



Ecosystem modeling as a framework to convert a multi-disciplinary research approach into a useful model for the Araçá Bay (Brazil)

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A B S T R A C T

A model-oriented research project can organize and systematize high quality sampling information and convert observed values into information needed to parameterize ecological models. In this paper, we describe the value parameterization process from an interdisciplinary project to the development of a food web model (using Ecopath) in order to comprehend the Araçá Bay ecosystem structure (Brazil) and to forecast the impact of a port expansion (São Sebastião Port) over a bay environment. Araçá Bay Ecopath model has 34 compartments, Phytoplankton, Phytobenthos, Mangrove, Zooplankton, 10 groups of benthos, 13 fish groups, Shrimp, Crabs, Turtles, two bird groups and two groups of Detritus. The model outputs showed that Araçá Bay is a mature and detritus-based ecosystem. It is highly influenced by the role of benthos groups which are responsible for a huge amount of detritus recycling due to their large biomass value. The simulation of port expansion (primary producers' reduction), using the Ecosim module, indicated negative impacts on almost all living groups and an increase in detritus accumulation, leading the entire bay ecosystem towards its collapse (in the short term). The interdisciplinary organized sampling process presented here is an example of how objectively planned sample design and modeling may guide scientists, local people and stakeholders' decisions with valuable integrated information and overall predictions in order to consider the sustainable use of natural areas and resources.

1. Introduction

The high biological production and species richness in marine and coastal environments have long provided several services to humans, especially in regards to food supply (Lopes et al., 2016; Erlandson et al., 2008). However, in recent decades, anthropogenic effects on marine environments has increased local impacts (Aarts et al., 2016), enlarging regional pressures on livestock (Piroddi et al., 2017) and strengthening global changes in climate (Ahmed et al., 2017).

Globally, many coastal ecosystems are being irreversibly modified and lost due to human interference. The complexity of these environments and their drivers (natural or human-induced) requires a broad approach in order to understand first the normal dynamics and

relationships among organisms and second, to forecast the effects of different impacts, such as ecological imbalance, loss of species and ecosystems services (Donohue et al., 2017).

Under the scenario of human-induced changes, small marine areas that shelter an array of environmentally-sensitive habitats are even more vulnerable. A clear understanding of the ecological processes and species interactions in multiple small marine habitats as well as their role as a refuge and species source to adjacent areas is key to evaluating the extent of impacts upon them (Bonaldo et al., 2017).

The Ecosystem Approach Management (EAF) assesses the ecological processes, species interactions and the integration of sustainable use with conservation in small marine ecosystems. Particularly, a key goal of the EAF is to unveil the drivers and consequences of fishing and other

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land activities in coastal areas upon individual species and habitats (Hutubessy et al., 2014).

Ecosystem models need define connections among organisms, with different roles on food web, into a single mathematical structure enabling the comprehension of complex systems and their drivers (Heymans et al., 2011). In this context, a fundamental phase of the modeling process is to convert observed field data into model parameter values minimizing biases and misrepresentations of the actual values (observed data).

One of the models to represent connections among organisms, i.e., a food web is the “Ecopath with Ecosim” (Polovina, 1984; Christensen and Pauly, 1992) that has substantially improved the capacity of scientists to understand complex marine ecosystems. Currently, more than 400 ecosystem models using the EwE approach have been published (Colléter et al., 2015) and there are more than 700 citations per year, on average over the last decade (Coll et al., 2015).

This study aimed to explore and show how to convert sampling records into input data for an Ecopath model for Araçá Bay, a small marine coastal environment in an urban area. The model was performed in order to integrate information about different organisms of a food web within an ecosystem context to be used to as a robust tool to predict the impact of the port expansion (São Sebastião Port, Brazil) over Araçá Bay. To achieve this, we converted multi-disciplinary research approach at into interdisciplinary model.

2. Material and methods

2.1. The study area: the Araçá Bay

Araçá Bay (23° 49'S, 45° 24'W) is a small and unique coastal ecosystem (345,000 m²) located in the central area of São Sebastião Channel, in the Southeast coastline of Brazil (Fig. 1). The bay reaches a maximum depth of 30 m in the main channel and the tides varies between 2.06 m and −0.04 m (Gubitoso et al., 2008). Adjacent to Araçá Bay is the São Sebastião Port, which is expected to expand toward the bay. The likely expansion (red lines in Fig. 1) would consist of concrete slabs supported by several pillars. If approved, the planned construction would advance approximately 20–42 m a year toward the bay and last for 10–20 years.

2.2. The Araçá Bay food web model

Araçá Bay model was developed using an Ecopath with Ecosim approach (EwE, versions 6.4). Ecopath, which is the mass-balance model of EwE, follows a mass-balance assumption allowing the description of a food web, its interactions and flows of energy and mass.

In the basic equation, the consumption by a predator (or group) leads to the mortality of its prey due to predation (Christensen and Pauly, 1992). This is mathematically described by:

$$B_i * PB_i * EE_i - \sum_j (B_j * QB_j * DC_{ji}) - EX_i = 0 \quad (1)$$

Where: B_i is the biomass of group i ; PB_i is the production/biomass rate of i , which is equal to the natural mortality M (Allen, 1971); EE_i is the ecotrophic efficiency of i , which varies from 0 to 1 and represents the fraction of the production of the group that is transferred to higher T_L s or exported from the system; B_j is the biomass of predator j ; QB_j is the food consumption per unit of biomass for predator j ; DC_{ji} is the fraction of i in the diet of j ; and EX_i is the export of i and represents the biomass that is caught through fishing and/or that migrates to other ecosystems. Because the complexity of tidal dynamics, EX_i was considered zero for all model's groups. The biomasses were expressed as gWW * m⁻² (grams of wet weight per square meter), and the flows in the food web were expressed in gWW m⁻² year⁻¹.

For an ecosystem with n compartments, the model builds a system of n linear equations. In the development of an Ecopath model, it is

necessary to include at least three of the four main input parameters (B_i , PB_i , QB_i , and EE_i). It is possible to estimate the missing parameter by connecting the production of one group with the consumption by the other groups. This is based on the assumption that the production of one group is utilized by another group inside the system (Christensen and Pauly, 1992). In the Araçá Bay model, EE_i was the parameter that was estimated by EwE, with a few exceptions (see below).

2.3. Dataset sampling

The Araçá Bay food web model has 34 compartments comprised by 32 groups of organisms (Phytoplankton, Phytobenthos, Mangrove, Zooplankton, 10 groups of benthos, 13 fish groups, Shrimp, Crabs, Turtles, and two bird groups) and two groups of Detritus. Groups are defined by considering the data about abundance in sampling and in the fish gut content analyses. *Taxa* were sampled by conventional methods (Table SM1).

2.4. Parameterization

The conversion of sampling data into parameter values for the Ecopath model required meticulousness and parsimony. The methods to convert basic data in values for the input parameters vary according to the biological groups chosen. Some of these methods are detailed below.

2.4.1. Phytoplankton and phytobenthos

At the total, nine samples of Phytoplankton were collected in Araçá Bay. They were divided in four fractions according to size: microplankton, nanoplankton, ultraplankton and picoplankton (Giannini and Cioti, 2016). The records were provided in milligrams of Carbon (mg C * m⁻³) and Chl a concentration in milligrams (mg * m⁻³), both by cubic meter (m⁻³).

To proceed with the conversion, we estimated the mean of all samples (Table SM1) of each Phytoplankton size. Afterwards, mean values were multiplied by two (2) to convert mg C into Dry Weight milligrams (mg DW). The resulting value was then multiplied by five (5) to convert mg DW to Wet Weight milligrams (mg WW) and divided by 1000 to convert milligrams to grams (g WW) (APHA, 2012). At the end, all values for each size fraction were summed because the Ecopath model was built with one Phytoplankton compartment only.

Values in g WW * m⁻³ needed to be converted in g WW * m⁻² (Ecopath model unit). In a step-by-step fashion, we first multiplied the bay area (345,000 m²) by its euphotic zone depth (1.5 m) to calculate the entire amount of water in the bay (m³). Subsequently, by multiplying the aforementioned value (in m³) by the value in g WW * m⁻³, we would have the total Phytoplankton biomass. Total biomass divided by bay area (m²) provides the Phytoplankton value in a suitable unit for the Ecopath model (g WW * m⁻²). Another practical and fast way to convert g WW * m⁻³ to g WW * m⁻² is to multiply the value in g WW * m⁻³ by the depth of euphotic zone (in m).

For converting Chlorophyll- a concentration (mg * m⁻³) in gWW * m⁻² for the Araçá Bay model, we first converted Chl- a concentration in Dry Weight, using the information that Chl- a corresponds to 1.5% of dry weight (APHA, 2012). After that, we used the conversions showed above.

Both results were similar. By using Chl a data the value found was 1.49 g WW * m⁻² while using mg C * m⁻³ the value was 1.286 g WW * m⁻². Such slight differences is acceptable and provides useful variation for model balancing process. In the final model we used the first value.

Production refers to the elaboration of tissue (whether it survives or not) by a group along a given period (Christensen et al., 2008). For Production/Biomass rate (g WW * m⁻² * year⁻¹), the estimation value was used for primary production (PP) calculated in the unit mg C * m⁻³ * hour⁻¹. We calculated the mean of all nine PP' estimates and

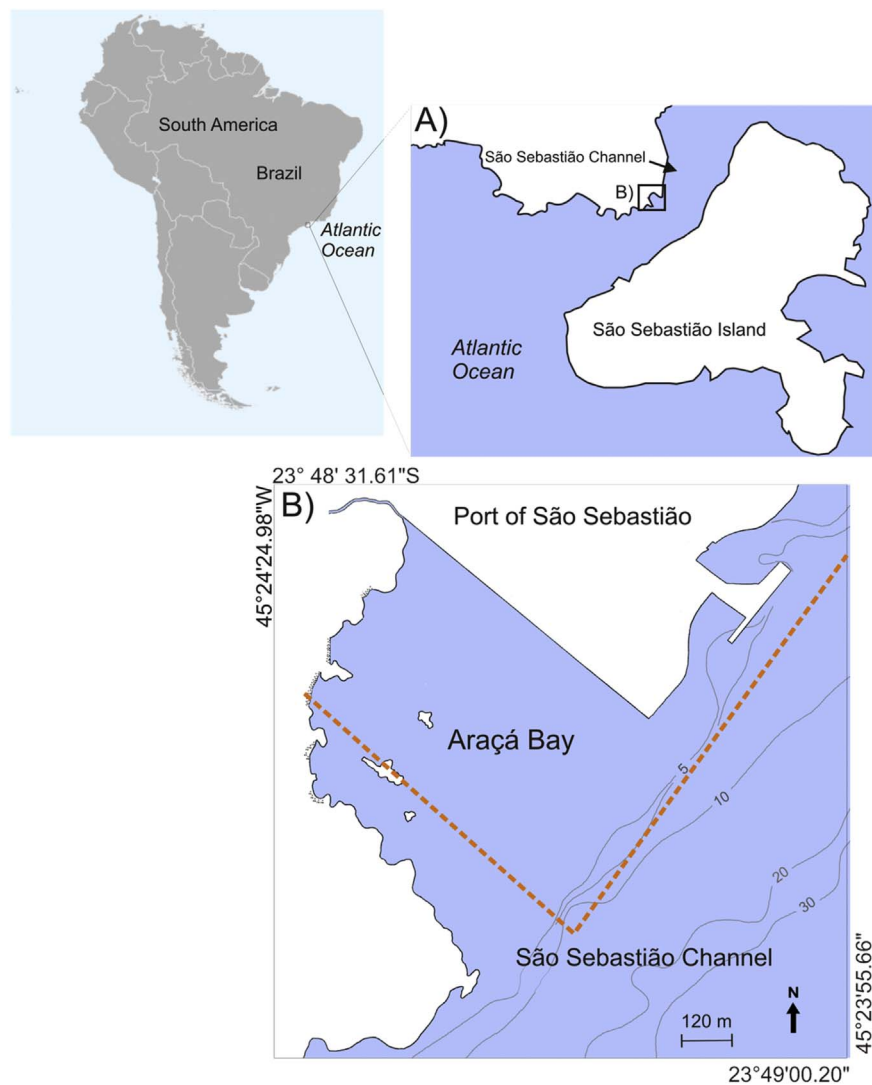


Fig. 1. Araçá Bay and São Sebastião Channel (São Paulo State, Brazil). The current port area borders the Bay and the port's expansion planned (red dashed line). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

multiplied it by 10 h (sunlight expected hours) resulting in $\text{mg C} \cdot \text{m}^{-3} \cdot \text{day}^{-1}$. After, we converted $\text{mg C} \cdot \text{m}^{-3}$ to $\text{g WW} \cdot \text{m}^{-2}$ (using the method explained above) and multiplied by 365 days, obtaining our input value for the model: $347.18 \text{ g WW} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$. This value suggests that the Phytoplankton standing crop almost produce its own weight every day through the year.

Phytoplankton biomass was also estimated using Chlorophyll-*a* pigments (Amaral, 2014) but in this case the unit was $\text{mg Chl-}a \cdot \text{m}^{-2}$ because the samples were collected at the bottom of the bay (Table SM1). Accordingly, using the same conversion mode for Phytoplankton (see above) we found a mean value of $27.5 \text{ g WW} \cdot \text{m}^{-2}$ with a standard deviation of $20.04 \text{ g WW} \cdot \text{m}^{-2}$. Unfortunately, it was not possible to estimate the PB rate for Phytoplankton, therefore the value = $121.6 \text{ g WW} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$ was adopted with the consideration that Phytoplankton could reproduce its own weight one time in three days ($365/3$).

2.4.2. Mangrove and Mangrove's Detritus

In general, many fish and invertebrate species are dependent on mangrove environments for spawning, growing and protection against predation. The mangrove area in Araçá Bay is 3445.24 m^2 (0.7% of bay area) with an estimate of trees biomass of $7000 \text{ g} \cdot \text{m}^{-2}$. For the complete area, mangrove Biomass reaches $49 \text{ g} \cdot \text{m}^{-2}$ and Production/Biomass is $0.173 \text{ g} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$, since local leaf production is around

1.73%. We allocated all detritus from Mangrove into a compartment named Detritus Mangrove without the initial value of biomass.

2.4.3. Zooplankton

Zooplankton is very important in an aquatic food web, since it is the first link between primary producers and main consumers such as fish species. In Araçá Bay, 169 trawls, using a plankton-net, were done during seven samplings periods (Table SM1) in seven sites. Individuals collected were digitalized using ZooScan (Biotom model) in the Zoo-Process software (Gorsky et al., 2010; <https://imagej.nih.gov/ij/>). Identification was made using the free software, Plankton Identifier (Gasparini and Antajan, 2013) and images were used to estimate an individual's area (in mm^2). Accordingly, these estimates were used to calculate individual biomass, applying some empirical regressions (Uye, 1982; Hernández-León and Montero, 2006; Lehet and Hernández-León, 2009) for different zooplankton groups of the sample (for example, Copepods (dominant group) such as Calanoida-Cyclopoida; Holoplankton: Appendicularia; Meroplankton: Decapoda).

For convenience, several identified zooplankton groups were grouping into only one compartment in the Ecopath model to represent zooplankton. We calculated the Zooplankton mean biomass, using all estimates and the result was $24.99 \text{ mg C} \cdot \text{m}^{-3}$. Therefore, we applied the same above-mentioned approach to convert units. The input

biomass to the Ecopath model for this group was $0.375 \text{ g WW} \cdot \text{m}^{-2}$ (standard deviation = 0.231).

There were no estimates available for production (PB) or for consumption (QB) of zooplankton groups. Thus, for these rates we used the values suggested by Rocha et al. (2007) who developed a preliminary model for Araçá Bay (then, $\text{PB} = 40 \text{ g WW} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$ and $\text{QB} = 160 \text{ g WW} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$). Diet composition for Zooplankton was 25% of Phytoplankton; 10% of Zooplankton and 65% of Detritus (Véga-Perez, 1993).

2.4.4. Benthos

Benthos samplings were taken during the low tide at 37 geo-referenced sites performed in four periods (Table SM1). Samples were taken using a corer of 10 cm inner diameter and 20 cm depth (Corte et al., 2017). Records were provided in species abundance by m^2 . The suitable input value for Ecopath model ($\text{g WW} \cdot \text{m}^{-2}$) was obtained by multiplying species (groups) individual weight by abundance mean. Due to the high benthos diversity at Araçá Bay (Corte et al., 2017) we had 10 compartments to represent this group (Table SM2), including four very abundant species considered exclusive compartments: *Olivella minuta*, *Anomalocardia brasiliensis*, *Laeonereis culveri*, and *Monokalliapseudes schubarti*.

Production/Biomass rate for the benthos groups were estimated using an empirical regression that assesses the annual somatic production of marine benthic invertebrate populations (Tumbiolo and Downing, 1994) as follow:

$$\text{Log(P)} = 0.24 + 0.96 \cdot \text{log(B)} - 0.21 \cdot \text{log(Mass)} + 0.03 \cdot \text{Temp} - 0.16 \cdot \text{log(D+1)} \quad (2)$$

where:

P: Annual Somatic Production ($\text{g DW} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$);
B: Biomass ($\text{g DW} \cdot \text{m}^{-2}$);
Mass: Maximum Individual Body Mass (mg DW ; $1 \text{ g DW} = 3.5 \text{ g WW}$);
Temp: Surface water Temperature (27°C);
D: Water depth (1.5 m).

Consumption/Biomass (QB) rate shows how much one component eats in relation of its own weight during a year (Christensen et al., 2008). In this case we used respiration rate estimates for invertebrates calculated by Humphreys (1979) equation:

$$\text{Log(R)} = 0.691 + 0.892 \cdot \text{log(P)} \quad (3)$$

where:

R: Respiration ($\text{K Joules} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$);
P: Production ($\text{K Joules} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$); P = P/B estimates;
Conversions rates: $1 \text{ KJ} = 238.85 \text{ calories}$ and $1 \text{ g WW} = 5 \text{ calories}$.
Consumption rate was calculated by:

$$\text{Q/B} = (\text{P/B} + \text{R/B})/\text{A} \quad (4)$$

where:

Q/B: Consumption/Biomass rate ($\text{g} \cdot \text{m}^{-2} \cdot \text{year}^{-1}$);
P/B: Production/Biomass (Eq. (2));
R/B: Respiration (Eq. (3)) divided by Biomass;
A: depends on feeding habit: filters and suspensivores: 0.6; others groups, including detritivores: 0.8.

Benthos' diet composition was organized using literature (Table SM2). All benthos components almost exclusively consumed Detritus. The only exceptions were Gastropoda, Polychaeta and *Olivella minuta*, which also consume other benthos and Echinodermata, which

consumes Phyto-benthos.

2.4.5. Fish

Fish samplings were made using gears, which allow for estimates of the weight of species caught (in grams) by area of environment (m^2) for each fish sampling operation. Using results of all gears by survey the biomass values of species ($\text{g} \cdot \text{m}^{-2}$) was estimated. In the model, only species caught in at least three from the five surveys were considered (tri-monthly; Table SM1).

The gears used in the sampling surveys were: i) Twin otter trawl with a total of four hauls carried out in each survey sampling, on average, $222 \pm 120 \text{ m}^2$; ii) Cast net with assumed area of the net to be round ($= 34.73 \text{ m}^2$), handled by skilled fisherman with 18 replicates per survey; iii) Encircling gill net, with 3 m in high and 590 m in length, to which fish are driven to become entangled in the net due to the noise and beating oars produced by fishermen. The mean sampled area was $4349 \pm 5315 \text{ m}^2$; iv) Beach Seine with 20 m wide and 3 m high with a 15 m long bag. Handling it produced an estimated mean sampled area of $378 \pm 153 \text{ m}^2$. Details about sampling surveys and each gear are explained in Supplementary Material (Table SM1) and Contente and Rossi-Wongtschowski (2017).

In total 126 fish species were sampled (Lamas et al., 2016) but only 49 occurred in more than three sampling surveys (Table SM3). We choose 13 fish compartments to represent the seven more abundant fish species (*Haemulopsis corvinaeformis*, *Mugil curema*, *Atherinella brasiliensis*, *Diapterus rhombeus*, *Trichiurus lepturus*, *Sardinella brasiliensis*, and *Mugil liza*), the two fish genera (*Centropomus* spp. and *Sphoeroides* spp.) and *Dasyatis* spp., because stingrays are 'charismatic' animals. We used three species groupings according to their feeding habit (Benthivore, Hyperbenthivore-piscivore, and Planktivore), which comprised 35 species (Table SM3).

The Production/Biomass (PB) for fish compartments was calculated using the Pauly (1980) equation for Natural Mortality (M):

$$\text{M} = 0.9849 \cdot \text{K}^{0.65} \cdot \text{L}_\infty^{-0.279} \cdot \text{T}^{0.463} \quad (5)$$

where:

M: Natural Mortality (year^{-1}) = Production/Biomass (Allen, 1971);
K: curvature parameter of the Von Bertalanffy Growth Function (year^{-1});
 L_∞ : asymptotic length (cm);
T: mean environmental temperature ($^\circ \text{C}$, in this case, 27°C).

The Consumption/Biomass (QB) rate is the intake of food by a group over the year relative to own weight. In our model, we calculated QB using the empirical regression of Palomares and Pauly (1998):

$$\text{log(QB)} = 7.964 - 0.204 \cdot \text{logW}_\infty - 1.965 \cdot \text{T} + 0.083 \cdot \text{Ar} + 0.532 \cdot \text{H} + 0.398 \cdot \text{D} \quad (6)$$

where:

Q/B: Consumption/Biomass rate (year^{-1});
 W_∞ : asymptotic weight (g WW);
T: is an expression for the mean annual temperature of the water: $\text{T} = 1000/(\text{Kelvin} = ^\circ \text{C} + 273.15)$;
Ar: aspect ratio of the caudal fin (measurement of the swimming and metabolic activity of the fish): $\text{Ar} = \text{h}^2/\text{S}$ (where: h - height of the caudal fin (mm) and S the surface area of the caudal fin (mm^2));
H and D: fish feeding habit: if Herbivores then $\text{H} = 1$ and $\text{D} = 0$; if Detritivores, $\text{H} = 0$, $\text{D} = 1$, for other feeding habit, $\text{H} = \text{D} = 0$.

We used the Fishbase platform (Froese and Pauly, 2017) for the input parameters values for equations (5) (PB) and (6) (QB).

2.4.6. Fish diet composition

Four sampling surveys were carried out in Feb–Mar/2013 and Jun–Jul/13 for fish collection following the same procedure as discussed above. In total, 879 gut contents of 23 species were analyzed with prey items being identified under stereomicroscope at different taxonomic levels. This depended on the preservation of their bodies and was quantified in grams (Amaral, 2015). Additionally, 1187 isotopes analyses for 20 fish species and food sources were performed (Soares et al., 2016). Both methods were applied in a complementary way mainly to confirm Detritus source for detritivore species.

2.4.7. Birds

Birds were sampled by visual observation during three-day sampling surveys monthly from June/2014 to June/2015 (2.5 h per day) with a total effort of 90 h of observation. A total of 74 bird species were observed. The most abundant was *Coragyps atractus* and we considered them as a unique compartment in the Ecopath model. In the other compartment (Water birds) we grouped the other species with the most representative ones being *Sula leucogaster*, *Fregata magnificens* and *Sterna hirundinacea*.

Biomasses were calculated, multiplying the mean abundance of samplings by individual mean weight of each species (Dunning, 1992). Afterward, we divided the biomass found by the Araújo Bay area.

For Consumption/Biomass rate estimating, we used the empirical regressions from Ellis and Gabrielsen (2002), which calculate the consumption based on species individual weight. For Production/Biomass we used a value for water birds (PB = 0.4) from an Ecopath model for Delaware Bay (Frisk et al., 2011). In this sense, we assumed PB = 0.1 for *C. atractus*, because it is much bigger (and weightier) than water birds from Araújo Bay.

2.4.8. Turtles

Sightings of turtles were made simultaneously from boats and at a high land points during four successive days in March, June, August and October 2014. All individuals observed (n = 144) were identified as *Chelonia mydas* juveniles with daily mean observation of 4.4 individuals. Using the mean weight of three individuals (= 5.36 kg) the biomass by the bay area was 0.068 g·m⁻². Production (PB) and Consumption (QB) rates were taken from the literature (Torres et al., 2013). Diet composition was determined by analysis of stable isotopes (Soares et al., 2016).

2.4.9. Crab and shrimp

Crabs and shrimp were sampled as by-catch in the fish sampling (see above). All individuals were weighted and standardized by fishing gear area in all sampling surveys. Biomasses of shrimp and crabs were 0.021 and 0.72 g · m⁻², respectively. PB and QB rates for crabs and for shrimp were taken from the literature (Frisk et al., 2011; Cheng et al., 2009). Diet compositions were based on literature for shrimp (Branco and Moritz Jr., 2001) and crabs (Mantelatto and Petracco, 1997; Mantelatto and Christofoletti, 2001).

2.5. Validation and balancing of the food web model

We followed the best practices in Ecopath modeling (Heymans et al., 2016) using the following steps: i) before the first run, we changed the excretion/egestion rate for Zooplankton, all benthos groups and other feeders groups on Phytoplankton to 40% and 30%, because it is more realistic from a physiological point of view (Ecopath input default is 20%); ii) after, we balanced the model to achieve the Ecotrophic Efficiency (EE) values lower than 1.0; iii) we also confirmed if Production/Consumption (P/Q or Gross Efficiency, GE) values were between 0.1 and 0.3; if Respiration/Assimilation rate values < 1.0; and if Respiration/Biomass rate values were between 1 and 10 for fish compartments and 50 to 100 for groups with higher turnovers rates (higher PB and QB values).

We also used the Pre-Balanced (PREBAL) diagnosis (Link, 2010) to identify issues in the model structure and in data quality before balancing the network model. We analyzed the main relationships among Biomass, Production and Consumption to Trophic Level. Biomass should span 5–7 orders of magnitude and PB and QB decrease when TL increases. We also observed vital rates ratios, for example, rates of predator must be lower than prey's rate and Respiration/Production rates need to be lower than 1 (Link, 2010).

In order to evaluate the input data quality, we estimated the Pedigree Index (IPdgr) attributing values between 0 (low quality) and 1 (high) for each input parameter value (B, PB, QB, and the diet matrix elements) according to the source of information. Then, the average values for all parameters and groups provided a general concise index of the model input data quality (Christensen et al., 2008).

2.6. Food web model results

The Ecopath food web model can be used to estimate general indicators for the food web aside from properties of each functional group. For each compartment, in order to investigate the strategy of feeding behavior, we used the Omnivory Index (Christensen et al., 2008), the number of paths in which energy passes until it has reached all groups, and the flow contribution to Detritus.

Regarding general indicators, we used the System Omnivory Index (SOI) and classical attributes (Odum, 1969) such as the Total Primary Production/Total Respiration, Total Primary Production/Total Biomass, Total Biomass/Total System Throughput, Connectance Index, Finn's Cycling Index, Overhead (O), Ascendency, Transfer Efficiency and the Detritivore/Herbivore ratio. These attributes measure a global development status for the ecosystem (*sensu* Odum, 1969) considering that “mature” environments are more resilient than “immature” ecosystems (see more details in Angelini et al., 2013).

The Mixed Trophic Impact (MTI) analysis was used to quantify the relative impact of biomass change within a component (impacting group) over the rest of the other components (impacted groups) in the food web (Ulanowicz and Puccia, 1990), accounting for all possible direct and indirect impacts from one component to another. Using MTI parameters, Libralato et al. (2006) and Valls et al. (2015) developed a keystone species index. A keystone species is defined as a species with low biomass but that could play an important role in the food web (Paine, 1995).

2.7. Time dynamic impact simulations

The temporal dynamic module of EwE (i.e., Ecosim) uses settings from the mass-balance module (i.e., Ecopath) as the initial conditions and parameter definitions (Christensen and Walters, 2004). Namely, the system equation (Eq. (1)) is transformed into a system of ordinary differential equation (Walters et al., 1997, 2000):

$$dB_i/dt = g_i \cdot \sum_j Q_{ji} - \sum_j Q_{ij} + I_i - (MO_i + F_i + e_i) \cdot B_i \quad (7)$$

where: dB_i/dt is the change in B of group i over time t ; g_i is the net growth efficiency; Q_{ji} is the consumption of group j by group i ; Q_{ij} is the consumption of group i by group j ; I_i is the extent of immigration of group i ; MO_i is the non-predation rate of natural mortality of group i ; F_i is the fishing mortality of group i (in this case zero (0) for all groups) and e_i is the emigration of group i .

In Eq. (2), the quantity of prey i consumed by predator j (Q_{ij}) is a nonlinear relationship based on the “foraging arena theory” (Walters et al., 2000; Walters and Christensen, 2007; Ahrens et al., 2012):

$$Q_{ij} = (a_{ij} \cdot v_{ij} \cdot B_i \cdot B_j) / (2 \cdot v_{ij} \cdot a_{ij} \cdot B_j) \quad (8)$$

Where: a_{ij} is the effective search rate of predator j feeding on prey i , B_i is the biomass of the prey, B_j is the predator biomass, and v_{ij} is the vulnerability of prey i to predator j . The foundation of Eq. (3) is the

“foraging arena concept”, in which the prey biomass is divided into vulnerable and non-vulnerable components and the transfer rate between these two components is the vulnerability rate (v_{ij}), which determines whether the flow control is top-down ($v_{ij} > 2$), bottom-up ($v_{ij} < 2$), or mixed ($v_{ij} = 2$; the default values in EwE).

Using Ecosim module, we simulated the temporal variation of relative biomass (end/initial Biomass) for all groups in the first fifteen years of port expansion using some values of vulnerability settings: $v_{ij} = 1.0$; $v_{ij} = 2.0$ and $v_{ij} = 10$, according to the theory of the foraging arena (Ahrens et al., 2012). Ecosim module contains a routine to allow a ‘forcing function’ (FF), which represents a physical driving influence on components and trophic interactions, varying the search rate values (a_{ij}). As the port's expansion could provide a floor deck over the bay waters, we simulated a vast shading, using a negative exponential function to all trophic relations linked with primary producers in the system, i.e., forcing a fast decreasing of the primary production for the next 15 years. The relative biomass for all compartments was analyzed in this simulation period. We also simulated (using $v_{ij} = 2$ and without forcing function) an increasing capture of the top five keystone components, in order to understand their role on other organisms of the food web.

3. Results

3.1. Araçá Bay Ecopath model

The input values for balanced Araçá Bay model are showed in Table 1 and the diet composition is displayed in Table 2. The resulting food web highlights the relevance of benthos biomass and their links to the overall system (Fig. 2).

The Pedigree index value for Araçá Bay model was markedly high

(0.84) because we trust in the biomass estimates and in the diet composition depicted (see Table SM4 for all pedigree index values). Values for these parameters did not change during the balancing procedure.

Consistency and coherence of the model were analyzed using rates and relations among compartments (Link, 2010; Heymans et al., 2016). We found out that QB rates for benthos (calculated by equations (3) and (4)) were overestimated because Production/Consumption (P/Q) rates were not between 0.1 and 0.3 (Table SM5). Notwithstanding this arrangement and likely due to high predation, some benthos compartments did not display Respiration/Biomass (R/B) lower than 100, as expected (Table SM5). Likewise, R/B rate for fish and bird compartments did not satisfy the predicted condition (R/B lower than 10 and P/Q higher than 0.1; Table SM5). Most likely these organisms were influenced by the tidal fluctuation, which leads them to feed mainly out of the bay area, resulting in the high import in their diet composition (Table 2). All the import values summed represent just 0.005% of total consumption, resulting in a remarkable imbalance between fish biomass at high trophic levels (TL > 3.0 and B = 7.7) and at low ones (TL < 3.0 and B = 2.5). Import consumption and predation on benthos groups support higher biomass at upper TL. Despite this, the relation of B, PB and QB with TL in the Araçá Bay model was inverse that of what was predicted (Fig. SM1 and SM2). Benthos groups, however, remained noticeable because they represented 97% of flow to Detritus, 93% of the total biomass (Table 1) and were responsible for 68% of total consumption.

Yet benthos groups have an omnivory index (OI) equal to zero since they have just one feeding path (Table 1). *Centropomus* spp. had the highest OI (0.78) since it was the food web's top-predator (TL = 4.01).

The Araçá Bay food web showed mature features (Table 3), being detritus-based and showing very high values of Finn' cycling index (34.7%) and Detritivore/Herbivore ratio (1122; Table 3). Conversely,

Table 1

Basic input parameters and outputs (in bold) for Ecopath of the Araçá Bay: Trophic Level (TL); B. Biomass ($\text{g}\cdot\text{m}^{-2}$); PB. Production/Biomass ($\text{g}\cdot\text{m}^{-2}$); QB. Consumption/Biomass ($\text{g}\cdot\text{m}^{-2}\cdot\text{year}^{-1}$); EE. Ecotrophic Efficiency; Flow detr. Flow to Detritus ($\text{g}\cdot\text{m}^{-2}\cdot\text{year}^{-1}$); OI. Omnivory Index.

n.	Group name	TL	B	PB	QB	EE	Flow detr	OI
1	Phytoplankton	1	1.286	347.17		0.959	18.16	
2	Phytobenthos	1	27.500	121.60		0.002	3337.19	
3	Mangrove	1	49.000	0.17		0.016	8.34	
4	Zooplankton	2.10	0.375	40.00	160.00	0.917	25.25	0.11
5	Gastropoda	2.53	20.770	12.25	65.00	0.022	788.84	0.29
6	<i>Olivella minuta</i>	2.97	130.780	69.82	219.00	0.001	20580.27	0.19
7	Bivalve	2.00	201.600	55.20	402.00	0.977	32671.60	0
8	<i>Anomalocardia brasiliana</i>	2.00	249.580	55.78	541.00	0.010	67788.57	0
9	Polychaeta	2.30	194.000	70.00	354.00	0.855	29443.88	0.21
10	Capitellidae	2.00	80.760	65.30	469.00	0.001	20417.09	0
11	<i>Laonereis culveri</i>	2.00	46.680	13.22	129.00	0.231	2883.34	0
12	Oligochaeta	2.00	15.520	5.21	50.00	0.089	384.15	0
13	<i>Monokalliapseudes schubarti</i>	2.00	224.190	114.27	780.00	0.894	72660.95	0
14	Echinodermata	2.00	0.560	0.60	6.00	0.000	1.68	0
15	<i>Dasyatis</i> spp.	3.23	0.001	0.50	6.35	0.020	0.00	0.65
16	<i>Haemulopsis corvinaeformis</i>	3.16	1.483	2.13	11.31	0.321	5.50	0.09
17	<i>Diapterus rhombeus</i>	3.20	0.444	1.20	10.50	0.907	0.98	0.08
18	<i>Mugil curema</i>	2.00	1.190	2.00	36.30	0.617	13.87	0.15
19	<i>Mugil liza</i>	2.00	0.058	0.56	21.60	0.015	0.41	0.15
20	<i>Atherinella brasiliensis</i>	2.38	0.792	1.78	15.90	0.988	3.79	0.28
21	<i>Centropomus</i> spp.	4.01	0.570	0.26	8.40	0.686	1.00	0.78
22	<i>Sphoeroides</i> spp.	3.00	0.340	1.25	8.72	0.268	0.90	0.25
23	<i>Trichinurus lepturus</i>	3.74	0.156	1.21	6.20	0.005	0.38	0.39
24	<i>Sardinella brasiliensis</i>	2.44	0.139	1.42	24.26	0.985	1.01	0.41
25	Planktivore	2.88	0.322	1.00	10.00	0.482	1.13	0.20
26	Benthivore	3.22	3.328	1.50	9.20	0.596	8.14	0.10
27	Hyperbenthivores-piscivores	3.40	1.187	0.71	4.68	0.923	1.18	0.65
28	Shrimp	2.00	0.021	7.75	26.70	0.683	0.28	0
29	Crabs	2.93	0.720	1.40	19.08	0.710	5.79	0.30
30	Turtles	2.53	0.068	0.15	2.54	0.000	0.06	0.27
31	<i>Coragyps atratus</i>	2.27	0.330	0.10	40.00	0.000	2.67	0.40
32	Waterbirds	3.41	0.200	0.40	50.00	0.000	2.08	0.24
33	Detritus Mangrove	1			Total	Input	8.34	
34	Detritus	1			Total	Input	251058.50	

Table 2
Diet composition for the Araçá Bay Ecopath model. Columns: consumer; Rows: food items. Sum of rows = 1.

	Prey	Consumer	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	
1	Phytoplankton		0.25	0.3									0.05				0.05	0.05	0.35				0.2	0.2			0.3					
2	Phytobenthos												0.1				0.05	0.05	0.3				0.1									
3	Mangrove																												0.8			
4	Zooplankton		0.1													0.02			0.35				0.2	0.8					0.01			
5	Gastropoda													0.12											0.15					0.1	0.1	
6	<i>Olivella minuta</i>													0	0.1										0.1			0.1	0	0.1	0.1	
7	Bivalve							0.05						0.05	0.1					0.7					0.1	0.14		0.1	0.1	0.1	0.1	
8	<i>A. brasiliiana</i>													0	0.1	0									0.1			0.1		0.1	0.1	
9	Polychaeta													0.18	0.22	0.83									0.15	0.12		0.1	0.1	0.1	0.1	
10	Capitellidae														0.1	0									0.1			0.1		0.1	0.1	
11	<i>L. culveri</i>														0.12	0									0.1			0.1		0.1	0.1	
12	Oligochaeta														0.14	0									0.1	0.07		0.1		0.1	0.1	
13	<i>M. schubarti</i>							0.25						0.15	0.12	0.1									0.1			0.1				
14	Echinodermata																															
15	<i>Dasyatis</i> spp.																															
16	<i>H. corvinaeformis</i>																														0.1	
17	<i>D. rhombeus</i>																			0.1												
18	<i>Mugil curema</i>																			0.05			0.22								0.1	
19	<i>Mugil liza</i>																															
20	<i>A. brasiliensis</i>																															
21	<i>Centropomus</i> spp.																			0.12			0.13			0.12						
22	<i>Sphaeroides</i> spp.																					0.1										
23	<i>Trichiurus lepturus</i>																									0.02						
24	<i>S. brasiliensis</i>																															
25	Planktivore																					0.2										
26	Benthivore																			0.25		0.1			0.01						0.1	
27	Hyperbenthivores-piscv																			0.15		0.05										
28	Shrimp																									0.02						
29	Crabs																									0.01						
30	Turtles																														0.05	
31	<i>Coragyps arratus</i>																															
32	Waterbirds																															
33	Detritus Mangrove																															
34	Detritus		0.65	0.2	0.15	1	1	0.7	1	1	1	1	0.85			0.05	0.25	0.25										0.7	0.05		0.1	0.2
35	Import													0.5			0.65	0.65	0.33	0.3			0.5		0.39					0.65		
36	Sum		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	

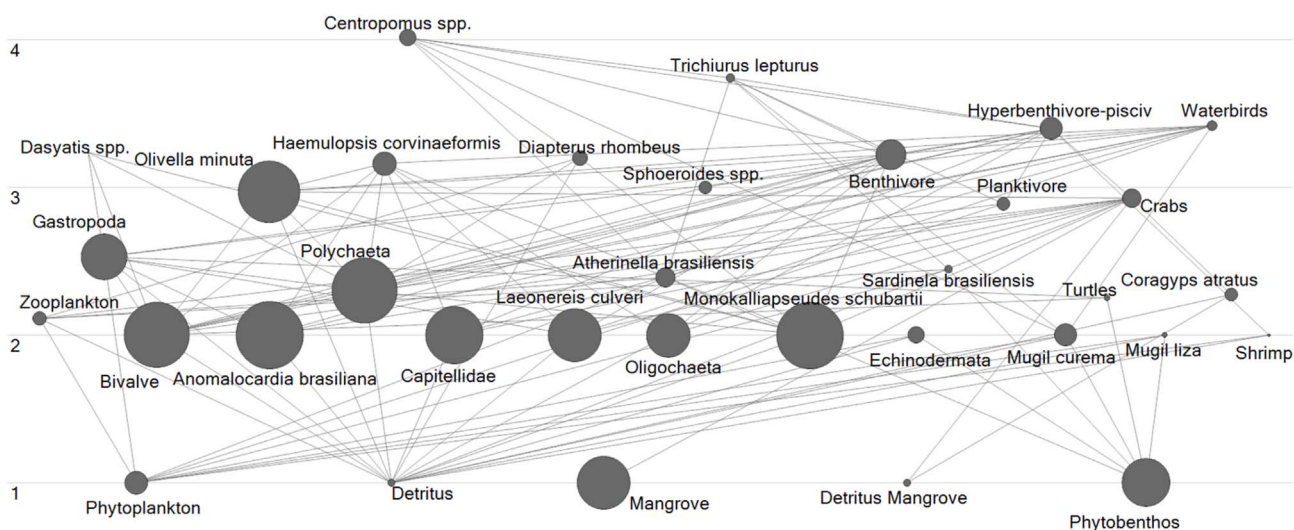


Fig. 2. Flow diagram of the Ecopath model for Araçá Bay (Brazil). Axes Y: Trophic Level position; Size of nodes represents compartment's biomass.

Table 3
Ecosystems attributes revealed by Araçá Bay Ecopath model.

Parameter	Value	Unit
Sum of all consumption	534506.2	$g^*m^{-2}year^{-1}$
Sum of all exports	0.09	$g^*m^{-2}year^{-1}$
Sum of all respiratory flows	241092.0	$g^*m^{-2}year^{-1}$
Sum of all flows into detritus	231060.5	$g^*m^{-2}year^{-1}$
Total system throughput	1006659.0	$g^*m^{-2}year^{-1}$
Sum of all production	83435.0	$g^*m^{-2}year^{-1}$
Calculated total net primary production	3798.9	$g^*m^{-2}year^{-1}$
Total Primary Production/Total Respiration	0.02	
Total Primary Production/Total Biomass	3.030	
Total Biomass/Total Throughput	0.001	
Total Biomass (excluding detritus)	1253.95	
Connectance Index	0.112	
System Omnivory Index	0.160	
Development Capacity (flowbits)	4138390	flowbits
Ascendency	24.08	%
Overhead	75.90	%
Finn's cycling index	34.70	% of total throughput
Total Transfer Efficiencies	1.65	%
Flow from PP to Trophic Level II	435.2	$g^*m^{-2}year^{-1}$
Flow from Detritus to Trophic Level II	488308.0	$g^*m^{-2}year^{-1}$
Ratio Detritivorie/Grazing	1122.03	
Pedigree index	0.844	

values for Total Primary Production/Total Respiration (TPP/TR), Total Biomass/Total Flow Throughput (TB/TFT) and Connectance index indicated an immature system (Table 3), but confirms the Detritus' relevance.

The Matrix Trophic Impact (Fig. 3) indicated that groups like *Trichiurus lepturus*, *Centropomus* spp., Waterbirds and Detritus have a greater influence on larger numbers of compartments than benthic groups. As a result, the keystone index indicates as key species in Araçá Bay (in order): *T. lepturus*, Waterbirds, *Coragyps atratus*, *Centropomus* spp., Hyperbenthivores-piscivores, Crabs, and Benthivores (see the full list in Table SM6).

3.2. Simulation outputs

The running of the Araçá Bay model using a negative exponential as a forcing function on all trophic relations linked with primary producers (to simulate a shadowing effect of port expansion) depicted the collapse of almost all groups (Fig. 4 with $v_{ij} = 2$). *Sardinella brasiliensis* is an exception and its final relative biomass would increase almost 500

times in 15 years after impact likely because its high import in diet composition. Detritus and Mangrove Detritus would also increase more than 100,000 times after five years, indicating a Detritus accumulation. Using vulnerability values ($v_{ij} = 10$ (top = down control) a very similar output to Fig. 4 was found (Fig. SM3). On the contrary, using $v_{ij} = 1$ (bottom-up control) all biomass compartments decreased quickly (Fig. 5).

We also simulated an increase catch for the top five keystone components (*T. lepturus*, Waterbirds, *C. atratus*, *Centropomus* spp., and Hyperbenthivores-piscivores) and the outputs show a relative influence on other components and on their own biomass (Fig. 6). It is interesting that despite increasing the catch, Hyperbenthivore-piscivore and *T. lepturus* could increase showing an unexpected result and the food web complexity.

4. Discussion

The Araçá Bay Ecopath food web model was constructed based on a multidisciplinary, model-oriented research project, making possible a high quality sampling design especially used to convert observed values into information needed to parameterize a food web model. The model outputs showed that Araçá Bay is a mature and detritus-based ecosystem and it is highly influenced by the role of benthos groups responsible for a large amount of Detritus recycling. The simulation of port expansion (primary producers' reduction) indicated a strong negative impact on almost all living groups and the increase in Detritus accumulation, leading the entire bay ecosystem to collapse (in the short term). Besides this, it seems that the food web is top-down control because the outputs using vulnerabilities rate values ($v_{ij} = 2$ or $v_{ij} = 10$) look similar and different to a bottom-up condition ($v_{ij} = 1$). This latter option seems unlikely since no ecological component showed an advantage with the simulated impact.

One of the main issues on ecological modeling is the model's representativeness raising the concerns whether the model is good enough to describe and simulate an ecosystem, markedly when severe changes are intended, such as in Araçá Bay. Usually, the confidence in Ecopath models is enhanced by its calibration using time series data on fishing and/or biomass of other organisms (Shannon et al., 2003). Like in many other Brazilian environments, there were no times series data available for Araçá Bay to allow for an appropriate calibration procedure. To overcome this paucity in data, model's consistency was verified through the Prebal analysis. This revealed realistic and coherent rates for the groups' metabolism (such as respiration, consumption, assimilation and other) in respect to their trophic levels. The quality of

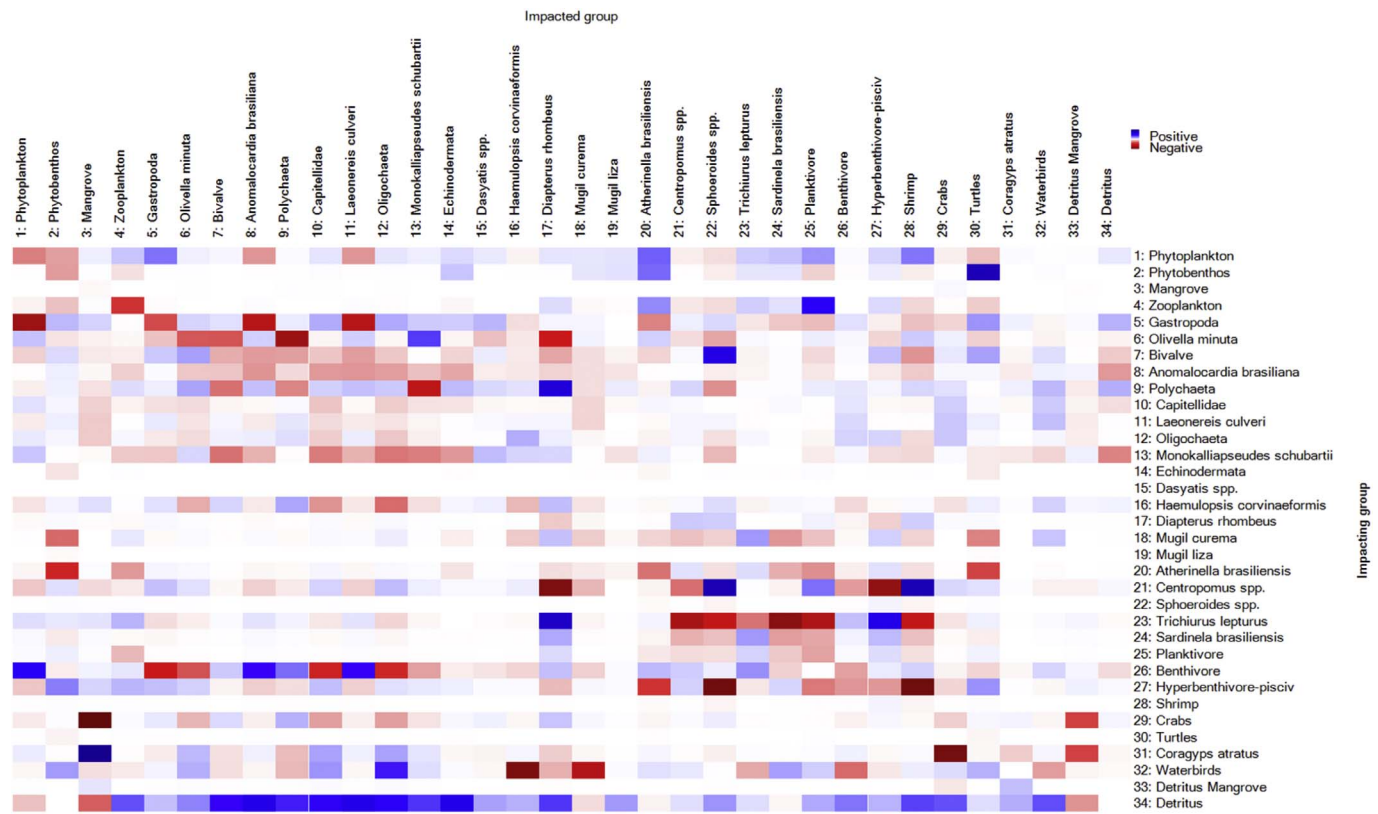


Fig. 3. Trophic Impact analysis matrix for Araçá Bay Ecopath model (Brazil). Rows: impacting group; Columns: Impacted groups. Blue: positive impact; Red: Negative impact. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

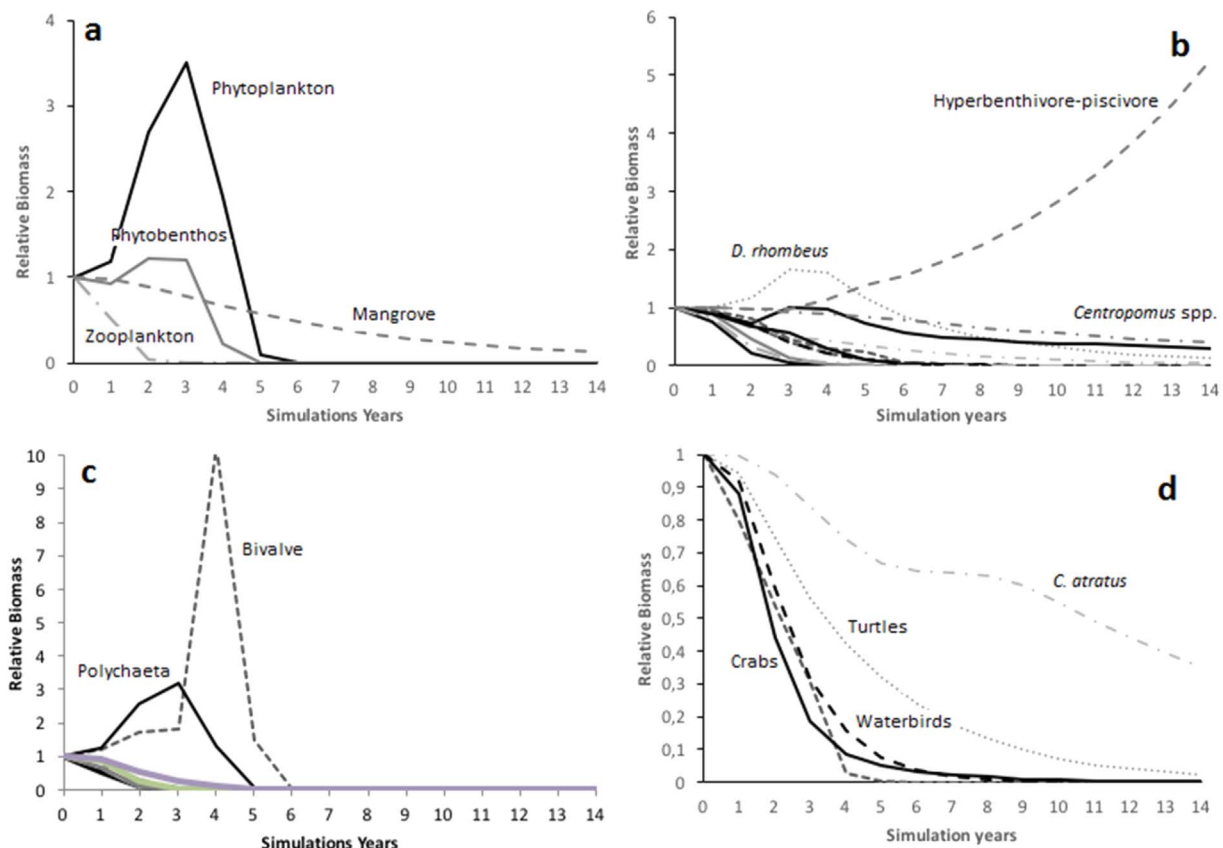


Fig. 4. Outputs of temporal simulations of Araçá Bay Ecopath model (Brazil) with forcing function reducing the primary producers and $v_{ij} = 2$ (vulnerabilities values). a) Primary Producers and Zooplankton; b) All fish compartments (exception is *S. brasiliensis*, see text); c) Benthos compartments; d) Other compartments. Some compartments were not highlighted.

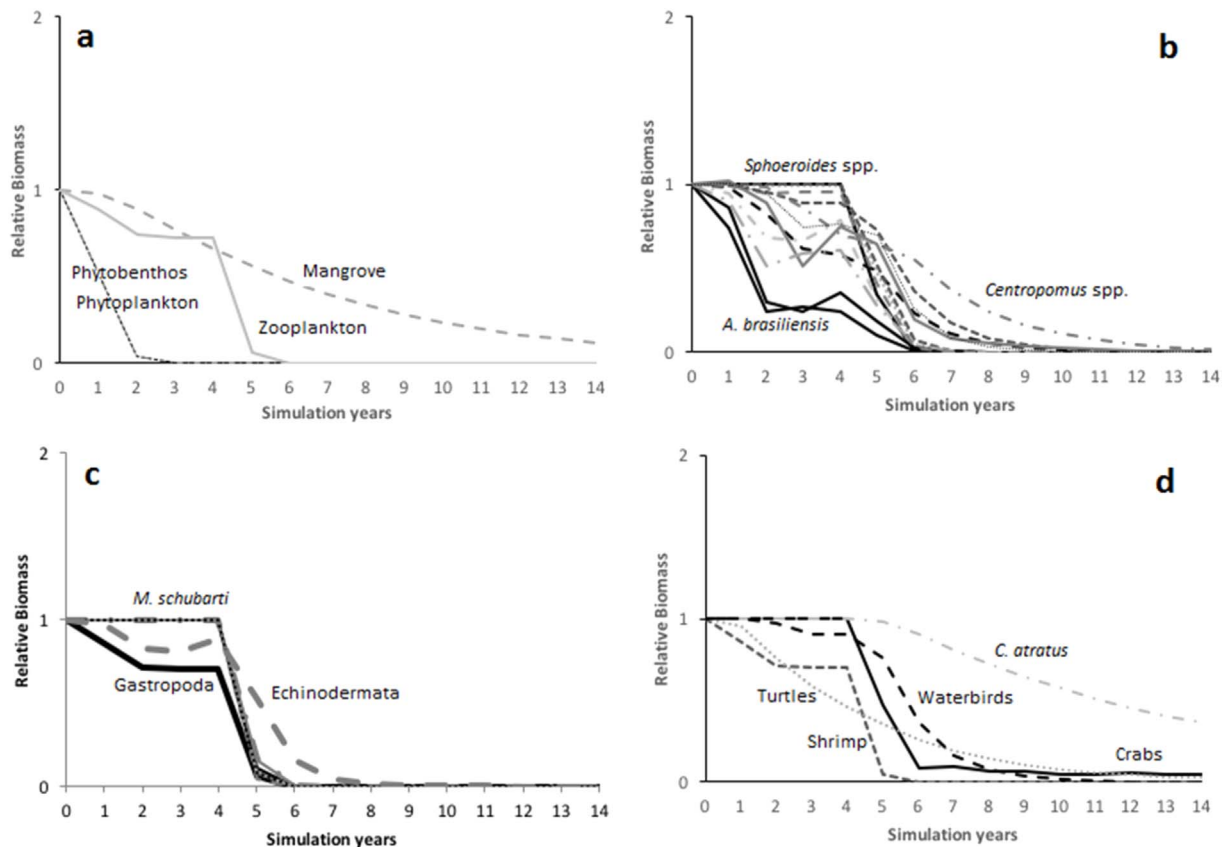


Fig. 5. Outputs of temporal simulations of Araçá Bay Ecopath model (Brazil) with forcing function reducing the primary producers and $v_{ij} = 1$ (vulnerabilities values). a) Primary Producers and Zooplankton; b) All fish compartments; c) Benthos compartments; d) Other compartments. Some compartments were not highlighted.

input data, valued by Pedigree index, was very high when compared to other models (see Colléter et al., 2015), emphasizing the value of a model-oriented research project. The systematically planned surveys methods provided the biomass estimates needed, which is the most sensitive parameter of Ecopath models and allowed the proper conversion from observed data to grams per square meter (Ecopath' unit). Besides, most rates are estimated for overall groups through broad equations like in Tumbiolo and Downing (1994), sometimes leading to poor estimates. Also, in the Araçá Bay model, the identification of overestimates in benthos consumption rate by the Prebal diagnosis underlined the shortage of good equations and rate estimates for tropical species.

To the extent of our knowledge, the absolute ($1163.88 \text{ g}\cdot\text{m}^{-2}$) and

relative (93%) biomasses of benthos recorded in Araçá Bay are the highest biomass entered in Ecopath models found so far. Despite the role of benthos' biomass, it has been shown relatively relevant in other bay Ecopath models (Du et al., 2015; Dutta et al., 2017) sometimes resulting in high recycling (Lin et al., 2004; Byron et al., 2011; Frisk et al., 2011). The biomass unveiled in Araçá Bay produced a high Detritivore/Herbivore rate (more than 1000) and a Finn recycling index of 32%, higher than values previously registered in Ecopath models in other bay areas (see for example, Sakamoto and Shirakihara, 2017; Chen et al., 2015).

Detritus-based ecosystems tend to be more resilient (sensu Odum, 1969) and are expected to hold up benthos groups that support high overhead value (75%), which measures the reserve of energy in the

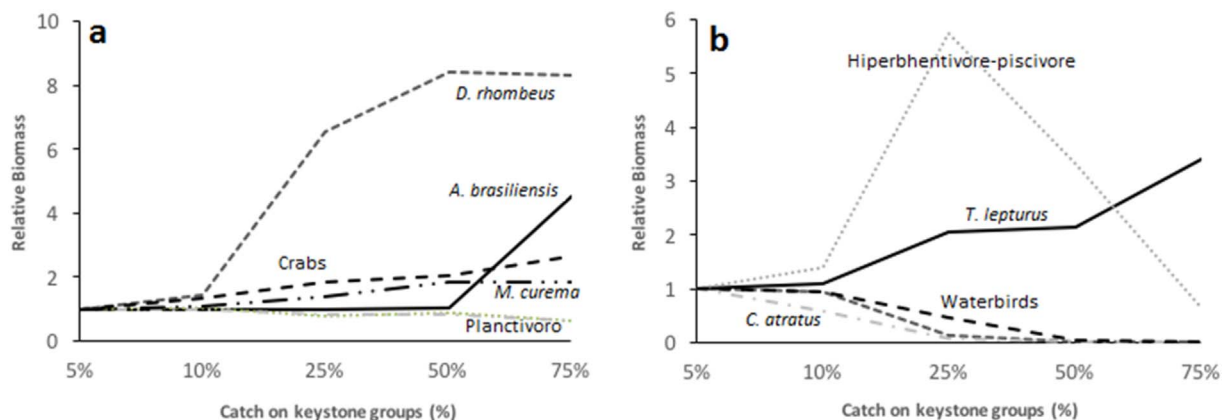


Fig. 6. Outputs of temporal simulation of catch on main five keystone groups. Catch percentage values are relative to initial biomass of each group. a) other groups; b) five keystone groups. Groups that are not shown did not have meaningful changes.

ecosystem (Ulanowicz, 1986). In bay environments, benthos groups are considered more resistant to climate change than other groups, especially if functional diversity is high (Taylor et al., 2008). Beyond the noteworthy biomass, benthos diversity is also high in Araçá Bay (Corte et al., 2017), turning the benthos groups into a permanent source of food for other organisms, acting as an efficient “engine” to recycle detritus and the main structuring live group in Araçá Bay. The role played by benthos groups is likely been influenced by its higher stability. While other groups are forced to leave the bay during low tide, the benthic groups remain in the bottom of the bay and are less influenced by tide fluctuation and other outside factors.

Notwithstanding the central importance of benthos, they are not the keystones group appointed by Ecopath outputs. Keystone species concept suggests that they have a low biomass and a high impact on other groups (Valls et al., 2015). In the Araçá Bay model the keystone groups identified (*T. lepturus*, Waterbirds, *C. atratus*, *Centropomus* spp., Hyperbenthivore-piscivore) have trophic level (TL) values higher than 3. Any change in these keystone species is expected to potentially alter the entire food web. Indeed, the absence of *T. lepturus* in the model simulations caused dissimilar dynamics in many species (see below). However, the simulation on these five key components did not disturbed the system compared to the port expansion impact.

Nevertheless, the resilient condition for Araçá Bay food web, simulation of the shading impact on the bay (due to the port expansion) indicates, at first, an increase of Phytoplankton, followed by increasing bivalves (Phytoplankton's consumer and benefited by predator's decline at the beginning of the simulations). However, with the large accumulation of Detritus on the bay, the majority of groups would be affected afterward and would tend to become extinct within a period of seven years. The exceptions would be *D. rhombeus*, while its main prey (Polichaetas) maintains itself, and Hyperbenthivore-piscivore that would grow probably due to the reduction in their main predators (*T. lepturus* and *Centropomus* spp.). Groups such as *Centropomus* spp. and *C. atratus* decrease slowly, likely because of the high percentage of imports in their diets. Accordingly, *S. brasiliensis*' biomass had a huge increase (almost 500 times) because of an import of 50% in its diet, which determines its low dependency on the bay environment, and because the decrease in its predator (*T. lepturus*). Consideration needs to be given as to the degree to which the bay turns shaded after the possible port expansion. It would be highly unlikely that the schools of *S. brasiliensis* would return to the bay.

In a broader view, simulation outputs showed that a port expansion of the Araçá Bay environment would cause an unrelenting impact on organisms and environmental quality (due to Detritus accumulation). However, like all mathematical models, our model portrays a picture of the reality. The inclusion of São Sebastião Channel area (Fig. 1) could substantially improve the model because Araçá Bay has a small area to which the majority of organisms move in and out according to tide fluctuations. In this sense, the use of Ecospace approach (Lewis et al., 2016) could be promising. It would allow for the inclusion of different habitats and the simulation of advantages and disadvantages of the implementation of a Marine Protected Area (MPA) on this small area, which could be considered a permanent “evolutionary hotspot” (Barthem and Goulding, 2007), to be used for migratory species and because it concentrates a high species richness, especially benthos groups.

5. Conclusion

All ecological investigation involves choices about researches priorities, which consequently define objectives, sampling design and outputs analysis (Jones and Paramor, 2010). Here, by carrying out an ecosystem-based research and model-oriented project, with specific sampling procedures per group of organism which could effectively integrate the multi-disciplinary information in a single mathematical structure (Ecopath model) which, in an interdisciplinary way, allowed the quantification of Araçá Bay food web. The Ecopath approach is a

key tool for the ecosystem-approach to fisheries and marine resources. It is useful to identify patterns and accessible to wide applications, because it was the first ecosystem-level simulation model to be freely available (Christensen and Maclean, 2011).

Our Ecopath model simulations indicated the probable harsh impact of a port expansion over Araçá Bay revealing that the environmental dynamic will be severely ruined due to the dangerous accumulation of Detritus, with negative consequences for human health.

The last Ecopath conference held in 2014 identified that modelers have failed to communicate the value and relevance of their work to management advisors (Coll et al., 2015). The model application and outputs presented here are an example of how objectively planned sample design and modeling may steer scientists, local people and stakeholders' decisions on the dilemma of conservation or ‘development’ and on the sustainable use of natural areas and its living resources.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at <http://dx.doi.org/10.1016/j.ocecoaman.2018.02.007>.

References

- Aarts, G., Benda-Beckmann, A., Lucke, K., Sertle, H.O., Bemmelen, R., Geelhoed, S.C.V., Brasseur, S., Scheidat, M., Lam, F.P.A., Slabbekoorn, H., Kirkwood, R., 2016. Harbour porpoise movement strategy affects cumulative number of animals acoustically exposed to underwater explosions. *Mar. Ecol. Prog. Ser.* 557, 261–275. <http://dx.doi.org/10.3354/meps11829>.
- Ahmed, N., Cheung, W.W.L., Thompson, S., Glaser, M., 2017. Solutions to blue carbon emissions: shrimp cultivation, mangrove deforestation and climate change in coastal Bangladesh. *Mar. Pol.* 82, 68–75. <http://dx.doi.org/10.1016/j.marpol.2017.05.007>.
- Ahrens, R.N.M., Walters, C.J., Christensen, V., 2012. Foraging arena theory. *Fish.* 13, 41–59.
- Allen, K.R., 1971. Relation between production and biomass. *J. Fish. Res. Board Can.* 28, 1573–1581.
- Amaral, A.C.Z., 2014. 2o Research Project Report: biodiversity and Functioning of a Subtropical Coastal Ecosystem: a Contribution to an Integrated Management. Benthic System. pp. 10–24 In Portuguese language. Biota/Fapesp (SP-Brazil). 51p.
- Amaral, A.C.Z., 2015. 2o Research Project Report: biodiversity and Functioning of a Subtropical Coastal Ecosystem: a Contribution to an Integrated Management. Nekton System. pp. 1–24 In Portuguese language. Biota/Fapesp (SP-Brazil). 29p.
- Angelini, R., Morais, R.J., Catella, A.C., Resende, E.K., Libralato, S., 2013. Aquatic food webs of the oxbow lakes in the Pantanal: a new site for fisheries guaranteed by alternated control? *Ecol. Model.* 253, 82–96.
- APHA, American Public Health Association, 2012. Standard Methods for the Examination of Water and Wastewater. APHA, AWWA, WEF 22nd Ed.
- Barthem, R., Goulding, M., 2007. An Unexpected Ecosystem: the Amazon as Revealed by Fisheries. Amazon Conservation Association, (ACA, Sociedade Civil Mamiurá). Biblos Grafica, Peru, pp. 241.
- Bonaldo, R.M., Pires, M.M., Guimar??es, P.R., Hoey Jr., A.S., Hay, M.E., 2017. Small marine protected areas in Fiji provide refuge for reef fish assemblages, feeding groups, and corals. *PLoS One* 12 (1). <http://dx.doi.org/10.1371/journal.pone.0170638>.
- Branco, J.O., Moritz Jr., H.C., 2001. Alimentação natural do camarão sete-barbas, *xi-phenaeus kroyeri* (heller) (Crustacea, Decapoda), na armação do Itapocory, Penha, Santa Catarina. *Rev. Bras. Zool.* 18 (1), 53–61.
- Byron, C., Link, J., Costa-Pierce, B., Bengtson, D., 2011. Calculating ecological carrying capacity of shellfish aquaculture using mass-balance modeling: Narragansett Bay, Rhode Island. *Ecol. Model.* 222 (10), 1743–1755. <http://dx.doi.org/10.1016/j>

- ecolmodel.2011.03.010.
- Chen, Z., Xu, S., Qiu, Y., 2015. Using a food-web model to assess the trophic structure and energy flows in Daya Bay, China. *Contin. Shelf Res.* 111, 316–326. <http://dx.doi.org/10.1016/j.csr.2015.08.013>.
- Cheng, J.H., Cheung, W.W.L., Pitcher, T.J., 2009. Mass-balance ecosystem model of the East China sea. *Prog. Nat. Sci.* 19, 1271–1280.
- Christensen, V., Walters, C.J., 2004. Ecopath with Ecosim: methods, capabilities and limitations. *Ecol. Model.* 172, 109–139 Amsterdam.
- Christensen, V., Pauly, D., 1992. ECOPATH II - a software for balancing steady-state ecosystem models and calculating network characteristics. *Ecol. Model.* 61, 169–185 Amsterdam.
- Christensen, V., Walters, C.J., Pauly, D., Forrest, R., 2008. Ecopath with Ecosim Version 6. User Guide. pp. 235.
- Christensen, V., Maclean, J., 2011. *Ecosystem Approaches to Fisheries: a Global Perspective*. Cambridge University Press, Cambridge, pp. 343.
- Coll, M., Akoglu, E., Arreguin-Sanchez, F., Fulton, E., Gascuel, D., Heymans, J., Libralato, S., Mackinson, S., Palomera, I., Piroddi, C., 2015. Modelling dynamic ecosystems: venturing beyond boundaries with the Ecopath approach. *Rev. Fish Biol. Fish.* 25, 413–424.
- Colléter, M., Valls, A., Guitton, J., Gascuel, D., Pauly, P., Christensen, V., 2015. Global overview of the applications of the Ecopath with Ecosim modelling approach using the EcoBase models repository. *Ecol. Model.* 302, 42–53.
- Contente, R.F., Rossi-Wongtschowski, C.L.D.B., 2017. Improving the characterization of fish assemblage structure through the use of multiple sampling methods: a case study in a subtropical tidal flat ecosystem. *Environ. Monit. Assess.* 189, 251. <http://dx.doi.org/10.1007/s10661-017-5954-y>.
- Corte, G.N., Checon, H.H., Fonseca, G., Vieira, D.C., Gallucci, F., Di Domenico, M., Amaral, A.C.Z., 2017. Cross-taxon congruence in benthic communities: searching for surrogates in marine sediments. *Ecol. Indic.* 173–182. <http://dx.doi.org/10.1016/j.ecolind.2017.03.031>.
- Donohue, I., Petchey, O.L., Kéfi, S., Genin, A., Jackson, A.L., Yang, Q., O'Connor, N.E., 2017. Loss of predator species, not intermediate consumers, triggers rapid and dramatic extinction cascades. *Global Change Biol.* 23, 2962–2972. <http://dx.doi.org/10.1111/gcb.13703>.
- Du, J., Cheung, W.W.L., Zheng, X., Chen, B., Liao, J., Hu, W., 2015. Comparing trophic structure of a subtropical bay as estimated from mass-balance food web model and stable isotope analysis. *Ecol. Model.* 312, 175–181.
- Dunning, J.B., 1992. *CRC Handbook of Avian Body Masses*. CRC Press, Boca Raton, Florida.
- Dutta, S., Chakraborty, K., Hazra, S., 2017. Ecosystem structure and trophic dynamics of an exploited ecosystem of Bay of Bengal, Sundarban Estuary, India. *Fish Sci.* 83, 145–159. <http://dx.doi.org/10.1007/s12562-016-1060-2>.
- Ellis, H.I., Gabrielsen, G.W., 2002. Energetics of free-ranging seabirds (Orgs.) In: Schreiber, E.A., Burger, J. (Eds.), *Biology of Marine Birds*, CRC Marine Biology Series. CRC Press, USA, pp. 359–407.
- Erlandson, J.M., Rick, T.C., Braje, T.J., Steinberg, A., Vellanoweth, R.L., 2008. Human impacts on ancient shellfish: a 10,000 year record from San Miguel Island, California. *J. Archaeol. Sci.* 35, 2144–2152.
- Frisk, M.G., Miller, T.J., Latour, R.J., Martell, S.J.D., 2011. Assessing biomass gains from marsh restoration in Delaware Bay using Ecopath with Ecosim. *Ecol. Model.* 222, 190–200. <http://dx.doi.org/10.1016/j.ecolmodel.2010.08.026>.
- Freese, R., Pauly, D., 2017. FishBase. World Wide Web Electronic Publication. version (02/2017). www.fishbase.org.
- Gasparini, S., Antajan, E., 2013. Plankton identifier software: guide. Available in: http://www.obs-vlfr.fr/~gaspari/Plankton_Identifier/userguide.html.
- Gorsky, G., Ohman, M.D., Picheral, M., Gasparini, S., Stemmann, L., Romagnan, J.B., Cawood, A., Pesant, S., García-Comas, C., Prejger, F., 2010. Digital zooplankton image analysis using the ZooScan integrated system. *J. Plankton Res.* 32 (3), 285–303. <http://dx.doi.org/10.1093/plankt/fbp124>.
- Giannini, M.F.C., Ciotti, A.M., 2016. Parameterization of natural phytoplankton photo-physiology: effects of cell size and nutrient concentration. *Limnol. Oceanogr.* 61 (4), 1495–1512. <http://dx.doi.org/10.1002/lno.10317>.
- Gubitoso, S., Duleba, W., Teodoro, A.C., Prada, S.M., d. Rocha, M.M., Lamparelli, C.C., Bevilacqua, J.E., Moura, D.O., 2008. Estudo geoambiental da região circunjacente ao emissário submarino de esgoto do Aracá, São Sebastião (SP). *Rev. Bras. Geociências* 38, 467–475.
- Hernández-León, S., Montero, I., 2006. Zooplankton biomass estimated from digitized images in Antarctic waters: a calibration exercise. *J. Geophys. Res.* 111, C05S03. <http://dx.doi.org/10.1029/2005JC002887>.
- Heymans, S., Coll, M., Libralato, S., Christensen, V., 2011. Ecopath theory, modelling and application to coastal ecosystems. In: In: McLusky, D., Wolanski, E. (Eds.), *Treatise on Estuarine and Coastal Science*, vol. 9. Elsevier, pp. 93–111. <http://dx.doi.org/10.1016/B978-0-12-374711-2.00905-0>.
- Heymans, J.J., Coll, M., Link, J.S., Mackinson, S., Steenbeek, J., Walters, C., Christensen, V., 2016. Best practice in Ecopath with Ecosim food-web models for ecosystem-based management. *Ecol. Model.* 331, 173–184.
- Humphreys, W.F., 1979. Production and respiration in animal populations. *J. Anim. Ecol.* 48, 427–453.
- Hutubessy, B.G., Mosse, J.W., van Zwieten, P.A.M., Hayward, P., 2014. Towards an ecosystem approach to small island fisheries: a preliminary study of a balanced fishery in Kotania Bay (Seram Island, Indonesia). *J. Mar. I. Cult.* 3, 98–105.
- Jones, K.E., Paramor, O.A.L., 2010. Interdisciplinary in ecosystems research: developing social robustness in environmental science. In: Raffaelli, D.G., Frid, C.L.J. (Eds.), *Ecosystem Ecology: a New Synthesis*. Cambridge Press, pp. 94–109.
- Lamas, R.A., Rossi-Wongtschowski, C.L.D.B., Contente, R.F., 2016. Checklist of the fish fauna of the Aracá bay, São Sebastião Channel, northern coast of São Paulo, Brazil. *Check List.* 12 (6), 2004. <http://dx.doi.org/10.15560/12.6.2004>.
- Lehette, P., Hernández-León, S., 2009. Zooplankton biomass estimation from digitized images: a comparison between subtropical and Antarctic organisms. *Limnol. Oceanogr. Methods* 7, 304–308.
- Lewis, K.A., Mutsert, K., Steenbeek, J., Peele, H., Cowan Jr., J.H., Buszowski, J., 2016. Employing ecosystem models and geographic information systems (GIS) to investigate the response of changing marsh edge on historical biomass of estuarine nekton in Barataria Bay, Louisiana, USA. *Ecol. Model.* 331, 129–141. <http://dx.doi.org/10.1016/j.ecolmodel.2016.01.017>.
- Libralato, S., Christensen, V., Pauly, D., 2006. A method for identifying keystone species in food web models. *Ecol. Model.* 195, 153–171.
- Lin, H.J., Shao, K.T., Hwang, J.S., Lo, W.T., Cheng, I.J., Lee, L.H., 2004. A trophic model for Kuosheng Bay in northern Taiwan. *J. Mar. Sci. Technol.* 12 (5), 424–432.
- Link, J.S., 2010. Adding rigor to ecological network models by evaluating a set of pre-balance diagnostics: a plea for PREBAL. *Ecol. Model.* 221, 1580–1591.
- Lopes, M.S., Bertucci, T.C.P., Tubino, R.A., Monteiro-Neto, C., Tomas, A.R.G., Tenório, M.A., Lima, T., Souza, R., Carrilo-Briceno, J.D., Haimovici, M., Macario, K., Csrvalho, C., Aguilera, O., 2016. The path towards endangered species: prehistoric fisheries in southeastern Brazil. *PLoS One* 11 e0154476–36.
- Mantelatto, F.L.M., Christofoletti, R.A., 2001. Natural feeding activity of the crab *Callinectes ornatus* (Portunidae) in Ubatuba Bay (São Paulo, Brazil): influence of season, sex, size and molt stage. *Mar. Biol.* 138, 585–594.
- Mantelatto, F.L.M., Petracco, M., 1997. Natural diet of the crab *Hepatus pubibundus* (Brachyura: calappidae) in Fortaleza bay, Ubatuba (SP), Brazil. *J. Crustac Biol.* 17 (3), 440–446.
- Odum, E.P., 1969. The Strategy of ecosystem development. *Science* 164, 262–270.
- Paine, R.T., 1995. A conversation on refining the concept of keystone species. *Conserv. Biol.* 9 (4), 962–964.
- Palomares, M.L.D., Pauly, D., 1998. Predicting food consumption of fish populations as functions of mortality, food type, morphometrics, temperature and salinity. *Mar. Freshw. Res.* 49 (5), 447–453.
- Pauly, D., 1980. On the interrelationships between natural mortality, growth-parameters, and mean environmental-temperature in 175 fish stocks. *J. Du Cons.* 39, 175–192.
- Piroddi, C., Coll, M., Lique, C., Macias, D., Greer, K., Buszowski, J., Steenbeek, J., Danovaro, R., Christensen, V., 2017. Historical changes of the Mediterranean Sea ecosystem: modelling the role and impact of primary productivity and fisheries changes over time. *Nat. Sci. Rep.* 7, 44491. <http://dx.doi.org/10.1038/srep44491>. 1–18pp.
- Polovina, J., 1984. Model of a coral reef ecosystem I: the Ecopath model and its application to French Frigate Shoals. *Coral Reefs* 3 (1), 1–11.
- Rocha, G.R.A., Rossi-Wongtschowski, C.L.D.B., Pires-Vanin, A.M.S., Soares, L.S.H., 2007. Trophic models of São Sebastião Channel and continental shelf systems, SE Brazil. *Panamias* 2 (2), 149–162.
- Sakamoto, A., Shirakihara, K., 2017. Ecosystem dynamics in Tokyo Bay with a focus on high trophic levels using Ecopath with Ecosim. *J. Mar. Sci. Technol.* 22, 1–10. <http://dx.doi.org/10.1007/s00773-016-0388-8>.
- Shannon, L.J., Moloney, C.L., Jarre, A., Field, J.G., 2003. Trophic flows in the southern Benguela during the 1980 and 1990. *J. Mar. Syst.* 39 (1–2), 83–116.
- Soares, L.S.H., Arantes, L.P., Pucci, M.C., 2016. Food web baseline of Aracá Bay, Atlantic southwestern: spatio-temporal variations in the d13C and d15N isotope values of suspended particulate matter, surface sediment organic matter and micro-phytobenthos. *Front. Mar. Sci. Conf. Abstract: XIX Iber. Symp. Mar. Biol. Stud.* <http://dx.doi.org/10.3389/conf.FMARS.2016.05.00163>.
- Taylor, M.H., Wolff, M., Mendo, J., Yamashiro, C., 2008. Changes in trophic flow structure of Independence Bay (Peru) over an ENSO cycle. *Prog. Oceanogr.* 79, 336–351. <http://dx.doi.org/10.1016/j.pocean.2008.10.006>.
- Torres, M.A., Coll, M., Heymans, J.J., Christensen, V., Sobrino, I., 2013. Food-web structure of and fishing impacts on the Gulf of Cadiz ecosystem (South-western Spain). *Ecol. Model.* 265, 26–44.
- Tumbiolo, M.L., Downing, J.A., 1994. An empirical model for the prediction of secondary production in marine benthic invertebrate populations. *Mar. Ecol.: Prog. Ser.* 114, 165–174. <http://dx.doi.org/10.3354/meps114165>.
- Uye, S., 1982. Length-weight relationships of important zooplankton from the Inland Sea of Japan. *J. Oceanogr. Soc. Jpn.* 38, 149–158. <http://dx.doi.org/10.1007/BF02110286>.
- Ulanowicz, R.E., 1986. *Growth and Development: Ecosystem Phenomenology*. Springer, New York, pp. 203.
- Ulanowicz, R.E., Puccia, C.J., 1990. Mixed trophic impacts in ecosystems. *Coenoses* 5, 7–16.
- Valls, A., Coll, M., Christensen, V., 2015. Keystone species: toward an operational concept for marine biodiversity conservation. *Ecol. Monogr.* 85 (1), 29–47.
- Véga-Pérez, L.A., 1993. Estudo do zooplâncton da região de Ubatuba. Estados de São Paulo. *Publção esp. Inst. Oceanogr.*, S Paulo 10, 65–84.
- Walters, C., Christensen, V., Pauly, D., 1997. Structuring dynamic models of exploited ecosystems from trophic mass-balance assessments. *Rev. Fish Biol. Fish.* 7, 139–172.
- Walters, C., Pauly, D., Christensen, V., Kitchell, J.F., 2000. Representing density dependent consequences of life history strategies in aquatic ecosystems: Ecosim II. *Ecosystems* 3, 70–83.
- Walters, C., Christensen, V., 2007. Adding realism to foraging arena predictions of trophic flow rates in Ecosim ecosystem models: shared foraging arenas and about feeding. *Ecol. Model.* 209, 34–350.