmose-
351 model.github.io/tree/master/data](https://github.com/osmose-model/osmose-model.github.io/tree/master/data)) (Step 2 in Fig. 1). To populate the JSON data archives, we
352 employed an existing routine³ to define functional groups for each of the marine regions
353 (marine ecosystems and combinations of a country, FAO area and state/province) that can

³ This (unpublished) routine is the routine used to provide some EwE parameters for aquatic ecosystems and national waters within FAO areas in the “Tools” section of FishBase (mentioned in the Introduction).

354 potentially be selected by the user. This routine considers: (1) the species inhabiting the
355 marine region of interest, according to FishBase and SeaLifeBase; and (2) the information
356 stored in FishBase/SeaLifeBase’s tables about the habitat (e.g., demersal, benthopelagic),
357 depth range, body size and high order (e.g., sharks, rays) of these species. The JSON data
358 archives also store the following information: (1) additional, related species (i.e., species that
359 belong to a related genus or family) for each of the functional groups defined for each of the
360 marine regions that can potentially be selected by the user (see Subsection 2.3.3); (2) the
361 maximum body size, habitat and depth range of all the species included in the JSON data
362 archives; and (3) “data richness” for all the species included in the JSON data archives (see
363 below). The JSON data archives created for our web application are automatically updated
364 every time changes are made in FishBase and SeaLifeBase (e.g., whenever mirror updates of
365 FishBase and SeaLifeBase are performed).

366 After the web UI has queried information from the JSON data archives, the first
367 definition of functional groups is displayed on a new webpage, along with two additional
368 generic functional groups (“phytoplankton” and “zooplankton”, which are both defined as
369 biotic resources) and instructions for the user (Step 3 in Fig. 1 and Fig. 3). Functional groups
370 are detailed in a table. A default name is assigned to them. Moreover, the class, Latin name,
371 maximum body size, habitat and depth range of the species comprising the functional groups
372 are provided. By default, all focal functional groups are defined as focal functional groups,
373 except the generic phytoplankton and zooplankton groups, which can both only be defined as
374 biotic resources.

375

Reorganize functional groups

Back **Proceed**

FishBase/SealifeBase defined functional groups for you

Please feel free to:

- (1) Indicate whether each functional group is a focal functional group or a biotic resource, using dedicated radio buttons.
- (2) Remove species from some functional groups.
- (3) Redistribute species between functional groups.
- (4) Remove functional groups from the table.
- (5) Create functional groups.
- (6) Rename functional groups.

Caution: The name of the functional groups should not include spaces nor underscores. For example, "SmallPelagics" is a valid functional group name, but not "Small pelagics" nor "Small_pelagics".

When you are ready, press Proceed to go to the next step.

Select/deselect	Functional Group	Focal Functional Group	Biotic Resource	Class	Species	Maximum length (cm)	Habitat	Depth
<input checked="" type="checkbox"/>	fishpelagicmd	<input checked="" type="radio"/>	<input type="radio"/>	<input checked="" type="checkbox"/> Actinopterygii	<input checked="" type="checkbox"/> <i>Decapterus macarellus</i>	46	pelagic-oceanic	400
<input checked="" type="checkbox"/>	fishdemersalm	<input type="radio"/>	<input type="radio"/>	<input checked="" type="checkbox"/> Actinopterygii	<input checked="" type="checkbox"/> <i>Hime japonica</i>	27.21	demersal	85-510
<input checked="" type="checkbox"/>	fishdemersalmd	<input type="radio"/>	<input type="radio"/>	<input checked="" type="checkbox"/> Actinopterygii	<input checked="" type="checkbox"/> <i>Antigonia capros</i>	30.5	demersal	50-900
<input checked="" type="checkbox"/>	fishbathypelagicmd	<input type="radio"/>	<input type="radio"/>	<input checked="" type="checkbox"/> Actinopterygii	<input checked="" type="checkbox"/> <i>Grammicolepis brachiusculus</i>	64	bathypelagic	300-1026
<input checked="" type="checkbox"/>	fishbenthopelagicmd	<input type="radio"/>	<input type="radio"/>	<input checked="" type="checkbox"/> Actinopterygii <input checked="" type="checkbox"/> Actinopterygii <input checked="" type="checkbox"/> Actinopterygii	<input checked="" type="checkbox"/> <i>Beryx splendens</i> <input checked="" type="checkbox"/> <i>Pentaceros wheeleri</i> <input checked="" type="checkbox"/> <i>Zenopsis nebulosa</i>	70 44 70	benthopelagic benthopelagic benthopelagic	25-1300 146-800 30-800
<input checked="" type="checkbox"/>	fishbenthopelagiclg	<input type="radio"/>	<input type="radio"/>	<input checked="" type="checkbox"/> Actinopterygii <input checked="" type="checkbox"/> Actinopterygii <input checked="" type="checkbox"/> Actinopterygii	<input checked="" type="checkbox"/> <i>Etelis carbunculus</i> <input checked="" type="checkbox"/> <i>Promethichthys prometheus</i> <input checked="" type="checkbox"/> <i>Ruvettus pretiosus</i>	140.97 122 300	benthopelagic benthopelagic benthopelagic	90-400 80-800 100-800
<input checked="" type="checkbox"/>	fishsharklg	<input type="radio"/>	<input type="radio"/>	<input checked="" type="checkbox"/> Elasmobranchii	<input checked="" type="checkbox"/> <i>Squalus blainville</i>	100	demersal	
<input checked="" type="checkbox"/>	zooplankton	<input type="radio"/>	<input type="radio"/>					
<input checked="" type="checkbox"/>	phytoplankton	<input type="radio"/>	<input type="radio"/>					

Back **Proceed**

376

377 **Fig. 3.** Snapshot of the second page of the web user interface for the Academician Berg, a seamount ecosystem
 378 belonging to the Hawaiian-Emperor seamount chain, which is located in the North Pacific.

379

380 The species composition of the functional groups defined in the JSON data archives
 381 and displayed on the second page of the web UI was determined using a “data richness”
 382 metric. Data richness was calculated on the basis of 18 FishBase/SeaLifeBase parameters
 383 (Table 3). For each species that could potentially be included in a functional group, it was
 384 determined whether a value is available (1) or not (0) for each of the 18
 385 FishBase/SeaLifeBase parameters to estimate data richness. For example, if, for a given
 386 species, 10 parameter values were available, the data richness of this species was equal to 10.
 387 For each functional group, the species that could potentially be included were ranked based on
 388 their data richness and those whose data richness was smaller than 2 were dropped. Then,
 389 some other species with the lowest data richness values were eventually dropped so as to keep

390 the number of species per functional group to a maximum of 30, for the sake of computational
 391 efficiency.

392 In the case of the generic phytoplankton and zooplankton groups, species are not
 393 defined and, therefore, data richness is not calculated. Instead, pre-specified parameter values
 394 for phytoplankton and zooplankton (i.e., which are the same for all marine regions; Table 4)
 395 are provided in the OSMOSE configuration files. These parameter values are those that are
 396 usually defined in existing OSMOSE applications (e.g., Travers-Trolet et al., 2014a; Grüss et
 397 al., 2015; Halouani et al., 2016; Fu et al., 2017). The rationale behind the definition of generic
 398 phytoplankton and zooplankton groups is that preliminary results revealed that data richness
 399 is equal to 1 for the great majority of the zooplankton species included in SeaLifeBase and for
 400 all the phytoplankton species included in SeaLifeBase. However, for some marine regions, the
 401 web application may define specific zooplankton groups in addition to the generic
 402 zooplankton group. This possibility was allowed, because, in addition to representing
 403 zooplankton groups as biotic resources, some existing OSMOSE models (Travers-Trolet et
 404 al., 2014a; Fu et al., 2013, 2017) represented euphausiids (order Euphausiacea, class
 405 Malacostraca) as a focal functional group.

406

407 **Table 4**

408 Parameter values for the generic phytoplankton and zooplankton groups defined by the web application for any
 409 marine region. Both the generic phytoplankton and zooplankton groups are defined as “biotic resources” by the
 410 web application.

OSMOSE parameter	OSMOSE parameter key	Value for phytoplankton	Value for zooplankton
Minimum body size (cm)	plankton.size.min.plk	0.0002	0.002
Maximum body size (cm)	plankton.size.max.plk	0.02	0.3
Trophic level	plankton.TL.plk	1	2
Theoretical accessibility coefficients	Content of the “predation-accessibility.csv” file	1	1

411

412 The user has the possibility to redefine functional groups (Step 4 in Fig. 1 and Fig. 3).
 413 First, a check box allows the user to select/deselect functional groups. Second, the user can
 414 modify the name of functional groups and redefine some focal functional groups as biotic
 415 resources. Third, check boxes are provided to the left of class names and Latin species names,
 416 which enable the user to deselect some classes or species if they wish. Fourth, “Edit” tools are

417 provided to the right of class names and Latin species names, which allow the user to add
418 classes or species to functional groups; suggestions are provided to the user as they start
419 typing something. Lastly, a “Plus” button at the bottom of the table enables the user to add
420 new functional groups to the table. A new functional group then needs to be defined either as
421 a focal functional group, in which case the user needs to fill in the “Species” column, or as a
422 biotic resource, in which case the user needs to fill in “Class” column; here, again,
423 suggestions are provided to the user as they start typing something⁴. The check boxes, “Edit”
424 tools and “Plus” button allow the user to define only focal species (i.e., focal functional
425 groups all comprising one unique species) for their OSMOSE model if they wish. The
426 redefined functional groups are for the local user only and are not saved in the JSON data
427 archives.

428 Once the user is satisfied with the (re)definition of functional groups, they need to
429 press “Proceed” to reach another webpage. This webpage offers the user the possibility to re-
430 order focal functional groups. Then, the user needs to press “Proceed” to reach another,
431 similar webpage, where they are invited to re-order biotic resources before proceeding to next
432 webpage.

433 The next webpage requests the user to indicate the number of time steps per year of
434 their future OSMOSE model (e.g., 12 if their future OSMOSE model has a monthly time
435 step). Afterwards, the user needs to press “Proceed”.

436

437 *2.3.3. Data query in TSV data archives*

438 In addition to the species comprising the defined functional groups that the user can
439 see on the second page of the web UI, additional, related species (i.e., species that belong to a
440 related genus or family) are included in each of the defined functional groups. We
441 implemented this so as to maximize one’s chances to obtain non-default values for the largest
442 possible number of OSMOSE input parameters. For each functional group defined for each
443 marine region that could be potentially selected by the user, potential additional species were
444 added to the JSON data archives and ranked based on their data richness, similarly to what is

⁴ A workaround to fill in the “Species” column for an additional biotic resource consists of: (1) temporarily defining the biotic resource as a “focal functional group”; (2) filling in the “Species” column”; and (3) redefining the functional group as a “biotic resource”; this workaround is mentioned by one of the “information buttons” of the web user interface.

445 described in Subsection 2.3.2. Potential additional species whose data richness was smaller
446 than 2 were dropped. Then, some other potential additional species were eventually dropped
447 so as to keep the total (i.e., original plus additional) number of species per functional group to
448 a maximum of 30, for the sake of computational efficiency. In the final list of species making
449 up a functional group in JSON data archives, the ranked list of original species precedes the
450 ranked list of additional species.

451 The list of the species (i.e., original plus additional) comprising the functional groups
452 and the number of time steps of the OSMOSE model are communicated to the web API via a
453 JSON file (Step 5 in Fig. 1). The web API then queries FishBase and SeaLifeBase data from
454 TSV data archives we compiled (compressed TSV files located in [https://github.com/FiN-](https://github.com/FiN-FBSLB/fishbase-sealifebase-archive)
455 [FBSLB/fishbase-sealifebase-archive](https://github.com/FiN-FBSLB/fishbase-sealifebase-archive); <https://doi.org/10.5281/zenodo.1418646>) (Steps 6 and 7
456 in Fig. 1). The TSV data archives were created from the information stored in the JSON data
457 archives, using the “rOpenSci FishBase API”, which is the API to the backend Structured
458 Query Language (SQL) database behind FishBase and SeaLifeBase (Boettiger et al., 2012).
459 The TSV data archives are automatically updated every time changes are made in FishBase
460 and SeaLifeBase (e.g., whenever mirror updates of FishBase and SeaLifeBase are performed).

461

462 *2.3.4. Generation of OSMOSE parameters*

463 The web API employs the data queried from the TSV data archives to derive values
464 for OSMOSE parameters (Step 8 in Fig. 1). For each functional group, to generate a value for
465 a given OSMOSE parameter, the web API deals with the species comprising the functional
466 group in turn, based on their rank. The web API first considers the first-ranked species and, if
467 FishBase/SeaLifeBase data are available for this species, then a value is calculated for the
468 OSMOSE parameter. The web API then considers the second-ranked species and, if
469 FishBase/SeaLifeBase data are available for this species, then a value is calculated for the
470 OSMOSE parameter. This process continues until the web API reaches the last-ranked species
471 of the functional group. If no FishBase/SeaLifeBase data are available for all of the species
472 making up the functional group (i.e., original plus additional), then the OSMOSE parameter
473 under consideration is set to its default value (Appendix C). NA (not available) is the default
474 value of 11 of the OSMOSE parameters for which our web application provides estimates
475 (Appendix C).

476 The web API either determines the value of an OSMOSE parameter directly from a
477 FishBase/SeaLifeBase parameter (e.g., longevity from the FishBase/SeaLifeBase parameter
478 “LongevityWild”), or it generates an estimate for the OSMOSE parameter from calculations
479 performed from several FishBase/SeaLifeBase parameters (e.g., critical predation efficiency
480 is estimated from the FishBase/SeaLifeBase parameters “PopQB” and “MaintQB”) (Table 3).
481 It was necessary to add new columns to FishBase/SeaLifeBase tables to enable the estimation
482 of some OSMOSE parameters. For example, we added the columns “PredPreyRatioMin” and
483 “PredPreyRatioMax” to the FishBase/SeaLifeBase table “estimate” to enable the production
484 of minimum and maximum predator/prey size ratio estimates for OSMOSE. When, for a
485 given species, the web API encounters several values (usually originating from studies
486 conducted in different regions) for a given FishBase/SeaLifeBase parameter in the TSV data
487 archives, it generates a median estimate for that FishBase/SeaLifeBase parameter before
488 doing any computations to derive an OSMOSE parameter estimate. Details about the
489 generation of OSMOSE parameter values with the web API are given in Appendix C. All
490 OSMOSE parameter values are entered by the web API into OSMOSE configuration files.

491

492 *2.3.5. Delivery of OSMOSE configuration files to the user*

493 Once the web API is done with the production of OSMOSE configuration files, an
494 “osmose_config.zip” file is passed to the web UI, which contains the OSMOSE configuration
495 files, as well as a CSV file listing the species making up the functional groups defined for the
496 OSMOSE model (“functional_groups.csv”) and a “README” file (Step 9 in Fig. 1). The
497 README file is a spreadsheet, whose individual tabs describe the content of each OSMOSE
498 configuration file. In each tab of the README file, information is provided about the
499 individual OSMOSE parameters, their default value, whether and how they were estimated by
500 the web application, and how they could be estimated if they are not covered by the web
501 application (similarly to Appendix B).

502 At the time the web API delivers the “osmose_config.zip” file to the web UI, the user
503 reaches a final webpage. This webpage informs the user that the configuration files for their
504 OSMOSE model are ready, and it also provides information on where to download OSMOSE
505 v3u2 and where to obtain technical assistance for OSMOSE. The user is instructed to press
506 the “Submit” button to obtain the “osmose_config.zip” file (Step 10 in Fig. 1).

507

508 **3. Results**

509 To demonstrate our web application, let us query OSMOSE configuration files for the
510 West Florida Shelf region, which is located within the Gulf of Mexico Large Marine
511 Ecosystem. The West Florida Shelf region is a marine ecosystem under strong and increasing
512 anthropogenic and environmental pressures (Brand and Compton, 2007; Chagaris, 2013;
513 Karnauskas et al., 2013, 2017). An OSMOSE model depicting the structure of the West
514 Florida Shelf ecosystem in the 2000s, referred to as “OSMOSE-WFS”, was developed in
515 Grüss et al. (2015). The OSMOSE-WFS model was later updated in Grüss et al. (2016b,
516 2016c). OSMOSE-WFS has a monthly time step, explicitly considers 12 focal functional
517 groups, and is forced by the biomass of seven biotic resources (Table 5). The two latest
518 versions of the OSMOSE-WFS model (Grüss et al., 2016b, 2016c) used the parameter values
519 defined in Grüss et al. (2015), except for the following parameters: (1) the minimum and
520 maximum predator/prey size ratios of focal functional groups, which were redefined; and (2)
521 the larval mortality rates of focal functional groups and the availability coefficients of biotic
522 resources, which were re-estimated during the calibration process of OSMOSE. The
523 parameter values employed in OSMOSE-WFS papers usually came from regional studies, or
524 they were established based on experts’ opinion (the accessibility coefficients of focal
525 functional groups and the theoretical accessibility coefficients of biotic resources). Here, we
526 compare the parameter values and functional relationships defined by our web application to
527 the parameter values and functional relationships used in OSMOSE-WFS papers (Grüss et al.,
528 2015, 2016b, 2016c).

529 **Table 5**

530 Functional groups represented in the OSMOSE model of the West Florida Shelf (“OSMOSE-WFS”). These functional groups include focal functional groups, whose entire
 531 life cycle is simulated in the OSMOSE-WFS model, and biotic resources, whose biomass is used to force OSMOSE-WFS. Species of a given focal functional group exhibit
 532 similar life history characteristics, body size ranges, diets and exploitation patterns. Some individual species constitute their own focal functional group, as they are
 533 emblematic to the West Florida Shelf and of high economic importance. * = Classes for which there is currently no information available in SeaLifeBase.

Functional group	Focal functional group or biotic resource?	Species making up the functional group
King mackerel	Focal functional group	King mackerel (<i>Scomberomorus cavalla</i>)
Amberjacks	Focal functional group	Greater amberjack (<i>Seriola dumerili</i>), lesser amberjack (<i>Seriola fasciata</i>), almaco jack (<i>Seriola rivoliana</i>)
Red grouper	Focal functional group	Red grouper (<i>Epinephelus morio</i>)
Gag	Focal functional group	Gag (<i>Mycteroperca microlepis</i>)
Red snapper	Focal functional group	Red snapper (<i>Lutjanus campechanus</i>)
Sardine-herring-scad complex	Focal functional group	Scaled sardine (<i>Harengula jaguana</i>), Spanish sardine (<i>Sardinella aurita</i>), Atlantic thread herring (<i>Opisthonema oglinum</i>), round scad (<i>Decapterus punctatus</i>), finescale menhaden (<i>Brevoortia gunteri</i>), Gulf menhaden (<i>Brevoortia patronus</i>), Atlantic menhaden (<i>Brevoortia tyrannus</i>)
Anchovies and silversides	Focal functional group	Bay anchovy (<i>Anchoa mitchilli</i>), striped anchovy (<i>Anchoa hepsetus</i>), inland silverside (<i>Menidia beryllina</i>), Alabama shad (<i>Alosa alabamae</i>)
Coastal omnivores	Focal functional group	Pinfish (<i>Lagodon rhomboides</i>), orange filefish (<i>Aluterus schoepfii</i>), fringed filefish (<i>Monacanthus ciliatus</i>), orangespotted filefish (<i>Cantherhines pullus</i>), honeycomb filefish (<i>Acanthostracion polygonius</i>), Atlantic spadefish (<i>Chaetodipterus faber</i>), scrawled cowfish (<i>Acanthostracion quadricornis</i>), bandtail puffer (<i>Sphoeroides spengleri</i>)
Reef carnivores	Focal functional group	White grunt (<i>Haemulon plumierii</i>), black sea bass (<i>Centropristis striata</i>), belted sandfish (<i>Serranus subligarius</i>), butter hamlet (<i>Hypoplectrus unicolor</i>), creole fish (<i>Paranthias furcifer</i>), slipperly dick (<i>Halichoeres bivittatus</i>), yellowhead wrasse (<i>Halichoeres garnoti</i>), bluehead (<i>Thalassoma bifasciatum</i>), reef croaker (<i>Odontoscion dentex</i>), jackknife-fish (<i>Equetus lanceolatus</i>), littlehead porgy (<i>Calamus proridens</i>), jolthead porgy (<i>Calamus bajonado</i>), saucereye progy (<i>Calamus calamus</i>), whitebone progy (<i>Calamus leucosteus</i>), knobbed progy (<i>Calamus nodosus</i>), French grunt (<i>Haemulon flavolineatum</i>), Spanish grunt (<i>Haemulon macrostomum</i>), margate (<i>Haemulon album</i>), bluestriped grunt (<i>Haemulon sciurus</i>), striped grunt (<i>Haemulon striatum</i>), sailor’s grunt (<i>Haemulon parra</i>), porkfish (<i>Anisotremus virginicus</i>)
Reef omnivores	Focal functional group	Doctorfish (<i>Acanthurus chirurgus</i>), blue tang (<i>Acanthurus coeruleus</i>), blue angelfish (<i>Holacanthus bermudensis</i>), gray angelfish (<i>Pomacanthus arcuatus</i>), rock beauty (<i>Holacanthus tricolor</i>), yellowtail damselfish (<i>Microspathodon chrysurus</i>), bridled goby (<i>Coryphopterus glaucofraenum</i>), Bermuda chub (<i>Kyphossus sectarix</i>), combtooth blenny (<i>Chasmodes saburrae</i>), banded blenny (<i>Paraclinus fasciatus</i>), twospot cardinalfish (<i>Apogon maculatus</i>), dusky jawfish (<i>Opistognathus whitehursti</i>), ocean surgeon (<i>Acanthurus bahianus</i>), banded butterfly (<i>Chaetodon striatus</i>), foureye butterfly (<i>Chaetodon capristratus</i>), reef butterfly (<i>Chaetodon sedentarius</i>), spotfin butterfly (<i>Chaetodon ocellatus</i>), French angel (<i>Pomacanthus paru</i>), queen angel (<i>Holacanthus ciliaris</i>), sergeant

Shrimps	Focal functional group	major damsel (<i>Abudefduf saxatilis</i>), blue parrot (<i>Scarus coeruleus</i>), queen parrot (<i>Scarus vetula</i>), rainbow parrot (<i>Scarus guacamaia</i>), redband parrot (<i>Sparisoma aurofrenatum</i>), spotlight parrot (<i>Sparisoma viride</i>), midnight parrotfish (<i>Scarus coelestinus</i>), princess parrotfish (<i>Scarus taeniopterus</i>), yellow chub (<i>Kyphosus incisor</i>), redband parrotfish (<i>Sparisoma chrysopterygum</i>), bucktooth parrotfish (<i>Sparisoma radians</i>)
Large crabs	Focal functional group	Pink shrimp (<i>Farfantepenaeus duorarum</i>), white shrimp (<i>Litopenaeus setiferus</i>)
Meiofauna	Biotic resource	Blue crab (<i>Callinectes sapidus</i>)
Small infauna	Biotic resource	Hexanauplia spp.*, Secernentea spp.*, Dorylaimida spp.*, Enoplea spp.*, Maxillopoda spp., Macrotracheata spp., Chaetognatha spp., Bdelloidea spp., Monogononta spp.*
Small mobile epifauna	Biotic resource	Aplousobranchia spp.*, Polychaeta spp.
Bivalves	Biotic resource	Ostracoda spp.*, Turbellaria spp.*, Cladocera spp.*, Brachiopoda spp.*
Echinoderms and gastropods	Biotic resource	Bivalvia spp.
Zooplankton	Biotic resource	Asterozoa spp., Echinozoa spp., Gastropoda spp., Holothurozoa spp.
Phytoplankton	Biotic resource	Zooplankton
		Phytoplankton

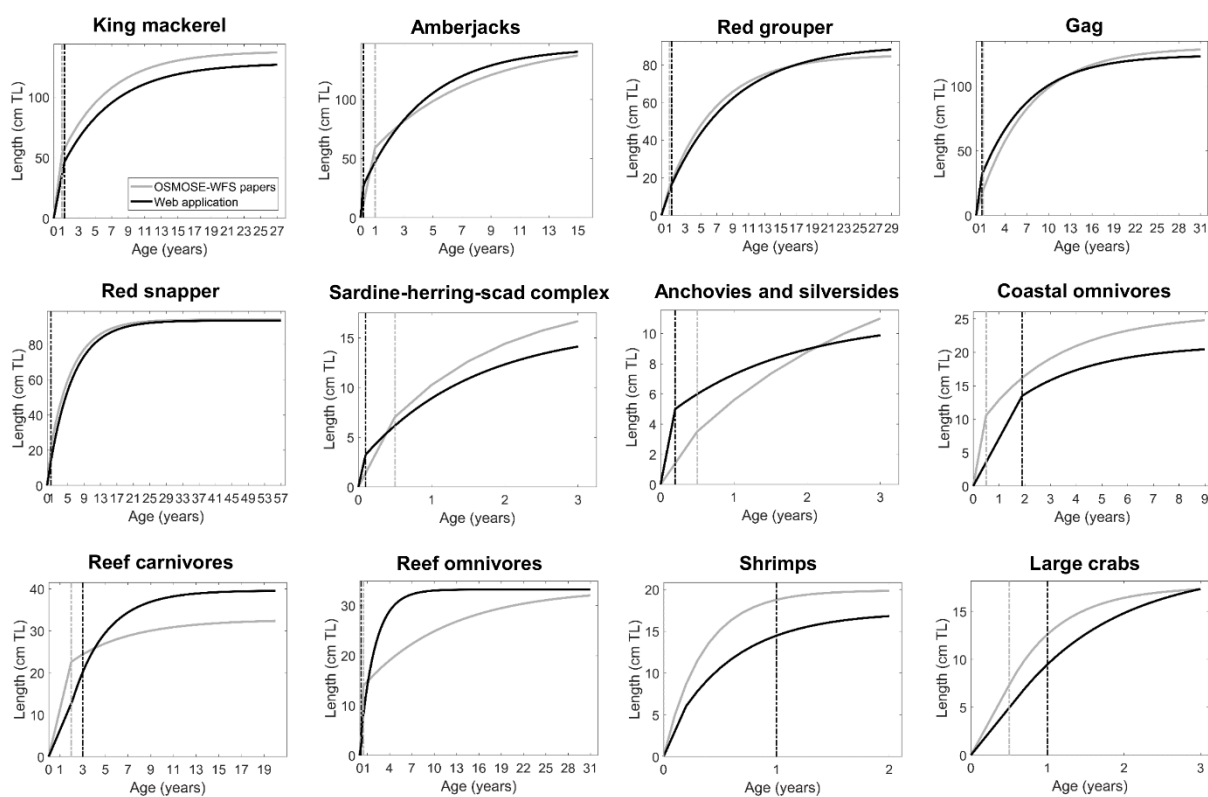
535 To obtain OSMOSE parameter estimates for the West Florida Shelf ecosystem with
536 our web application, we proceeded as follows. First, in the first page of the web UI, we
537 selected the Gulf of Mexico (Fig. 2). Second, in the second page of the web UI, we employed
538 the different tools available (i.e., the check boxes, the Edit tools and the Plus button; Fig. 3) to
539 define focal functional groups and biotic resources according to Table 5. With respect to
540 biotic resources, there was at the time of writing (September 2018) no information available
541 in SeaLifeBase for some of the classes comprising the meiofauna and small infauna groups
542 and all of the classes comprising the small mobile epifauna group; this entails that we were
543 unable to define a small mobile epifauna group for the West Florida Shelf ecosystem with the
544 web application. Third, we re-ordered focal functional groups and biotic resources according
545 to Table 5. Fourth, we indicated to the web UI that the OSMOSE model for the West Florida
546 Shelf has a monthly time step, i.e., we set the number of time steps per year to 12 in the fifth
547 page of the web UI. Finally, we pressed the “Submit” button in the last page of the web UI to
548 obtain an “osmose_config.zip” file containing all the OSMOSE configuration files populated
549 by the web API. The entire process took around 15 minutes with a laptop with a 2.6 GHz Intel
550 Core i5-6440HQ processor.

551 To compare the information provided by our web application to the information used
552 in OSMOSE-WFS papers (Grüss et al., 2015, 2016b, 2016c), we examined the following: (1)
553 the length-at-age relationship of focal functional groups; (2) the weight-at-age relationship of
554 focal functional groups; (3) the longevity (i.e., maximum age), body size at sexual maturity,
555 relative fecundity (i.e., annual number of eggs per g of mature female), reproduction
556 seasonality, minimum and maximum predator/prey size ratios, accessibility coefficients,
557 annual natural mortality rate due to marine organisms and events (e.g., harmful algal blooms)
558 that are not explicitly considered in OSMOSE, critical predation efficiency, maximum annual
559 ingestion rate, proportion of females, egg size, and egg weight of focal functional groups; and
560 (4) the theoretical accessibility coefficients, minimum and maximum sizes, and TL of biotic
561 resources.

562 We first examine the length-at-age relationship of the 12 focal functional groups
563 represented in the OSMOSE-WFS model (Fig. 4). In OSMOSE, schools are assumed to grow
564 in size only when the amount of food they ingested fulfills maintenance requirements, and, if
565 that condition is met, the growth in length of schools is calculated as a function of predation
566 efficiency and the mean length increase from the von Bertalanffy growth model (Appendix
567 A). The length-at-age relationships we examine here were established outside of OSMOSE

568 (i.e., ignore predation efficiencies) from the values of the following parameters: (1)
 569 instantaneous growth rate at small size (K , in year⁻¹); (2) asymptotic size (L_{∞} , in cm); (3)
 570 theoretical age of zero length (t_0 , in years); and (4) the age below which a linear function is
 571 employed, and above which a von Bertalanffy growth function is employed, to model body
 572 growth (A_{thres} , in years) (Appendix A). The length-at-age relationships established from the
 573 parameter estimates provided by the web application and from the parameter estimates used in
 574 OSMOSE-WFS papers are similar (Fig. 4). The largest discrepancies between OSMOSE-
 575 WFS and our web application were observed for reef carnivores and shrimps (Fig. 4).

576



577

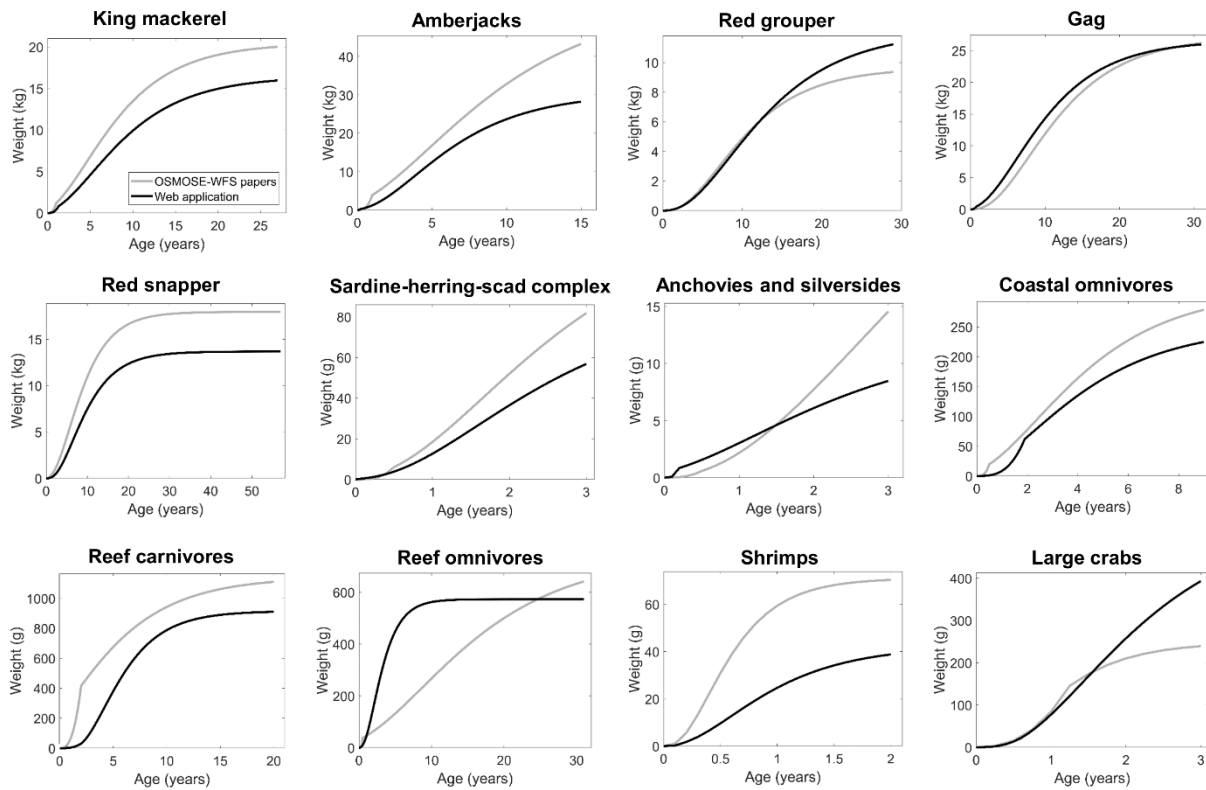
578 **Fig. 4.** Comparison of the length-at-age relationships used in previous papers (Grüss et al., 2015, 2016b, 2016c;
 579 gray curves) and predicted by our web application (black curves) for the 12 focal functional groups represented
 580 in the OSMOSE model of the West Florida Shelf (“OSMOSE-WFS”). The vertical lines indicate the age below
 581 which a linear function is employed, and above which a von Bertalanffy growth function is employed, to model
 582 body growth.

583

584 We next examine the weight-at-age relationship of the 12 focal functional groups
 585 represented in OSMOSE-WFS (Fig. 5). In OSMOSE, the body weight of a school is
 586 estimated from its body length using a classic allometric function, while the body length of

587 the school is itself estimated based on von Bertalanffy parameters and predation efficiency, as
588 explained earlier. The weight-at-age relationships we examine here were also established
589 outside of OSMOSE (i.e., they also ignore predation efficiencies), from the values of the
590 following parameters: (1) the von Bertalanffy parameters K , L_∞ and t_0 ; (2) the A_{thres} parameter;
591 and (3) the constant of proportionality (c) and exponent (b) of the allometric length-weight
592 relationship (Appendix A). The weight-at-age relationships established from the parameter
593 estimates provided by the web application and from the parameter estimates used in
594 OSMOSE-WFS papers tend to be similar (Fig. 5). However, the individual body weights of
595 red snapper (*Lutjanus campechanus*), the sardine-herring-scad complex, the anchovies and
596 silversides' group and shrimps are noticeably larger when employing the parameter estimates
597 used in OSMOSE-WFS papers, while the individual body weights of reef omnivores and
598 large crabs are generally markedly larger when employing the parameter estimates provided
599 by the web application (Fig. 5). Yet, these differences usually do not alter the rankings of the
600 maximum individual body weights of focal functional groups (computed outside of
601 OSMOSE, i.e., ignoring predation efficiencies; Table 6). An exception to this usual pattern is
602 observed for coastal omnivores, whose maximum individual body weight is greater than that
603 of large crabs when employing the parameters used in OSMOSE-WFS papers, while the
604 opposite is observed when the parameters provided by the web application are employed
605 (Table 6).

606



607

608 **Fig. 5.** Comparison of the weight-at-age relationships used in previous papers (Grüss et al., 2015, 2016b, 2016c;
 609 gray curves) and predicted by our web application (black curves) for the 12 focal functional groups represented
 610 in the OSMOSE model of the West Florida Shelf (“OSMOSE-WFS”).

611

612 **Table 6**

613 Comparison of the maximum individual body weights of the 12 focal functional groups represented in the
 614 OSMOSE-WFS ecosystem model computed outside of OSMOSE (i.e., ignoring predation efficiencies) when
 615 using the parameter estimates employed in previous studies (Grüss et al., 2015, 2016b, 2016c) vs. the parameter
 616 estimates provided by our web application. Some of the mean individual weights are in kg, while the others are
 617 in g.

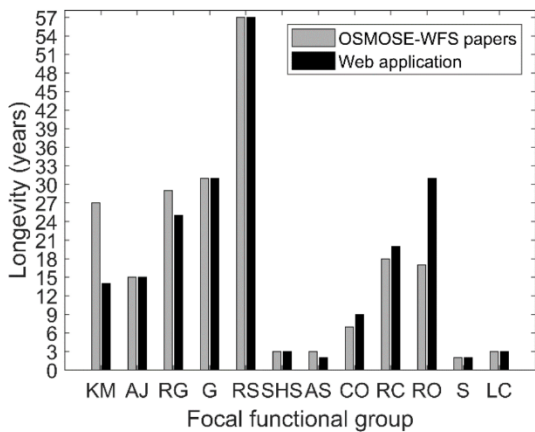
Focal functional group	Maximum individual body weight when using the parameter estimates from previous studies	Maximum individual body weight when using the parameter estimates from the web application
Amberjacks	44.1 kg	28.2 kg
Gag	26.2 kg	26.0 kg
King mackerel	20.0 kg	16.0 kg
Red snapper	17.9 kg	13.7 kg
Red grouper	9.4 kg	11.2 kg
Reef carnivores	1,109.3 g	909.6 g
Reef omnivores	440.6 g	572.7 g
Coastal omnivores	278.8 g	224.7 g
Large crabs	239.2 g	393.2 g
Sardine-herring-scad complex	81.8 g	56.8 g
Shrimps	70.3 g	38.8 g

618

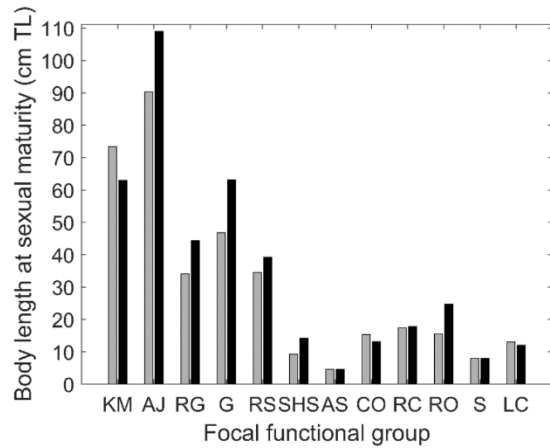
619 We now compare the longevity and body size at sexual maturity (L_{mat}) estimates
 620 provided by the web application to those used in OSMOSE-WFS papers (Figs. 6A and B). In
 621 general, there are no marked differences between the longevity and L_{mat} estimates delivered
 622 by the web application and those used in OSMOSE-WFS papers. Exceptions to this general
 623 pattern include: (1) king mackerel (*Scomberomorus cavalla*), whose longevity is set to 14
 624 years by the web application vs. 27 years in OSMOSE-WFS papers; (2) gag (*Mycteroperca*
 625 *microlepis*), whose L_{mat} is set to a larger value by the web application (63.2 cm vs. 46.8 cm in
 626 OSMOSE-WFS papers); and (3) reef omnivores, whose longevity is set to 31 years by the
 627 web application vs. 17 years in OSMOSE-WFS papers, and whose L_{mat} is set to a larger value
 628 by the web application (24.7 cm vs. 15.5 cm in OSMOSE-WFS papers).

629

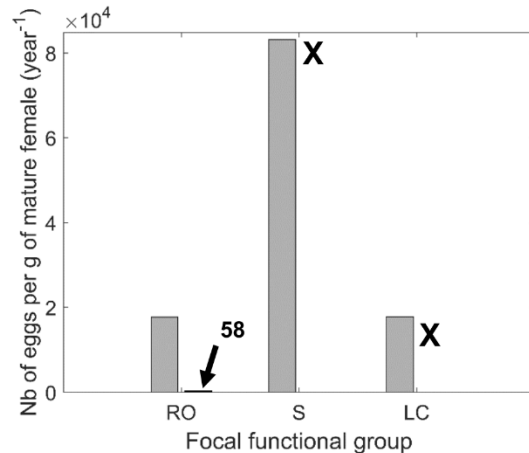
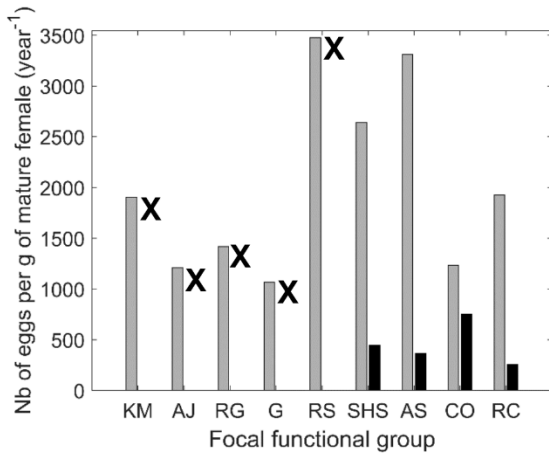
(A) Longevity



(B) Body length at sexual maturity



(C) Relative fecundity



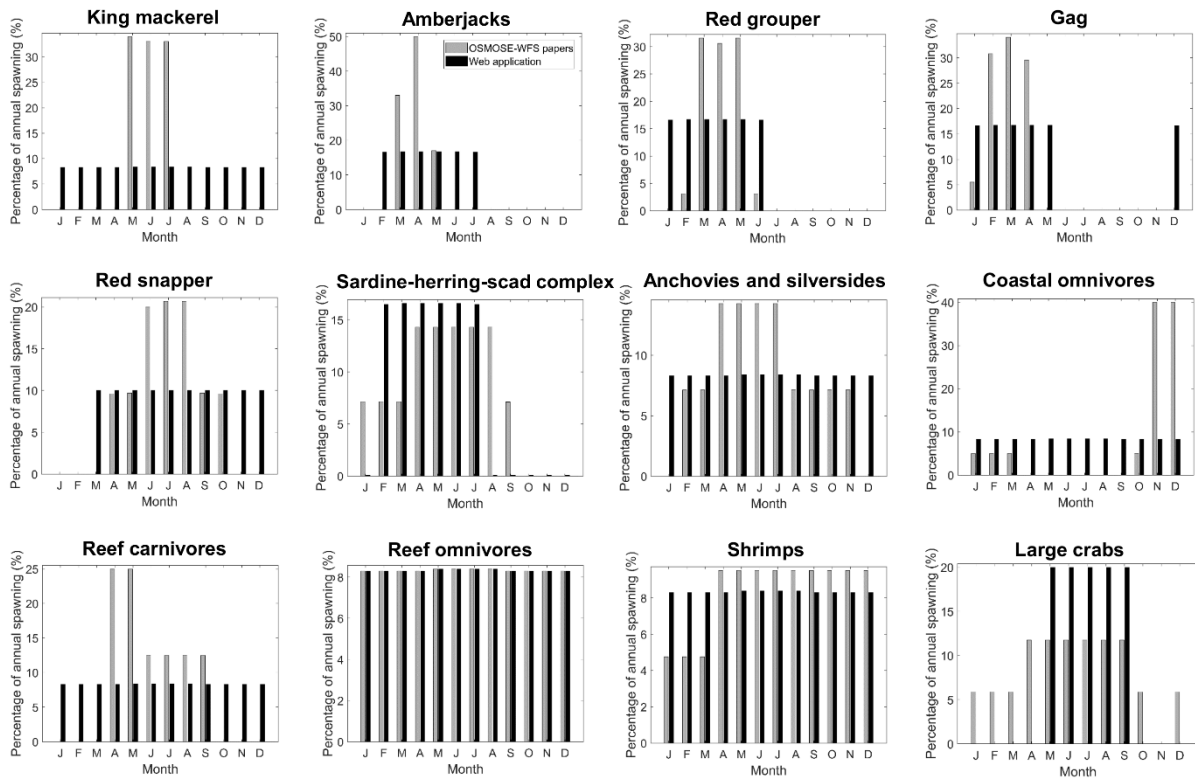
630

631 **Fig. 6.** Comparison of the (A) longevity, (B) body length at sexual maturity and (C) relative fecundity estimates
632 used in previous papers (Grüss et al., 2015, 2016b, 2016c; gray bars) and provided by our web application (black
633 bars) for the 12 focal functional groups represented in the OSMOSE model of the West Florida Shelf
634 (“OSMOSE-WFS”). Relative fecundities are expressed as the annual number of eggs per g of mature female.
635 Black crosses indicate when the web application was unable to provide a relative fecundity estimate. The relative
636 fecundity of reef omnivores estimated by our web application (58 eggs per g of mature female per year) is
637 pointed out by an arrow. The focal functional groups represented in OSMOSE-WFS include: KM = king
638 mackerel; AJ = amberjacks; RG = red grouper; G = gag; RS = red snapper; SHS = the sardine-herring-scad
639 complex; AS = anchovies and silversides; CO = coastal omnivores; RC = reef carnivores; S = shrimps; and LC =
640 large crabs.

641

642 Next, we compare the relative fecundity and reproduction seasonality estimates
643 delivered by the web application to those used in OSMOSE-WFS papers (Figs. 6C and 7).
644 The web application was able to produce a relative fecundity estimate for only five of the 12
645 focal functional groups represented in the OSMOSE-WFS model: the sardine-herring-scad
646 complex; anchovies and silversides; coastal omnivores; reef carnivores; and reef omnivores
647 (Fig. 6C). For these five focal functional groups, the web application provided a relative
648 fecundity estimate that is considerably smaller than the estimate employed in OSMOSE-WFS
649 papers. Moreover, the web application was able to define reproduction seasonality patterns for
650 only six of the 12 focal functional groups represented in OSMOSE-WFS: amberjacks; red
651 grouper (*Epinephelus morio*); gag; red snapper; the sardine-herring-scad complex; and large
652 crabs (Fig. 7). For these six focal functional groups, the web application and OSMOSE-WFS
653 papers defined similar reproduction seasonality patterns. When the web application was
654 unable to define reproduction seasonality patterns for a given focal functional group, it
655 assumed that this functional group had a probability of 1/12 to reproduce each month of the
656 year (Fig. 7).

657



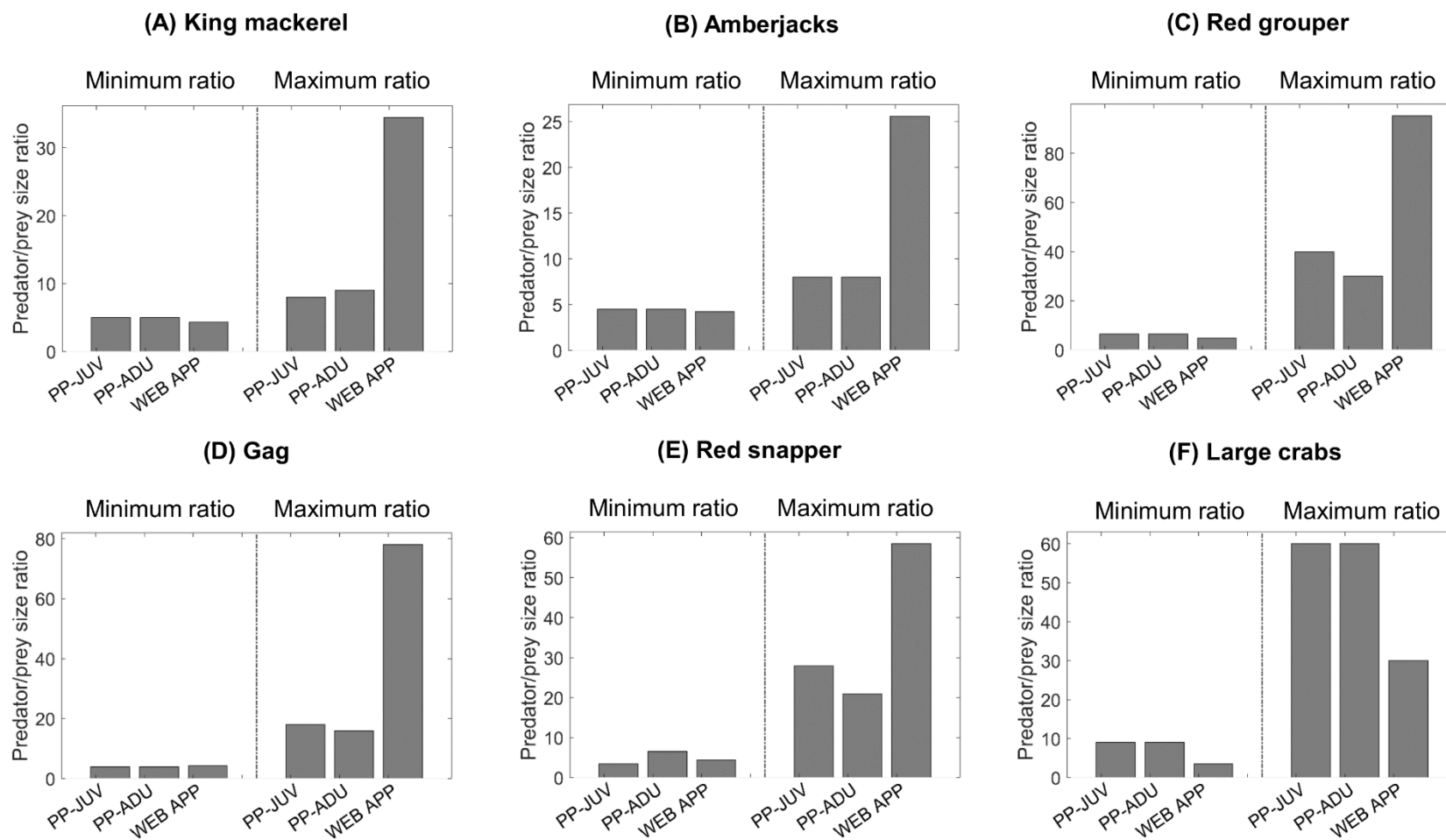
658

659 **Fig. 7.** Comparison of the reproduction seasonalities used in previous papers (Grüss et al., 2015, 2016b, 2016c;
 660 gray bars) and estimated by our web application (black bars) for the 12 focal functional groups represented in the
 661 OSMOSE model of the West Florida Shelf (“OSMOSE-WFS”).

662

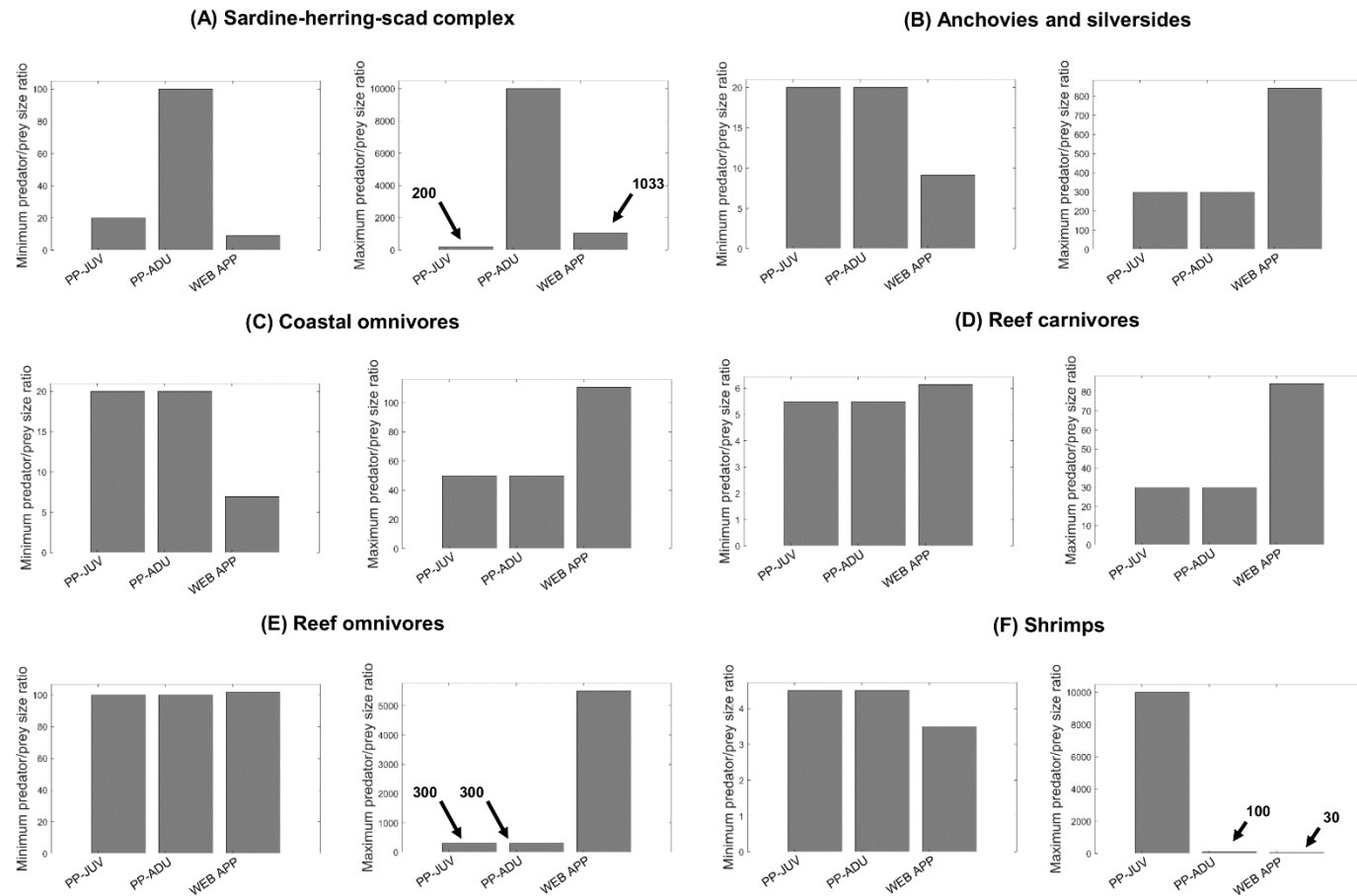
663 We now compare the minimum predator/prey size ratio ($(L_{pred}/L_{prey})_{min}$) and maximum
 664 predator/prey size ratio ($(L_{pred}/L_{prey})_{max}$) estimates provided by the web application to those
 665 used in OSMOSE-WFS papers (Figs. 8 and 9). For each focal functional group, the
 666 OSMOSE-WFS papers relied on four predator/prey size ratio estimates: one $(L_{pred}/L_{prey})_{min}$
 667 estimate for juveniles; one $(L_{pred}/L_{prey})_{min}$ estimate for adults; one $(L_{pred}/L_{prey})_{max}$ estimate for
 668 juveniles; and one $(L_{pred}/L_{prey})_{max}$ estimate for adults. In contrast, for each focal functional
 669 group, the web application delivers one $(L_{pred}/L_{prey})_{min}$ estimate for all life stages combined
 670 and one $(L_{pred}/L_{prey})_{max}$ estimate for all life stages combined. In general, the web application
 671 and OSMOSE-WFS papers defined very similar $(L_{pred}/L_{prey})_{min}$ estimates (Figs. 8 and 9).
 672 Exceptions to these general patterns occurred for three focal functional groups, for which the
 673 web application defined a markedly smaller $(L_{pred}/L_{prey})_{min}$ estimate: the sardine-herring-scad
 674 complex; anchovies and silversides; and coastal omnivores (Figs. 9A-C). On the other hand,
 675 there are marked differences between the $(L_{pred}/L_{prey})_{max}$ estimates delivered by the web
 676 application and those employed in OSMOSE-WFS papers (Figs. 8 and 9). In general, the web
 677 application defined larger $(L_{pred}/L_{prey})_{max}$ values than OSMOSE-WFS papers. Exceptions to

678 this general pattern included: (1) large crabs and shrimps, for which the web application
679 provided a smaller $(L_{pred}/L_{prey})_{max}$ estimate (Figs. 8F and 9F); and (2) the sardine-herring-scad
680 complex, for which the web application delivered a $(L_{pred}/L_{prey})_{max}$ estimate much larger than
681 the estimate defined for juveniles in OSMOSE-WFS papers, but substantially smaller than the
682 estimate defined for adults in OSMOSE-WFS papers (Fig. 9A).



683

684 **Fig. 8.** Comparison of the minimum and maximum predator/prey size ratios used in previous papers (Grüss et al., 2015, 2016b, 2016c) and estimated by our web application
 685 for six of the 12 focal functional groups represented in the OSMOSE model of the West Florida Shelf (“OSMOSE-WFS”): (A) king mackerel; (B) amberjacks; (C) red
 686 grouper; (D) gag; (E) red snapper; and (F) large crabs. Previous papers defined minimum and maximum predator/prey size ratios for the juvenile and adult stages of focal
 687 functional groups (PP-JUV and PP-ADU, respectively), while our web application estimated minimum and maximum predator/prey size ratios for all the life stages of focal
 688 functional groups combined (WEB APP).



689

690 **Fig. 9.** Comparison of the minimum and maximum predator/prey size ratios used in previous papers (Grüss et al., 2015, 2016b, 2016c) and estimated by our web application
 691 for six of the 12 focal functional groups represented in the OSMOSE model of the West Florida Shelf (“OSMOSE-WFS”): (A) the sardine-herring-scad complex; (B)
 692 anchovies and silversides; (C) coastal omnivores; (D) reef carnivores; (E) reef omnivores; and (F) shrimps. Previous papers defined minimum and maximum predator/prey
 693 size ratios for the juvenile and adult stages of focal functional groups (PP-JUV and PP-ADU, respectively), while our web application estimated minimum and maximum
 694 predator/prey size ratios for all the life stages of focal functional groups combined (WEB APP).

695 We now compare the accessibility coefficients of focal functional groups and the
696 theoretical accessibility coefficients of biotic resources that are provided by the web
697 application to the coefficients that are used in the OSMOSE-WFS papers (Appendix D).
698 These two types of coefficients describe the accessibility of a potential prey item (the age
699 class of a focal functional group or a biotic resource) to a potential predator (a given age class
700 of a focal functional group). The web application set accessibility coefficients to 0.8 much
701 more often than OSMOSE-WFS papers (Appendix D). The web application set accessibility
702 coefficients to 0.4 only when there was limited overlap in the water column between the
703 potential prey item and the potential predator (e.g., the accessibility of adults of anchovies and
704 silversides, which are pelagic, to adult large crabs, which is benthic, was set to 0.4). With
705 respect to the generic phytoplankton and zooplankton groups, the web application
706 automatically sets all of their theoretical accessibility coefficients to 1, while OSMOSE-WFS
707 papers set some of their accessibility coefficients to 0 (e.g., their theoretical accessibility to
708 adult red snapper; Appendix D). With respect to the other biotic resources defined with the
709 web application (i.e., meiofauna, small infauna, bivalves, and echinoderms and gastropods),
710 their theoretical accessibility coefficients were usually set to 0.4, reflecting their limited
711 overlap in the water column with the great majority of the focal functional groups represented
712 in the OSMOSE-WFS model (Appendix D).

713 Next, we compare the annual natural mortality rates due to marine organisms and
714 events not explicitly considered in OSMOSE that are provided by the web application to those
715 that are used in the OSMOSE-WFS papers (Table 7). These types of mortality rates are
716 referred to as “diverse natural mortality rates”. The web application was able to deliver an
717 estimate different from the 0.2 year⁻¹ default value for only four of the 12 focal functional
718 groups represented in OSMOSE-WFS: red snapper; the sardine-herring-scad complex;
719 anchovies and silversides; and reef carnivores (Table 7). The diverse natural mortality rates of
720 red snapper and of the sardine-herring-scad complex delivered by the web application and
721 those employed in OSMOSE-WFS papers are similar. By contrast, the diverse natural
722 mortality rate of anchovies and silversides used in OSMOSE-WFS papers is *ca.* twice larger
723 than that provided by the web application, while the diverse natural mortality rate of reef
724 carnivores delivered by our web application is around twice larger than that employed in
725 OSMOSE-WFS papers (Table 7).

726

727 **Table 7**

728 Comparison of the “diverse natural mortality rate” estimates used in previous papers (Grüss et al., 2015, 2016b,
 729 2016c) and provided by our web application for the 12 focal functional groups represented in the OSMOSE
 730 model of the West Florida Shelf (“OSMOSE-WFS”). “Diverse natural mortality” is the mortality due to marine
 731 organisms and events (e.g., harmful algal blooms) that are not explicitly considered in OSMOSE.

Focal functional group	Diverse natural mortality estimate in OSMOSE-WFS papers (year⁻¹)	Diverse natural mortality estimate provided by our web application (year⁻¹)
King mackerel	0.28	0.2
Amberjacks	0.01	0.2
Red grouper	0.02	0.2
Gag	0.01	0.2
Red snapper	0.19	0.25
Sardine-herring-scad complex	1.43	1.09
Anchovies and silversides	2.29	1.05
Coastal omnivores	1.1	0.2
Reef carnivores	0.35	0.64
Reef omnivores	0.55	0.2
Shrimps	1.58	0.2
Large crabs	0.74	0.2

732

733 We now consider five parameters that are usually set to their default value for all focal
 734 functional groups in OSMOSE models: (1) critical predation efficiency (default value: 0.57);
 735 (2) maximum annual ingestion rate (default value: 3.5 year⁻¹; but see Brochier et al. (2013));
 736 (3) proportion of females (default value: 0.5; but see OSMOSE-WFS papers); (4) egg size
 737 (default value: 0.1 cm; but see Halouani et al. (2016)); and (5) egg weight (default value:
 738 0.00053669 g; but see Halouani et al. (2016)). Regarding critical predation efficiency, the web
 739 application was able to provide an estimate different from the 0.57 default value for only two
 740 of the 12 focal functional groups represented in the OSMOSE-WFS model: red snapper; and
 741 reef carnivores (Table 8). The web application was able to deliver a maximum annual
 742 ingestion rate estimate different from the 3.5 year⁻¹ default value for five of the 12 focal
 743 functional groups represented in OSMOSE-WFS: red snapper; the sardine-herring-scad
 744 complex; anchovies and silversides; reef carnivores; and reef omnivores (Table 8). The web
 745 application set the proportion of females of four of the 12 focal functional groups represented
 746 in OSMOSE-WFS to a value different from 0.5: red snapper; anchovies and silversides; reef
 747 carnivores; and reef omnivores (Table 8). Finally, the web application set egg size and weight
 748 to their default values for all the focal functional groups represented in the OSMOSE-WFS
 749 model.

750

751 **Table 8**

752 Estimates of critical predation efficiency, maximum annual ingestion rate and proportion of females provided by
 753 our web application for the 12 focal functional groups represented in the OSMOSE model of the West Florida
 754 Shelf (“OSMOSE-WFS”). * = The web application set the parameter to its default value, because too little or no
 755 information was available in FishBase/SeaLifeBase to produce an estimate.

Focal functional group	Critical predation efficiency	Maximum ingestion rate (year⁻¹)	Proportion of females
King mackerel	0.57*	3.5*	0.5*
Amberjacks	0.57*	3.5*	0.5*
Red grouper	0.57*	3.5*	0.5*
Gag	0.57*	3.5*	0.5*
Red snapper	0.64	5.24	0.49
Sardine-herring-scad complex	0.57*	8.1	0.5*
Anchovies and silversides	0.57*	10.1	0.49
Coastal omnivores	0.57*	3.5*	0.5*
Reef carnivores	0.23	7.98	0.74
Reef omnivores	0.57*	3.21	0.82
Shrimps	0.57*	3.5*	0.5*
Large crabs	0.57*	3.5*	0.5*

756

757 Finally, we consider the minimum size, maximum size and TL of biotic resources. The
 758 web application and OSMOSE-WFS papers usually provided identical minimum size,
 759 maximum size and TL estimates for phytoplankton and zooplankton. The exception to this
 760 usual pattern was the TL of zooplankton, which was set to a slightly higher value in
 761 OSMOSE-WFS papers than in the configuration files delivered by the web application (2.19
 762 vs. 2). The web application was unable to supply any minimum size and maximum size
 763 estimates for meiofauna, small infauna, bivalves, and echinoderms and gastropods. It was also
 764 unable to supply a TL estimate for meiofauna. The TL values provided by the web application
 765 and OSMOSE-WFS papers for small infauna and bivalves were similar (web application: 2
 766 for both biotic resources; OSMOSE-WFS papers: 2.25 for small infauna, and 2 for bivalves),
 767 while the TL of echinoderms and gastropods was set to a larger value in the configuration
 768 files delivered by the web application than in OSMOSE-WFS papers (3.3 vs. 2.5).

769

770 **4. Discussion**

771 In the present study, we introduced a web application we created, which generates
 772 configuration files for applications of an ecosystem modeling platform, OSMOSE, from
 773 FishBase and SeaLifeBase data. Our web application is user-friendly and entirely relies on an
 774 openly accessible API and free technologies. We provided a demonstration of this tool by

775 querying OSMOSE configuration files for the West Florida Shelf ecosystem. This
 776 demonstration showed the potential of our web application, but also highlighted research
 777 avenues for enhancing it (see Subsection 4.1). Our web application and its associated
 778 resources (its associated GitHub repositories, and Appendix A of the present paper) contribute
 779 to the “toolkit for OSMOSE users” (Table 9).

780

781 **Table 9**

782 Resources of the toolkit for OSMOSE users.

Resource	Comments
User guide	This resource is currently being developed (https://documentation.osmose-model.org). Its dedicated GitHub repository is: https://github.com/osmose-model/user_documentation .
Reference paper on OSMOSE	This resource is currently being developed. Meanwhile, Appendix A of the present paper is a useful resource.
OSMOSE Java code	The Java code of the latest version of OSMOSE (considered in the present paper), i.e. OSMOSE v3u2, is available for download from http://www.osmose-model.org/downloads .
Template OSMOSE configuration files	The template configuration files for OSMOSE v3u2 can be downloaded from http://www.osmose-model.org/downloads .
Our web application	The web application introduced in the present paper provides OSMOSE configuration files for any marine region that is of interest to the user. The Github repositories dedicated to this tool are: https://github.com/osmose-model/osmose-model.github.io , https://github.com/osmose-model/osmose-web-api and https://github.com/osmose-model/osmose-web-api-js .
Calibration guidelines	This resource is currently being developed and can be found in its preliminary form in OSMOSE user guide (https://documentation.osmose-model.org). Oliveros-Ramos (2014), Oliveros-Ramos and Shin (2016) and Oliveros-Ramos et al. (2017) are other useful resources.
Postprocessing of OSMOSE outputs	A R package called “osmose”, which is now available on CRAN, was primarily developed for OSMOSE output post-processing. The Github repository dedicated to this R package is: https://github.com/osmose-model/osmose .
OSMOSE user forum	OSMOSE users can ask questions to other users and OSMOSE developers on the following webpage: http://www.osmose-model.org/forum .

783

784 A key resource for our web application are its dedicated GitHub repositories
 785 (<https://github.com/osmose-model/osmose-model.github.io>, [https://github.com/osmose-](https://github.com/osmose-model/osmose-web-api)
 786 [model/osmose-web-api](https://github.com/osmose-model/osmose-web-api) and <https://github.com/osmose-model/osmose-web-api-js>). Among
 787 other purposes, these GitHub repositories intend to keep track of the issues faced by the
 788 developers and users of the web application and to find solutions to these issues and, more
 789 generally, ways to continuously enhance the web application. We strongly encourage the
 790 users of our web application to remain critical towards the OSMOSE parameter values
 791 provided by the web application and to accept or reject these values based on their expertise

792 of their study marine region. Users are strongly encouraged to create new issues in the GitHub
793 repositories: (1) to indicate critical missing parameter values (e.g., parameter values missing
794 for species that are emblematic to a marine region or of high economic importance to that
795 region); (2) to indicate problematic parameter values; but, also: (3) to provide suggestions as
796 to how the web application could come up with better estimates for the parameters it currently
797 covers and with non-default values for the parameters it currently does not cover.

798 In our demonstration, we simply examined the parameter estimates for the West
799 Florida Shelf delivered by the web application and did not attempt to re-calibrate the
800 OSMOSE-WFS model. In brief, the calibration of OSMOSE is a process which, usually: (1)
801 ensures that, on average, the biomasses of focal functional groups predicted by OSMOSE are
802 within realistic intervals; and (2) enables the estimation of two types of parameters, the larval
803 mortality rates of focal functional groups and the availability coefficients of biotic resources
804 (Oliveros-Ramos and Shin, 2016). In general, the calibration process of OSMOSE also
805 involves refining the minimum and maximum predator/prey size ratios of focal functional
806 groups to help the biomasses of focal functional groups predicted by the OSMOSE model to
807 be, on average, within realistic intervals (Grüss et al., 2015, 2016c). The calibration of an
808 OSMOSE model is the most difficult process that OSMOSE users have to go through and can
809 easily take several months (Oliveros Ramos, 2014; Grüss et al., 2016c). For this reason, we
810 did not try to re-calibrate the OSMOSE-WFS model for the present study. This endeavor was
811 also beyond the scope of the present study. However, the evaluation of our web application
812 did not require a calibrated OSMOSE model and it was possible to conduct this evaluation
813 directly from the OSMOSE configuration files provided by the web application.

814 In the following, we first discuss the insights provided by our demonstration for the
815 West Florida Shelf ecosystem and identify attendant avenues for future research. Then, we
816 identify other avenues for future research. The sets of research recommendations we are
817 providing below are certainly not exhaustive and, again, we strongly encourage the users of
818 our web application to suggest other research recommendations as they see fit by opening
819 new issues in our GitHub repositories ([https://github.com/osmose-model/osmose-](https://github.com/osmose-model/osmose-model.github.io)
820 [model.github.io](https://github.com/osmose-model/osmose-model.github.io) and <https://github.com/osmose-model/osmose-web-api>).

821

822 *4.1. Insights from the demonstration for the West Florida Shelf and attendant avenues for* 823 *future research*

824 Overall, the issues we raised earlier during our demonstration for the West Florida
825 Shelf are not worrisome. We discuss below how each of the issues raised can be addressed,
826 and we also identify the OSMOSE parameters that should be the main focus of future research
827 efforts.

828 A result that was unexpected was the relatively low longevity of king mackerel
829 defined by the web application (14 years vs. 27 years in OSMOSE-WFS papers). This result
830 can be explained by the fact that the web API derives OSMOSE parameters from global
831 median estimates, while the king mackerel longevity estimate used in OSMOSE-WFS models
832 came from a regional study (SEDAR 5, 2004).

833 The web application was able to provide a relative fecundity estimate for only five of
834 the 12 focal functional groups represented in the OSMOSE-WFS model, and the resulting
835 estimates were all substantially smaller than the relative fecundity estimates used in
836 OSMOSE-WFS papers. Nevertheless, relative fecundity is the most uncertain OSMOSE
837 parameter (Shin et al., 2004; Travers, 2009; Grüss et al., 2015), so that it is not possible to
838 state whether the relative fecundity estimates derived from the results of regional studies or
839 those derived from FishBase/SeaLifeBase data are more reliable. For example, the web
840 application and OSMOSE-WFS papers established that the relative fecundity of the sardine-
841 herring-scad complex was 445 and 2,640 eggs per g of mature female per year, respectively;
842 the estimate used in OSMOSE-WFS papers came from a Gulf of Mexico study on scaled
843 sardine (*Harengula jaguana*) (Houde, 1976). However, the relative fecundity of *Sardinops*
844 *sagax* in the OSMOSE model of the Humboldt ecosystem was 8,000 eggs per g of mature
845 female per year (Marzloff et al., 2009) and that of *S. sagax* in the OSMOSE model of the
846 Southern Benguela was 2,400 eggs per g of mature female per year (Travers-Trolet et al.,
847 2014a), while the relative fecundity of *Sardina pilchardus* in the OSMOSE model of the Gulf
848 of Gabes was only 360 eggs per g of mature female per year (Halouani et al., 2016). Another
849 example is that of the anchovies and silversides' group, for which the web application and
850 OSMOSE-WFS papers established a relative fecundity of 366 and 3,313 eggs per g of mature
851 female per year, respectively; the estimate used in OSMOSE-WFS papers came from a study
852 on bay anchovy carried out in Chesapeake Bay, in the mid-Atlantic region (Wang and
853 Houde, 1995). However, the relative fecundity of *Engraulis rigens* in the OSMOSE model of
854 the Humboldt ecosystem was 13,200 eggs per g of mature female per year (Marzloff et al.,
855 2009) and that of *Engraulis encrasicolus* in the OSMOSE model of the Southern Benguela
856 was 8,000 eggs per g of mature female per year (Travers-Trolet et al., 2014a), while the

857 relative fecundity of *E. encrasicolus* in the OSMOSE model of the Gulf of Gabes was only
858 444.6 eggs per g of mature female per year (Halouani et al., 2016). An important avenue for
859 future research is to populate FishBase/SeaLifeBase tables so that the web application is
860 capable of providing a relative fecundity estimate for as many species/functional groups as
861 possible. More specifically, the literature should be screened to fill in gaps in the columns
862 “SpawningCycles” and “RelFecundityMean” of FishBase/SeaLifeBase table “fecundity”
863 (Table 10).

864 Overall, the web application delivered satisfactory $(L_{pred}/L_{prey})_{min}$ and $(L_{pred}/L_{prey})_{max}$
865 estimates, even if the $(L_{pred}/L_{prey})_{max}$ estimates delivered tended to be larger than the
866 $(L_{pred}/L_{prey})_{max}$ estimates employed in OSMOSE-WFS papers. For the present study,
867 generalized additive models (GAMs) were fitted to the $(L_{pred}/L_{prey})_{min}$'s and $(L_{pred}/L_{prey})_{max}$'s
868 used in existing OSMOSE models to predict the $(L_{pred}/L_{prey})_{min}$ and $(L_{pred}/L_{prey})_{max}$ of the
869 species included in FishBase and SeaLifeBase (see Appendix C). The $(L_{pred}/L_{prey})_{min}$ and
870 $(L_{pred}/L_{prey})_{max}$ estimates employed in published OSMOSE papers were established based on
871 experts' opinion or on the limited diet data for which one had both predator length and prey
872 length information (e.g., Travers, 2009; Grüss et al., 2015; Halouani et al., 2016).
873 Furthermore, as mentioned earlier, the $(L_{pred}/L_{prey})_{min}$ and $(L_{pred}/L_{prey})_{max}$ estimates initially
874 defined for an OSMOSE model are, in general, tweaked during the calibration process of
875 OSMOSE; $(L_{pred}/L_{prey})_{min}$ estimates tend to be increased, while $(L_{pred}/L_{prey})_{max}$ estimates tend to
876 be decreased, so as to help the biomasses of focal functional groups to be, on average, within
877 realistic intervals (Grüss et al., 2015, 2016c). Therefore, the fact that two of the $(L_{pred}/L_{prey})_{min}$
878 estimates provided by the web application were markedly smaller than those used in
879 OSMOSE-WFS papers, and the fact that the $(L_{pred}/L_{prey})_{max}$ estimates provided by the web
880 application tended to be larger than those used in OSMOSE-WFS papers, are not an issue.
881 Nonetheless, an important avenue for future research is to enhance our web application so that
882 it can deliver potentially differing $(L_{pred}/L_{prey})_{min}$ and $(L_{pred}/L_{prey})_{max}$ estimates for the juvenile
883 and adult stages of focal functional groups; to enable this, individual statistical models (not
884 necessarily GAMs) should be developed for juvenile and adult fish and juvenile and adult
885 invertebrates. Moreover, to allow $(L_{pred}/L_{prey})_{min}$ and $(L_{pred}/L_{prey})_{max}$ estimates to be more
886 accurate (e.g., to allow $(L_{pred}/L_{prey})_{max}$ estimates to be lower for species like king mackerel, red
887 grouper and gag; Fig. 8), the statistical models developed should be more flexible (i.e. their
888 degree of freedom should be as little restrained as possible), and these models should also

889 ideally not be sensitive to correlated continuous predictors so as to be able to integrate as
890 many continuous predictors as possible.

891 The accessibility coefficients of focal functional groups and the theoretical
892 accessibility coefficients of biotic resources, along with distribution maps and $(L_{pred}/L_{prey})_{min}$
893 and $(L_{pred}/L_{prey})_{max}$ estimates, influence predation mortalities and diet compositions in
894 OSMOSE (Grüss et al., 2016c; Fu et al., 2017). However, the great majority of the
895 accessibility coefficients of focal functional groups and of the theoretical accessibility
896 coefficients of biotic resources other than phytoplankton and zooplankton are set to 0.8 in
897 OSMOSE, so as to let diet compositions be determined primarily from the degree of spatial
898 overlap between predators and their potential prey (determined by distribution maps) and size
899 adequacy between predators and their potential prey (determined by $(L_{pred}/L_{prey})_{min}$ and
900 $(L_{pred}/L_{prey})_{max}$ estimates) (Travers, 2009; Grüss et al., 2015). Thus, the accessibility
901 coefficients of focal functional groups and the theoretical accessibility coefficients of biotic
902 resources other than phytoplankton and zooplankton defined by the web application, which
903 are most often equal to 0.8, are satisfactory. Yet, we envision two avenues for future research
904 with respect to accessibility coefficients and theoretical accessibility coefficients. First, for
905 increased ecological realism in the OSMOSE model, the web API should be able to set the
906 theoretical accessibility of phytoplankton and zooplankton to the adult stages of some focal
907 functional groups to 0 (Travers, 2009; Grüss et al., 2015). Second, still to increase ecological
908 realism in OSMOSE, ecological information should be used by the web API to set some of
909 accessibility coefficients to 0 when predator-prey interactions are not possible (e.g., when the
910 potential prey have spikes that dissuade the predator from attacking them; Fu et al., 2013).

911 The web application provided a diverse natural mortality rate estimate different from
912 the 0.2 year^{-1} default value for only four of the 12 focal functional groups represented in the
913 OSMOSE-WFS model. This result highlights the need to screen the literature to fill in gaps in
914 the column “mortality” of FishBase/SeaLifeBase table “popqb” (Table 3), so as to enable the
915 web application to set the diverse natural mortality rate of the largest possible number of focal
916 functional groups to a value other than the 0.2 year^{-1} default value. In general, the diverse
917 natural mortality rate of a focal functional group represented in an OSMOSE model is
918 assumed equal to the total predation mortality rate of that functional group in an Ecopath
919 model of the same ecosystem that is due to the marine organisms that are represented in the
920 Ecopath model but not in the OSMOSE model (e.g., Marzloff et al., 2009; Travers-Trolet et
921 al., 2014a; Grüss et al., 2015; Halouani et al., 2016). Recently, a large repository called

922 “EcoBase” was constructed to gather a very large fraction of the EwE models published
923 around the world (Colléter et al., 2015). Thus, we envision building upon the EcoBase
924 repository to develop a database gathering predation mortality rate estimates for the species
925 included in FishBase and SeaLifeBase for various marine regions. It would then be possible
926 for the web API to query this new database to derive diverse natural mortality rate estimates
927 for an OSMOSE model, given the ultimate focal functional groups defined for that OSMOSE
928 model via the interactions between the web UI and the user.

929 The web application was able to deliver a non-default estimate for only two of the 12
930 OSMOSE-WFS focal functional groups with respect to critical predation efficiency, five
931 OSMOSE-WFS focal functional groups with respect to maximum annual ingestion rate, and
932 four OSMOSE-WFS focal functional groups with respect to proportion of females. An avenue
933 for future research is to screen the literature to fill in gaps in relevant FishBase/SeaLifeBase
934 tables, so as to enable the web application to provide non-default estimates of critical
935 predation efficiency, maximum annual ingestion rate and proportion of females for as many
936 species/functional groups as possible (Table 10). However, because critical predation
937 efficiency, maximum annual ingestion rate and proportion of females are usually set to their
938 default value for all focal functional groups in OSMOSE models (but see Brochier et al.
939 (2013) and OSMOSE-WFS papers), the above-mentioned research recommendation is
940 secondary compared to others (Table 10).

941 In addition to relative fecundity and diverse natural mortality rate, the following
942 OSMOSE parameters should be the primary focus of future research efforts: (1) the
943 reproduction seasonality of focal functional groups, given that the web application was able to
944 define reproduction seasonality patterns for only six of the 12 focal functional groups
945 represented in OSMOSE-WFS; and (2) the minimum and maximum sizes and TL of biotic
946 resources, given that the web application was generally unable to provide values for all these
947 parameters for the biotic resources other than phytoplankton and zooplankton that are
948 represented in OSMOSE-WFS. For all these OSMOSE parameters, efforts should be made to
949 screen the literature to fill in gaps in relevant FishBase/SeaLifeBase tables, so as to maximize
950 the chances of the web application providing non-default estimates for them (Table 10). By
951 contrast, we do not recommend more emphasis on the egg size and egg weight of focal
952 functional groups. The web application set these parameters to their default values for all the
953 focal functional groups represented in OSMOSE-WFS. However, these parameters, which
954 have usually been set to their default values in published OSMOSE-WFS models (but see

955 Halouani et al. (2016)), have virtually no impact on OSMOSE predictions and, therefore, do
 956 not deserve further consideration compared to parameters such as the relative fecundity and
 957 reproduction seasonality of focal functional groups (Table 10).

958

959 **Table 10**

960 OSMOSE parameters for which efforts should be made to screen the literature to fill in relevant
 961 FishBase/SeaLifeBase tables, so as to maximize the chances of our web application providing a non-default
 962 estimate for these parameters.

OSMOSE parameter	Priority for future research efforts?	FishBase/SeaLifeBase fields that need to be populated
Relative fecundity of focal functional groups	Yes	SpawningCycles, and RelFecundityMean (FishBase/SeaLifeBase table: fecundity)
Reproduction seasonality of focal functional groups	Yes	Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, and Dec (FishBase/SeaLifeBase table: spawning)
Diverse natural mortality rate of focal functional groups	Yes	mortality (FishBase/SeaLifeBase table: popqb)
Minimum size of biotic resources	Yes	LengthMin (FishBase/SeaLifeBase table: popll)
Maximum size of biotic resources	Yes	LengthMax (FishBase/SeaLifeBase table: popll)
Trophic level of biotic resources	Yes	Troph (FishBase/SeaLifeBase table: estimate)
Critical predation efficiency of focal functional groups	No	MaintQB, and PopQB (FishBase/SeaLifeBase table: popqb)
Maximum annual ingestion rate of focal functional groups	No	PopQB (FishBase/SeaLifeBase table: popqb)
Proportion of females of focal functional groups	No	SexRatiomid (FishBase/SeaLifeBase table: spawning)

963

964 ***4.2. Other avenues for future research***

965 We also envision the following additional improvements: (1) introducing new
 966 invertebrate classes in SeaLifeBase and populating SeaLifeBase tables for these new classes;
 967 (2) allowing the web API to derive OSMOSE parameter values from the regional estimates
 968 available in FishBase/SeaLifeBase rather than from median estimates; (3) improving the
 969 computational efficiency of our web application so that there is no restriction on the total (i.e.,
 970 original plus additional) number of species per functional group included in the JSON data
 971 archives; (4) enhancing our web application so that it covers more OSMOSE parameters; (5)
 972 allowing the web application to also define “background functional groups” for OSMOSE
 973 models; and (6) building upon the generic software architecture on which our web application
 974 relies to develop other web applications delivering a diversity of products needed to advance
 975 EBFM.

976 The demonstration for the West Florida Shelf ecosystem revealed that a number of
977 small invertebrate classes are not covered by SeaLifeBase (Table 5). Importantly, because
978 there is currently no information on the Ostracoda, Turbellaria, Cladocera and Brachiopoda
979 classes in SeaLifeBase, it was impossible to define a small mobile epifauna group for the
980 West Florida Shelf ecosystem. The literature on small invertebrate species is scarce. Yet, if
981 small invertebrate species are considered in an OSMOSE model, they will be represented as
982 biotic resources, for which OSMOSE only needs a limited number of parameters, of which
983 the great majority could be defined somehow. In particular, we suspect that it will be possible
984 to define the minimum and maximum sizes and TL of most of the species belonging to small
985 invertebrate classes. Therefore, we encourage efforts to populate SeaLifeBase tables for
986 species belonging to small invertebrate classes.

987 There are cases where, for a given species, several values (usually generated by studies
988 conducted in different regions) are available for a given FishBase/SeaLifeBase parameter. In
989 these cases, the web API produces a median estimate for the FishBase/SeaLifeBase parameter
990 before doing any calculations to derive an OSMOSE parameter estimate. However, two
991 populations of the same species inhabiting different regions can differ in many traits (e.g.,
992 Branstetter et al., 1987; Carlson et al., 2006; Cope, 2006; Alheit and Pitcher, 2012), notably
993 their body size, which is usually a function of temperature (Pauly, 2010). Therefore, it would
994 be advantageous to improve the web API so that it can select the most appropriate regional
995 estimate for a given FishBase/SeaLifeBase parameter and species rather than relying on a
996 median estimate for that FishBase/SeaLifeBase parameter and species.

997 For the sake of computational efficiency, the total number of species (i.e., original plus
998 additional) per functional group in JSON data archives is restricted to 30 currently. In the
999 future, this restriction should be abandoned to enable the web API to set the maximum
1000 possible number of OSMOSE parameters to their non-default values. However, for this to
1001 happen and, also, because our web application will need to be continuously enhanced, it will
1002 be necessary to first find a way to improve the computational efficiency of our web
1003 application.

1004 There are a couple of OSMOSE parameters that our web application does not cover
1005 currently. For example, the web API does not attempt to estimate the maximum annual
1006 starvation mortality rate of focal functional groups, which is set to a default value instead (0.3
1007 year⁻¹), as is the case in all existing OSMOSE applications. As previous studies (e.g., Shin and

1008 Cury, 2001a; Shin et al., 2004; Travers, 2009), we were unable to establish a method for
1009 estimating a maximum annual starvation mortality rate for individual species; however, we
1010 feel that developing such a method is not a priority for future research efforts. In contrast, it
1011 would be interesting to enhance our web application so that it provides a spatial grid for the
1012 OSMOSE model and distribution maps for focal functional groups. For example, a page could
1013 be added to the web UI to query additional information to the user, including the desired
1014 longitudinal and latitudinal ranges of the OSMOSE spatial grid and the desired resolution of
1015 that grid. This information would then be handled by a geographic information system (GIS)
1016 tool. The GIS tool would produce distribution maps for focal functional groups in the form of
1017 CSV files (Appendix B), based on the depth ranges of the species making up the focal
1018 functional groups entered in FishBase/SeaLifeBase tables. Finally, the CSV files generated by
1019 the GIS tool would be passed to the web API, which would include them in the
1020 “osmose_config.zip” file delivered to the user.

1021 The latest version of OSMOSE (OSMOSE v3u2) and our web application consider
1022 two types of functional groups: focal functional groups, and biotic resources. However, it is
1023 planned to introduce a third type of functional groups in the template version of OSMOSE:
1024 “background functional groups”. The concept of background functional groups was
1025 introduced in Fu et al. (2017). Background functional groups are functional groups that are of
1026 secondary importance for the study envisioned by the user, but that have the potential to be
1027 non-negligible predators or prey items of focal functional groups. As the full life cycle of
1028 background functional groups is not modeled (contrary to focal functional groups), the
1029 number of inputs needed for background functional groups is less important than that needed
1030 for focal functional groups, but more important than that needed for biotic resources (Fu et al.,
1031 2017). Once the next version of OSMOSE that integrates background functional groups is
1032 released, we will modify the web application so that it can also deliver parameter estimates
1033 for this new type of functional groups.

1034 The software architecture used to build our bridge between FishBase/SeaLifeBase and
1035 the OSMOSE ecosystem modeling platform can serve as a basis for designing other advanced
1036 web applications processing FishBase/SeaLifeBase data to produce parameter values for other
1037 EBFM tools. A logical future use of this software architecture would be the development of
1038 web applications producing parameter estimates for Atlantis and EwE ecosystem models from
1039 FishBase/SeaLifeBase data. Such web applications would consider not only the information
1040 on fish compiled in FishBase and the information on invertebrates compiled in SeaLifeBase,

1041 but also the information on other marine organisms compiled in SeaLifeBase. The generic
1042 framework we designed could also be used in many other ways, for example, to develop a
1043 simple web application defining functional groups for any marine region, or to derive
1044 parameter estimates from FishBase/SeaLifeBase data for dynamic multispecies models
1045 (Kinzey and Punt, 2009; Holsman et al., 2016). However, it is important to emphasize that the
1046 web application bridging FishBase/SeaLifeBase and OSMOSE does not allow for quality
1047 control at the species level. Yet, many modelers employ FishBase and SeaLifeBase as starting
1048 points for finding parameter values for individual species, which they then possibly alter or
1049 replace using available regional information. Thus, we recommend that some of the future
1050 versions of our framework do not aggregate species into functional groups and rather provide
1051 parameter values for individual species; users will then have the possibility to gauge
1052 parameter values for individual species, eventually alter or replace some of these parameter
1053 values using regional information, and group some individual species into groups as they see
1054 fit.

1055

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1064 A.G., M.L.D.P., J.H.P., J.R.B., C.D.A. and S.R.O. performed the research; A.G., M.L.D.P.,
1065 J.H.P., J.R.B. and D.P. analyzed the data; and A.G., M.L.D.P., J.H.P., J.R.B., C.D.A., S.R.O.,
1066 N.B., Y.-J.S., J.S. and D.P. wrote the paper.

1067

1068 **Supplementary data**

1069 Supplementary data associated with this article can be found in the online version of the
1070 manuscript.

1071

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