Potential combined impacts of climate change and nonindigenous species arrivals on Bay of Biscay trophic network structure and functioning

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Abstract :

The consequences of climate change for marine organisms are now well-known, and include metabolism and behavior modification, distribution area shifts and changes in the community. In the Bay of Biscay, the potential environmental niches of subtropical non-indigenous species (NIS) are projected to expand as a response to sea temperature rise by the mid-century under the RCP8.5 climate change scenario. In this context, this study aims to project the combined effects of changes in indigenous species distribution and metabolism and NIS arrivals on the functioning of the Bay of Biscay trophic network. To do this, we created six different Ecopath food web models: a "current situation" trophic model (2007-2016) and five "future" trophic models. The latter five models included various NIS biomass combinations to reflect different potential scenarios of NIS arrivals. For each model, eight Ecological Network Analysis (ENA) indices were calculated, describing the properties of the food web resulting from the sum of interactions between organisms. Our results illustrate that rising temperature increases the quantity of energy passing through the system due to increased productivity. A decrease in the biomass of some trophic groups due to the reduction of their potential environmental niches also leads to changes in the structure of the trophic network. The arrival of NIS is projected to change the fate of organic matter within the ecosystem, with higher cycling, relative ascendency, and a chain-like food web. It could also cause new trophic interactions that could lead to competition and thus modify the food-web structure, with lower omnivory and higher detritivory. The combined impacts (increasing temperatures and NIS arrivals) could lower the resilience and resistance of the system.

Highlights

▶ Increasing temperature could have impacts on the current trophic network. ▶ NIS arrival could change the structure and the functioning of the trophic network. ▶ The combined impacts could lower the resistance and resilience of the system.

Keywords : Climate change, Non-indigenous species, Ecological Network Analysis, Food web modeling, Fisheries

42 **1. Introduction**

The impacts of climate change on marine biodiversity and ecosystem functioning have 43 been extensively studied over the last two decades (Harvell et al., 2002; Poloczanska et al., 44 2013; Lenoir et al., 2020). At the global scale, several studies have predicted the effects of 45 climate change on marine ecosystems (Parmesan and Yohe, 2003; Butchart et al., 2010; 46 47 Poloczanska et al., 2013; Lotze et al., 2019), but there remains a need for local studies that take into account environmental drivers in order to adapt management policies (Lopez y 48 49 Royo et al., 2009; Riera et al., 2016), especially in coastal areas already subject to different 50 human-induced pressures (eutrophication, fishing, recreational activities, pollution, marine 51 structures such as windfarms, etc.). Furthermore, climate change is expected to have greater 52 impacts on coastal areas than on the open ocean (Wong et al., 2014). As a consequence of 53 rising temperatures and the arrival of subtropical species (Cheung et al., 2012), marine 54 communities in temperate coastal areas are increasingly subject to tropicalization (Vergés et 55 al., 2014; Montero-Serra et al., 2015).

The Bay of Biscay is located in the northeastern part of the Atlantic Ocean, along the 56 west coast of France, in temperate latitudes already affected by warming temperatures 57 (Michel et al., 2009; Irigoien et al., 2011; Costoya et al., 2015). This temperature change has 58 induced a modification in local fish communities, with decreasing abundance and a shift in 59 distribution range (Costoya et al., 2015; Iglésias and Lorance, 2016; Delgado et al., 2018). 60 Indeed, a recent study projecting the potential environmental niches of 163 indigenous 61 62 species revealed that some of these species would shift westward or northward by 2050 under scenarios RCP2.6 and RCP8.5 (Le Marchand et al., 2020). This study also projected the 63 64 arrival of southern non-indigenous species (NIS) in the Bay of Biscay as a consequence of a 65 northward shift of their native ranges. A major limitation of this study, however, was that it 66 did not consider trophic interactions. Indeed, trophic interactions among species create a complex network of fluxes, as a result of organism feeding suitability, such as in terms of 67 68 predation or herbivory (Montoya et al., 2006). There is now evidence that warming temperatures affect ecosystem trophic dynamics (Lercari et al., 2018; Kwiatkowski et al., 69 70 2019; Baird et al., 2019), notably due to the effects of trophic cascades (Doney et al., 2012). Furthermore, it has been proven that the arrival of invasive species may alter the structure 71 72 and functioning of food webs (Baxter et al., 2004; Nehls et al., 2006; Baird et al., 2012). 73 However, to our knowledge, there are very few studies on the consequences for a local 74 trophic network of the arrival of NIS due to a shift of their distribution area under climate 75 change, in a temperate ecosystem (Moullec et al., 2019a).

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In the Bay of Biscay, Le Marchand et al. (2020) revealed that under the RCP8.5 scenario, 54% of fish and cephalopod species would not undergo any range shift by 2050. . These authors defined NIS as species currently beyond the southern border of the Bay of Biscay and whose area of presence is projected to expand with climate change. These are not invasive species *sensu stricto* (i.e., introduced by humans, having no predators,

opportunistic, and capable of rapid and dramatic increases in abundance; Mack et al., 2000).
In the context of climate change, little work has been done on the combined impacts of
changes on (1) indigenous species distribution and metabolism, and (2) NIS arrivals affecting
trophic network properties. These aspects are, nevertheless, crucial for ecosystem
management and policies (Halpern et al., 2015).

Given the impacts of climate change on the structure and functioning of marine 87 ecosystems, it is necessary to have reliable indicators that make it possible to follow and 88 anticipate ecosystem changes. Several types of indicators, such as Ecological Network 89 90 Analysis (ENA) indices, describe ecosystem functioning. Ecological network analysis provides 91 a set of indicators based on the analysis of the quantified flux (carbon or energy) within a 92 trophic network (Ulanowicz, 1986; Niquil et al., 2012). The main goal of these indicators is to characterize the functioning of a system (Niguil et al., 1999) and to emphasize the holistic 93 94 properties of the food web (Fath et al., 2007). They make it possible to assess how the 95 trophic network may be modified following different changes in the ecosystem (Baird et al., 96 1991). For instance, ENA indices can be used to explore how a system will evolve following 97 environmental change (Paar et al., 2019) or anthropogenic pressure (Bueno-Pardo et al., 98 2018). In recent years, ENA indices have been proposed as highly promising indicators for assessing the "Good Environmental Status" of marine ecosystems (Niquil et al., 2012), 99 100 targeted by the "Food Webs" descriptor of the Marine Strategy Framework Directive (Safi et al., 2019; Fath et al., 2019) and proposed as tools for environmental managers (Schukel et 101 102 al., 2018).

The aim of the present study was to investigate the possible consequences of climate 103 104 change by coupling effects on indigenous species, consisting in a potential decrease in their environmental niches and modifications to their metabolism, with the arrival of NIS in the 105 106 same area. The trophic functioning of the Bay of Biscay ecosystem was assessed by applying various biological hypotheses for the mid-century and the RCP8.5 climate change scenario. 107 108 To do this, Ecopath models and ENA indicators were applied to the Bay of Biscay. To consider the potential future NIS biomass, six models were built that progressively varied 109 110 the NIS biomass.

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- 112 **2.** Material and methods
- 113 *2.1. Study area*



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Figure 1: Geographical location of the study area: in grey, the French part of the Bay of Biscay continental shelf (30–200 meters depth)

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The Bay of Biscay is a large gulf located on the Eastern side of the North Atlantic Ocean 118 119 (Figure 1). It is bordered by the Spanish (43.5°N) and French coasts and by the English Channel and the Celtic Sea to the north (48.3°N). It is the top fishing area in Europe (ICES, 120 121 2020), with about 100,000 tonnes of fish and shellfish caught every year by French and other European fishermen (http://ices.dk/marine-data). Our study focused on the French part of 122 123 the Bay of Biscay continental shelf (30–200 m depth). The Bay of Biscay is already affected by climate change, with its sea temperature in the upper 200 m layer increasing by 124 0.2°C.decade⁻¹ between 1965 and 2004 (Michel et al., 2009) and general trends of changes in 125 temperature seasonality have already been observed (Costoya et al., 2015). In addition, 126 Chust et al. (2021) reported an increase in chlorophyll concentrations measured by satellite 127 of 0.054±0.012 mg m⁻³ dec⁻¹ in the Bay of Biscay during the last two decades. 128

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130 *2.2. Ecopath model*

The Ecopath with Ecosim (EwE) model is a tool used worldwide for modeling marine trophic networks. In this study, the 6.6 version of Ecopath was used. The Ecopath routine provides a snapshot of energy fluxes between different functional groups, from plankton to marine mammals (Christensen and Walters, 2004). A functional group is composed of one to several species with identical trophic behavior.

136 With Ecopath, the energy fluxes are modeled using two main equations. The first 137 equation calculates production. It corresponds to the sum of all the outgoing fluxes and is 138 defined as:

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Production = fishery catch + predation mortality + net migration + biomass accumulation
 + other mortalities

142 143 Formally, for a functional group i and a predator j (j being a predator of i), this equation can 144 be written as: 145 146 $B_i \times (P/B)_i = Y_i + \sum_i (B_i \times (Q/B)_i \times DC_{ij}) + Ex_i + Bacc_i + B_i(1 - EE_i) \times (P/B)_i$ (1) 147 148 where B is the biomass density (t.km⁻²), P/B is the production rate (year⁻¹), Y is the total catch (t.km⁻²), Q/B is the consumption rate (year⁻¹), DC is the diet composition (DC_{ii} is 149 the proportion of *i* in the diet of *j*), Ex is the net migration rate (year⁻¹), Bacc is the biomass 150 accumulation (year⁻¹), and EE is the ecotrophic efficiency (meaning the proportion of the 151 trophic group's biomass consumed by a predator or caught by fisheries). 152 153 154 The second equation represents the mass balance of the compartment, i.e., the inflows are 155 equal to the sum of the outflows of the compartment: 156 157 Consumption = production + respiration + unassimilated food 158 159 Formally, this equation for a functional group *i* and a predator *j* (*j* being a predator of *i*) can be written as: 160 161 162 $B_i x (Q/B)_i = B_i x (P/B)_i + R_i + U_i$ (2) 163 where R is the respiration (t.km⁻²) and U is the unassimilated food rate. 164 165

The models are then balanced by adjusting the EE when it is greater than 1. Indeed, the EE represents the part of the group production that is consumed or fished, so it cannot be higher than 1. The EE of each functional group was adjusted by modifying the predation control in the diet composition matrix.

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171 2.3. The "Current" model, based on data from 2007–2016

172 *2.3.1. Structure*

173 The "Current" model developed in this paper is composed of 52 compartments 174 ranging from detritus to mammals and seabirds. Among these, 44 compartments, corresponding to species indigenous to the Bay of Biscay, were taken from a previous 175 176 Ecopath model (Moullec et al., 2017), itself based on a model by Lassalle et al. (2011). These 177 two models differ by their currency: wet weight for the former and carbon for the latter. We 178 used data from both models. Indeed, Moullec et al. (2017) used the values from Lassalle et 179 al. (2011), but chose to give their biomass in wet weight t.km², as did we. We primarily used the data from Lassalle et al. (2011), except for those in kgC.km, for which we used the values 180 181 from Moullec et al. (2017), who converted those from Lassalle et al. In addition, we 182 performed some corrections in the composition of fish trophic groups and fisheries. Marine 183 mammals are divided into two groups according to their size. Seabirds are also divided into two groups, according to their feeding strategies. There are 21 groups of fishes: two groups 184 of chondrichthyans (large piscivorous sharks and small sharks and rays), 11 monospecific 185 groups of fishes targeted by fisheries (seabass, blue whiting, hake, whiting, megrim, sole, 186 187 plaice, horse mackerel, sardine, anchovy, and pout) and eight multispecific groups: anglerfishes (two species), mackerels (two species), flatfishes (benthos feeders), demersal 188 189 benthos feeders, demersal piscivores, demersal planktivores, pelagic piscivores, and pelagic planktivores. Cephalopods are separated into two groups: benthic and pelagic. There are 190 eight benthic invertebrate groups (Norway lobster, lobsters/crabs, shrimps, carnivorous and 191 necrophagous benthic invertebrates, subsurface deposit feeding invertebrates, surface 192 suspension and deposit feeders, benthic meiofauna, and suprabenthic invertebrates). 193 194 Zooplankton are divided into three groups according to their size: microzooplankton (<200 195 μ m), mesozooplankton (200–2000 μ m), and macrozooplankton (>2000 μ m). Phytoplankton 196 are divided into two groups (small and large), in addition to a primary benthic producers 197 group. There are also groups for bacteria, detritus, and discards.

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199 In addition to these 44 compartments, we considered 8 groups of NIS fishes, which were not included in the two previous models (Lassalle et al., 2011; Moullec et al., 2017). 200 They are composed of three monospecific groups of fishes targeted by fisheries in their 201 202 original habitat and that would potentially be targeted by the Bay of Biscay fisheries (hake, Merluccius senegalensis; horse mackerel, Trachurus trecae; and gilt sardine, Sardinella 203 aurita) and five multispecific groups (flatfishes, demersal benthos feeders, demersal 204 piscivores, pelagic piscivores, and pelagic planktivores). Potential environmental niche 205 206 models run by Le Marchand et al. (2020) predicted the arrival of 57 NIS in the study area by 207 2050 under the IPCC RCP8.5 scenario. The NIS modeled in the present study are the same as 208 those modeled by Le Marchand et al. (2020) (Table S1 in the Supplementary data). These 209 species were selected because their current distribution areas are limited to northwest 210 Africa and are thus most likely to arrive in the Bay of Biscay.

NIS groups have the same preys and predators as those already present in the Bay of Biscay, which we have named "mirror groups" in this study. Their diet proportions are identical to their mirror groups.

The consistency of the Current model was checked with the Ecopath PREBAL tool (Link, 2010) (Figure S2 in the Supplementary data).

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217 2.3.2. Inputs in the Current model

The current biomass of monospecific fish groups targeted by fisheries were calculated from total biomass values given by Ifremer and reported in t.km² (Ifremer 2021), and averaged over the 2007-2016 period. Due to a lack of data, the current biomass of the six multispecific fish groups were estimated by Ecopath using an EE of 0.8 for the pelagic piscivorous group and of 0.95 for the other groups (Table S3 in the Supplementary data). The current biomass of large piscivorous sharks and small sharks and rays were estimated by Ecopath with EE values of 0.6 and 0.8, respectively (Moullec et al., 2017). The diet matrix was obtained from
previous Ecopath models of the Bay of Biscay (Lassalle et al., 2011; Moullec et al., 2017).

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To maintain the same structure for the different models, because ENA indices are sensitive to model topology (Fath et al., 2013), the NIS were considered in the Current model with a biomass close to 0 (i.e., 0.0001t.km⁻², Table 1). The diets of the NIS multispecific group were the same as for their current mirror groups, due to a lack of information on the diets of those species. The diets of the three monospecific NIS groups were compiled from Fishbase (Froese and Pauly, 2021). The NIS group contribution to the diet of their predators was kept very low.

234

The P/B and Q/B parameters were updated for all fish groups. The P/B ratios for a fish
species *i* were calculated with the empirical equation (Allen, 1971; Pauly, 1980) (Table S3 in
Supplementary data):

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$$P/B = M_i + F_i = (K_i^{0.65} \times L^{\infty} I^{-0.279} \times T^{0.463}) + (Y_i / B_i)$$
(3)

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where K is the growth parameter from the Von Bertalanffy growth function (year⁻¹) for each species (Froese and Pauly, 2021), L^{∞} is the asymptotic length (cm), T is the mean temperature (°C) over the Current model period (i.e., 2007–2016), Y is the yield (kg.year⁻¹) and B is the biomass (kg.year⁻¹). The temperature assigned depends on the species' vertical habitat, which was provided by Le Marchand et al. (2020): 9.74°C for benthic and demersal (bottom temperature), 11.66°C for benthopelagic (mean water column temperature), and 12.26°C for pelagic species (surface temperature).

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For all fish groups, the Q/B ratios were calculated for a species *i*, with the empirical equation (Palomares and Pauly, 1998) (Table S3 in the Supplementary data):

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252 $Log_{10}(Q/B) = 6.37 - 1.5045 \times log_{10}T' - 0.168 \times log_{10}W_{\infty_i} + 0.1399 \times Pf + 0.2765 \times HD$ (4) 253

where T' is the mean temperature of seawater calculated by 1000/(T + 273.75), W ∞ is the asymptotic weight (g), and Pf and HD are two dimensionless variables (Pf = 0 for herbivorous and detritivorous species, 1 for others; HD = 0 for carnivorous species, 1 for others).

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258 As ENA indices are sensitive to model topology (Fath et al., 2013), the topology of all models 259 was standardized. So, the eight NIS groups were considered in the Current model. However, 260 their biomass was close to 0 (i.e., 0.0001t.km⁻², Table 1). The diets of the three monospecific NIS groups were compiled from Fishbase (Froese and Pauly, 2021). Their proportion in their 261 262 predator's diet was kept low in the Current model, given the low biomass (due to absence) of the group. The P/B and Q/B ratios of the NIS monospecific groups were calculated using 263 264 equations (3) and (4). For the five NIS multispecific groups (i.e., NIS flatfishes, NIS demersal benthos feeders, NIS piscivores, demersal planktivores, and NIS pelagic planktivores), some 265

of the species in the groups had not been sufficiently documented to calculate the Q/B. So, the choice was made to use the default P/Q ratio of 0.25 instead (Table S3 in the Supplementary data) (Christensen et al., 2005).

269

Depending on the pertinence of the data they relied upon, the biomass for other EwE functional groups were taken from Lassalle et al. (2011) and Moullec et al. (2015). The detailed information is provided in Table 3 in the Supplementary data.

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274 2.3.3. Fisheries

275 Landings data were obtained from the International Council for the Exploration of the 276 Sea (ICES; http://ices.dk/marine-data/Pages/default.aspx) for the period 2007 to 2016. To 277 obtain a more realistic Ecopath model, we integrated the 10 main French fleets operating in the area: bottom trawlers targeting demersal fishes, purse seiners, bottom trawlers 278 279 targeting Norway lobster, gillnetters larger than 15 meters, pelagic trawlers targeting small pelagic fishes, gillnetters smaller than 15 meters, pelagic trawlers targeting demersal fish, 280 281 long-liners and line vessels, pelagic trawlers targeting tuna, and Danish seine. Other European fleets were also included, mostly from Spain (29% of catches from foreign ships), 282 283 the United Kingdom (10%), and Belgium (6%). This information was included in the ICES 284 data.

The proportions contributing to the landings by each fleet were calculated from OBSMER reports (Fauconnet et al, 2011; Dubé et al, 2012; Cornou et al, 2013; 2015a; 2015b; 2016; 2017; 2018). ICES data provided the total biomass caught for each species per year. We applied the percentage calculated from OBSMER to the ICES data and obtained for the total biomass of each Ecopath group caught by every fleet from 2010 to 2016. The landings inputs were annual means of these results.

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Discards were calculated similarly to landings. Indeed, OBSMER reports include the discard rates for each species and each fleet, from 2010 to 2016. These rates were applied to the ICES catches to obtain annual mean discards over this period.

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296 2.4. Projections

To study the effects of NIS arrivals, we developed a comparative approach by creating five 297 other Ecopath models based on different community changes caused by the arrival of NIS, 298 compared with the current situation (2007-2016). We built these models for the mid-299 century period (2041–2050) under the IPCC scenario RCP8.5. While the previous version of 300 the work conducted by Le Marchand et al. (2020) was based on both RCP2.6 and RCP8.5, we 301 302 chose to focus only on the latter. Including RCP2.6 would have considerably increased the number of models. Additionally, the aim of our study was to explore the effects of NIS arrival 303 304 on native communities, which would be limited under scenario RCP2.6 according to the 305 results from Le Marchand et al. (2020). Thus, we therefore chose to only work with RCP8.5. 306 Into these models, we integrated the impacts of climate change on Bay of Biscay species by considering (i) the evolution of fish and cephalopod biomass (based on Chaalali et al., 2016)
due to the projected evolution (gain or loss) of their suitable habitat (calculated in Le
Marchand et al., 2020); and (ii) the changes in the organisms' production and consumption.
The five hypotheses of the future evolution of the Bay of Biscay food web illustrate both
climate change effects and variation in NIS biomass.

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313 2.4.1. The common basis of the five future models

The five hypotheses simulate progressive variation of the NIS biomass, which is the only parameter to change between the five models. The common basis of the five hypotheses integrates the effects of climate change on fish and cephalopod distributions predicted for the mid-century under RCP8.5 as presented in the previous section.

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319 Future biomass: Species that are projected to show no range shift maintain the same 320 biomass as in the Current model. For the species that are projected to undergo a range loss 321 (Le Marchand et al., 2020), a proportional reduction in biomass is applied according to the 322 reduction in their potential environmental niche (called "ecological niche" in Le Marchand et 323 al., 2020) by 2050 under RCP8.5 (see Chaalali et al., 2016): anglerfishes (-3.12%), whiting (-324 17.15%), megrim (-3.75%), plaice (-9.73%), flatfishes (-4.89%), demersal benthos feeders (-325 0.21%), demersal piscivores (-18.64%), pelagic planktivores (-1.21%), and sharks and rays (-326 0.07%) (Table S4 in the Supplementary data).

The biomass values of cephalopods, benthic invertebrates, zooplankton, phytoplankton, and bacteria estimated by the Current model were used as inputs for the five future hypotheses without any changes, since changes in their potential environmental niches were not considered in this study.

331

Future P/B and Q/B: The future P/B and Q/B ratios of fishes were calculated using equations 332 (3) and (4) and considering the water temperature projected by mid-century under RCP8.5. 333 334 The latter has already been calculated by Le Marchand et al. (2020), based on information taken from three general circulation models (GFDL, IPSL, and MPI) (Taylor et al., 2012). The 335 336 temperature depth was integrated to produce values for the different fish habitat depths: 10.03°C for benthic and demersal, 12.34°C for benthopelagic, and 13.03°C for pelagic 337 338 species. For groups with several species, the P/B and Q/B were averaged and weighted 339 according to the biomass of each species. The resulting P/B and Q/B differed from those of 340 the Current model (Table S5 in the Supplementary data), which integrates the effects of 341 climate change on metabolism.

For cephalopods, benthic invertebrates, zooplankton, and primary producers, we decided to apply the same alterations (+2%) of P/B and Q/B ratios as those observed for fishes. Thus, the differences between current and projected fish P/B and Q/B values were calculated and it appeared that future P/B and Q/B were 2% greater than current values. As a consequence, a 2% increase of the P/B and Q/B was applied to the cephalopods, benthic invertebrates, zooplankton, and primary producers. Finally, as mammals and seabirds are homeotherms, their P/B and Q/B ratios remained unchanged in the climate change models.

350

Fisheries: For the future models, we hypothesized that fishing effort would be the same as in the Current model. The NIS were hypothesized to be fished at the same rate and by the same fleet as their mirror group. However, to take into account the European "zero discard" objective, discards were set to zero in the 2050 models for species under quota. Consequently, landed discards were added to the landings inputs.

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357 2.4.2. Specificities of the projection models

The five hypotheses of the future evolution of the Bay of Biscay food web illustrate both climate change effects and variation in NIS biomass.

360

361 *Model 1 – ClimOnly:* No NIS arrive in the Bay of Biscay. This model integrates only the effects 362 of climate change on the species present in the Current model in the Bay of Biscay (i.e., 363 decrease in the biomass of certain fish species due to the reduction of their potential 364 environmental niches and increased P/B and Q/B ratios). For the ClimOnly model, the NIS 365 biomass were set at 0.0001 t.km⁻² and maintained at fully consumed (EE > 0.95) (Figure 2) 366 (Table S6 in the Supplementary data).

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The following four models are based on the conditions of ClimOnly, to which we added NIS parameters.

370

Model 2 – NISPel: Only pelagic NIS arrive in the Bay of Biscay, as they are expected to shift
 more rapidly than demersal species in the Bay of Biscay under climate change. For the NISPel
 model, the biomass of flatfishes and demersal NIS was set at 0.0001 t.km⁻² and the NIS
 pelagic biomass was estimated by Ecopath, using an EE of 0.8 for piscivores and 0.95 for
 other groups (Figure 2) (Table S7 in the Supplementary data).

376

Model 3 – NISEqual: In this model, we considered that the environmental niches freed by 377 indigenous species are immediately occupied by NIS with same trophic function. The NIS 378 379 arrivals counterbalance the loss of biomass due to species impacted by climate change in the 380 Bay of Biscay. The biomass values of the main functional groups remain the same as in the 381 ClimOnly model. As the groups impacted by climate change are mainly demersal and benthic 382 species, this hypothesis mostly models the arrival of demersal and benthic NIS. For the NISEqual model, the NIS group biomass values were equal to the biomass reduction of their 383 384 mirror current trophic groups due to climate change (Figure 2) (Table S8 in the 385 Supplementary data).

386

387 Model 4 – NISMax: In this model, there is no restriction on NIS arrivals. The biomass values
 388 are not a priori estimated but calculated by Ecopath by balancing the two model equations

((1) and (2)). An EE of 0.8 is applied for pelagic piscivorous NIS and 0.95 for other groups, as
we supposed their EE would be the same as those of the indigenous groups (Table S9 in the
Supplementary data).

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393 *Model 5 – NISInt:* This is a conservative option. A preliminary analysis of the potential 394 impacts of NISMax on the NIS biomass level estimate suggested that a good intermediate 395 situation between NISMax and other models would be obtained by dividing the NISMax 396 biomass by five (Figure 2).

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Figure 2: Diagram showing the Current model (2007–2016) and the five projected models (2041–2050). The blue shapes represent the Bay of Biscay species (light blue for species not impacted by climate change and dark blue for species with a reduced biomass due to climate change). The green shapes represent nonindigenous species (NIS). The tuna-shaped symbol represent pelagic and benthopelagic species, the flatfish profile represents benthic and demersal species. The size of the green circle is relative to the NIS biomass.

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408 2.5. ENA

Ecological network analysis (ENA) indices, which reveal the hidden properties of food webs, were used to highlight the effect of climate change and arrivals of new species in the Bay of Biscay. A set of five indices currently calculated in the Matlab routine ENATool (Guesnet et al., 2015) were selected: Mean Trophic Level 2 (MTL₂), Total System Throughput
(TST), Finn Cycling Index (FCI), relative ascendency (A/C), and System Omnivory Index (SOI).

In addition, three new indices (Averaged Mutual Information, AMI; Mean Trophic Level 3.25,

415 MTL_{3.25}; and Detritivory/Herbivory ratio, D/H) added to this routine were calculated to 416 provide a detailed description of food web structure and functioning (Table 2).

The Matlab routine ENATool takes into account Ecopath input uncertainties. It runs 417 418 Monte-Carlo simulations to create a set of different versions of one Ecopath model, whose input parameters vary according to the Ecopath pedigree. The pedigree represents the 419 coefficient of variation of every input and varies from 1 (the data are reliable) to 0 (the data 420 estimated by Ecopath are not coherent) (Guesnet et al., 2015) (Table S11 in the 421 Supplementary data). For each model, the ENATool routine created 100 simulations, varying 422 the inputs for biomass and P/B and Q/B ratios, and the diet composition according to the 423 pedigree. All simulations were balanced. For each model, we obtained 100 values for each 424 425 ENA indicator.

The significant difference between the ENA values of each model was tested by a Kruskal–Wallis non-parametric test, as conditions of normality were not met. Then, the hypotheses were compared with each other using Dunn tests.

For greater clarity in the results, we separated the ENA indices into two groups according
to what they reflected: network ENA (TST, FCI, AC, and AMI) and diet ENA (MTL₂, MTL_{3.25},
SOI, and D/H).

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Table 1: Description of the ENA indices. T_{ij} is the flux from group i to group j; TSTc is the sum of cycling fluxes; TL_i is the trophic level of group i; B_i is the biomass of group i; Q_i is the consumption of group i; Ol_i is the omnivory index of group i; D is the fluxes from detritus; Z_i is the import into the system through compartment I; y_i is the output of the system from compartment I; T_{.j} is the flow to compartment j, DCij is the proportion of i in the diet of group j, and H is the flux from primary producers. The * specifies the indicators that were added to the basic

438 ENAtool routine.

Indicators	Definition	Formula	Interpretation of an	
			increase in value	
Total System	Sum of all fluxes		The overall activity of	
Throughput (TST)	in the system	$\sum T_{i,i} + Z_i + v_i$	the system is increasing	
/t.year ⁻¹		$\sum_{ij} ij + i + ji$		
Ulanowicz (1986)				
Finn's Cycling Index	Fraction of all		The system has more	
(FCI) %	system fluxes that	$\sum \sum T_{i} \pm z_{i}$	complex internal links,	
Finn (1980)	are recycled	$\sum \frac{\sum_{i=1}^{i} \sum_{j=1}^{i} \sum_{j=1}^{i}}{TST}$	a better use of energy	
		j 151	system	
			System	
Relative ascendency	Quantification of	$(T_{ij}TST)$	The system has a higher	
(A/C), no units	the degree of	$\sum_{i,j} T_{ij} \log\left(\frac{T_j - T_j}{T_i T_j}\right)$	degree of organization,	
Ulanowicz (1986)	organization of	$-\frac{1}{\sum_{i=1}^{n} T_{i} + T_{i}}$	the direct pathways are	
	the system	$\Sigma_{i,j} T_{ij} \log \left(\overline{TST} \right)$	favored, chain-like	
Averaged Mutual	Quantification of		The system is more	
Information* (AMI),	the exchange	$K\sum \left(\frac{T_{ij}}{T_{ij}}\right)T_{ij}\log\left(\frac{T_{ij}TST}{T_{ij}}\right)$	constrained and energy	
no units	between	$\prod_{i,j} \langle TST \rangle^{T_{ij}} \langle T_i, t_{.j} \rangle$	flows through particular	
(Hirata and Ulanowicz,	compartments		pathways	

1984)			
Mean Trophic Level 2	Mean trophic		The proportion of high
(MTL ₂), no units	level of	$\Sigma_i TL_i \times B_i$	trophic levels increases
(Pauly, 1998)	consumers (all	$\frac{\underline{\Delta t} + \underline{\Delta t}}{\sum B_{i}}$	In the whole system
	species with TL >	$\Delta_l D_l$	
	2)		
Mean Trophic Level	Mean trophic		The proportion of the
3.25* (MTL _{3.25}), no	level of predators	$\sum_i TL_i \times B_i$	higher trophic levels
units	(all species with	$\sum_i B_i$	has grown in the
Shannon et al. (2014)	TL > 3.25)		predators
System Omnivory	Mean consumer	$\sum_{i} \sum_{j} [TL_{j} \times (\sum_{j} TL_{j} \times DC_{ji})] \times \log T_{j}$	The predators are less
Index (SOI), no units	omnivory index	$\sum_i \log T_{.j}$	specialized. They feed
(Christensen et al.,			on various trophic
1993)			levels, this leads to
			more parallel flows in
			the system
Detritivory/Herbivory*	Ratio between		A greater proportion of
(D/H) no units	detritivory and	\sum Detritivory/ \sum Herbivory	the system is supported
(Kay et al., 1989)	herbivory		by detritus

439 440

Moreover, we explored ENA index behavior according to the different models using a Principal Component Analysis (PCA). The PCA was performed with the *ade4* package for R Core Team 2019 software (v 3.6.1), with the ENA indices as variables and the models as individuals.

445

446 **3. Results**

447 3.1. General trends

In the Current model, the trophic levels ranged from 1 to 4.49 (large pelagic sharks). 448 449 Trophic Level (TL) I was composed of five groups (three groups of primary producers, detritus, and discards) and represented 63.59% of the total biomass. TL II encompassed 450 451 heterotrophic bacteria, zooplankton, and some of the zoobenthos species, mainly 452 subsurface deposit feeders; it represented 26.76% of the total biomass. TL III was composed 453 of the majority of the fish groups (e.g., demersal piscivores Trachurus trachurus, Solea solea, 454 etc.) and represented 9.29% of the total biomass. TL IV corresponded to top predators and 455 represented only 0.96% of the total biomass.

456 3.2. ENA indices

The first two axes of the PCA (Figure 3) explain 69% of the variance, and only these are presented. The table on the top left of the figure gives information on the percentage contribution of each variable for each of the two dimensions. The first axis (horizontal: 460 49.2% of the variance) is accounted for by the indices MTL_{3.25} (19.26%), AMI (18.57%), A/C (18.20%), SOI (16.04%), and TST (14.56%). The second axis (vertical: 17.8% of the variance) is accounted for by FCI (50.87%) and D/H (24.58%). All of the models are distinguished on axis 463 1, with a clear separation of the Current model. The five other models form a group centered on axis 1 and progressively extend toward the right of axis 1. Thus, the Current and 464 465 NISPel models show opposite positions on axis 1. The Current model stands out by having lower TST, AMI, A/C, and MTL_{3.25} than the other models, but a stronger SOI. Thus, in this 466 467 model, the lower contribution of trophic level >3.25 seemed to lead energy to flow through multiple parallel pathways that favored omnivory. On the contrary, in the five other models, 468 469 energy was channeled to particular pathways, limiting feeding on several trophic levels (i.e., omnivory). The models are not really distinguishable from one other on axis 2, although four 470 models (ClimOnly, NISMax, NISInt, and NISEqual) seem to present a slightly higher FCI and 471 472 D\H ratio.



473

474 Figure 3: Principal component analysis of the six models (Current, ClimOnly, NISPel, NISEqual, 475 NISMax, and NISInt) and the eight ENA indices (Total System Throughput, TST; Finn's Cycling, FCI; 476 Relative ascendency, A/C; Averaged Mutual Information, AMI; Mean Trophic Level 2, MTL₂, Mean 477 Trophic Level 3.25, MTL_{3.25}; System Omnivory Index, SOI; and Detritivory/Herbivory ratio, D/H). Each 478 model includes all 100 simulations performed with ENATool. The solid dots with a black border 479 represent the initial models before applying any changes to parameters based on the ENAtool routine. The white dots represent the average model (i.e., the centroid of each model). The table at 480 481 the top left shows the absolute contributions of each ENA index for the two axes (in %). The table on 482 the top left gives information on the percentage contribution of each variable for each dimension.

483 484

485 *3.2.1. Network ENA*

486 TST increased significantly between the Current model and the projected models 487 (Figure 4, Table 2). The total flux in the system was $6255 (\pm 261) \text{ t.km}^{-2}$. year⁻¹ in the Current 488 model and increased by 15% on average under the future hypotheses. The projected
489 hypotheses presented significantly different TST values, with the exception of NISEqual and
490 NISInt, which showed similar TST.

The mean A/C ratio in the Current model was 0.223 and increased significantly up to 0.230 under ClimOnly (Figure 4, Table 2). Significant differences were observed between projected models, with the exception of NISPel and NISEqual, which had A/C ratios that were similar and the highest. Mean values of 0.245 and 0.242 were recorded for NISPel and NISEqual, respectively.

The AMI increased significantly between the Current model and ClimOnly (Figure 4, Table 2). All NIS hypotheses showed a significantly higher AMI than Current and ClimOnly models. A significant decrease in the AMI value was observed from NISPel (mean of 1.19) to NISInt (mean of 1.13), with intermediate values recorded by NISEqual and NISMax.

A significant increase of the FCI was obtained with the projected models (Figure 4, Table 2). The Current model showed a significantly lower FCI value than all the other models (mean of 16.85%). The NISInt model had the highest FCI values followed by ClimOnly and NISEqual, which showed similar FCI. The NISPel and NISMax models had intermediate values between the Current model and the other three models.



Figure 4: Boxplots of network ENA index values (Total System Throughput, TST; Averaged Mutual Information, AMI; Relative ascendency, A/C; and Finn's cycling, FCI), comparing the Current model and the five projected models (ClimOnly, NISPel, NISEqual, NISMax, and NISInt). The letters correspond to the significance of the differences between the models, based on a Kruskal–Wallis (KW) test (p-value < 0.01) and Dunn tests: two models with a different letter are significantly different. The central dot represents the mean and the standard deviation.

514

According to these results, climate change is expected to cause system productivity (TST) and recycling (FCI) to increase and to modify the structure of the trophic network (AMI and A/C). Index values varied greatly according to the NIS model. The highest values of AMI and A/C for NISPel and NISEqual imply that in these two models, energy would be forced to flow through direct pathways in order to reach higher trophic levels.

520

521 *3.2.2. Diet ENA*

522 There was no significant difference in the MTL₂ of the ClimOnly model compared with 523 the Current model (Figure 5, Table 2). A significant decrease of MTL₂ was recorded for the 524 NISPel hypothesis (mean of 2.54) due to the strong increase in biomass of small pelagic fish 525 of low trophic level such as *Sardinella aurita*. A significant increase was calculated for the 526 NISEqual and NISMax hypotheses (means of 2.66 and 2.70, respectively), due to the arrival 527 of non-indigenous demersal benthos feeders and piscivorous fishes, which replaced

indigenous species heavily impacted by climate change. The NISInt MTL₂ was slightly higherthan the Current and ClimOnly values.

530 The current MTL_{3.25} value (mean 3.48) increased significantly with climate change to 531 reach 3.62 in the ClimOnly model (Figure 5, Table 2). NISPel and NISEqual models showed 532 the highest MTL_{3.25} (means of 3.70 and 3.69, respectively), which can be explained by the 533 increase in fishes of high trophic levels such as tunas for NISPel and demersal piscivorous 534 fishes for NISEqual. The lowest MTL_{3.25} calculated were obtained under the NISInt and 535 NISMax hypotheses (means of 3.61 and 3.65, respectively).

536 The SOI showed a significant decrease between the Current model and all the other projected models (Figure 5, Table 2). There were also significant differences among the 537 future hypotheses. The NISPel model presented the lowest SOI (mean 0.15), whereas the 538 NISEqual model registered the highest among the five future hypothesis values (mean 0.19). 539 However, the NISInt and NISMax values were intermediate (means of 0.16 and 0.17, 540 respectively). The groups with the most marked decrease in omnivory were the top 541 predators (e.g., seabirds, mammals, and sharks) and the pelagic fishes (e.g., planktivores and 542 piscivores) (Table S12 in the Supplementary data). 543

544 The D/H ratio was significantly lower for the future hypotheses compared with the 545 Current model (Figure 5, Table 2). The decrease in D/H ratio was related to an increase in the 546 flux from primary producers. Detritivory was projected to increase by 4% and herbivory by 547 22% in the future. The increase in herbivory was higher than the increase in detritivory, 548 resulting in a decrease in the D/H ratio.



549

NISPel NISEqual NISMax NISInt Current ClimOnly NISPel NISEqual NISMax Current ClimOnly NISInt

550 Figure 5: Boxplots of the values of diet ENA indices (Mean Trophic Level 2, MTL₂; Mean Trophic Level 3.25, MTL_{3.25}; System Omnivory Index, SOI; and Detritivory/Herbivory ratio, D/H), comparing the 551 552 Current model and the five projected models (ClimOnly, NISPel, NISEqual, NISMax, and NISInt). The 553 letters correspond to the significance of the differences between the models, based on a Kruskal-554 Wallis (KW) test (p-value <0.01) and Dunn tests: models with different letters are significantly 555 different. The central dot represents the mean and the standard deviation.

556 Climate change is expected to affect the relative contribution of primary producers 557 and detritus to the feeding of primary consumers. In addition, the effects of both climate 558 change (i.e., decreased biomass of some groups) and of NIS arrivals would modify trophic 559 interactions, especially by decreasing the mean omnivory (SOI) in a various ways, according 560 to the NIS model. The mean trophic level indices (MTL₂ and MTL_{3.25}) showed changes in the 561 community, with variations according to the trophic functions of arriving NIS.

562 Table 2: Synthesis of trends of ENA indices (Total System Throughput, TST; Finn's cycling, FCI; Relative 563 ascendency, A/C; Averaged Mutual Information, AMI; Mean Trophic Level 2, MTL₂; Mean Trophic Level 3.25, MTL_{3.25}: System Omnivory Index, SOI; and Detritivory/Herbivory ratio, D/H), comparing 564 565 each future model (2041 – 2050) to the Current model (2007 – 2016). The symbol ↗ indicates a 566 significant increase of the index value in the future model, \searrow represents a significant decrease and 567 an equal sign '=' means that the Current model and the future model are significantly identical. A 568 single arrow indicates a slight variation, a double arrow indicates stronger variation and a triple 569 arrow indicates maximal variation.

ENA	ClimOnly	NISPel	NISEqual	NISMax	NISInt
TST	N N	NNN	<u>ZZ</u>	קק	קע
FCI	Z Z	NN	ZZ	קק	N NN
A/C	7	N N N	NNN	קק	קע
AMI	7	NNN	ZZ	קק	קע
MTL ₂	=	Ы	ZZ	NNN	=
MTL _{3.25}	Z Z	NNN	ZZ	קק	קע
SOI	עע	תתת	תע	עע	עע
D/H	И	Ы	Ы	И	Ы

571

572 **4. Discussion**

573 In this study, we projected the potential response of the Bay of Biscay trophic network to 574 changes in species composition and relative abundances driven by a rise in sea temperature. 575 Our results can be interpreted on three levels. Firstly, the comparison of ENA indices between the Current model and the ClimOnly hypothesis gives us information about the 576 577 effects of species distribution range reduction due to climate change and increasing metabolism. Secondly, the comparison of ENA indices between the ClimOnly hypothesis and 578 579 the four others (i.e., NISPel, NISInt, NISEqual, and NISMax) enables us to examine the 580 consequences of NIS arrivals. Finally, the comparison of ENA indices between the Current 581 model and the four NIS hypotheses reveals the combined effects of biomass decreases of 582 some local species and biomass increases of NIS. Several previous studies have investigated 583 the consequences of the arrival of invasive species (Miehls et al., 2009; Baird et al., 2012; 584 Libralato et al., 2015; Goren et al., 2016) or of climate change (Albouy et al., 2014; Raoux et 585 al., 2018; Bourdaud et al., 2021) in food webs structured by native species. A previous study 586 has dealt with the arrival of non-indigenous species in the Mediterranean sea as a result of 587 climate change (Moullec et al., 2019b). These species are expected to arrive due to a northward or southward shift of their range following an increase in water temperature, but 588 589 are not necessarily expected to become invasive (Lenoir et al., 2020; Urban, 2020).

590

591 4.1. Model limitations

We tried to build our models to be as exhaustive as possible. However, some aspects were not taken into account, even though they could play an important role in predicting the future of the ecosystem. Firstly, the models we used did not integrate the organisms' adaption capability. For example, generalist species might experience a diet shift, which would redesign the trophic network. Moreover, the opportunistic processes of fishes and cephalopods in predation cannot be integrated into Ecopath, as the diet matrix is predefined 598 and fixed. Thus, this study does not accurately reflect diet adaptability due to community changes. Furthermore, we did not model a decrease in the native species P/B, even if their 599 600 biomass declined due to climate change. This suggests that these species are currently at their optimum productivity. Based on this assumption, increasing the native species P/B in 601 602 the future models as we did hypothesizes that the native species could further develop in 603 the Bay of Biscay and could limit the development of NIS by contrasting with a strong 604 competition. The study of NIS arrivals could be improved by the use of Ecosim and Ecospace. 605 The study could also be improved by forcing the lower trophic level food web according to 606 biogeochemical models. This would make it possible to fit the trophic networks with more 607 realistic phytoplankton and zooplankton biomass variation. Indeed, in the study, we chose to model an increase in primary production, which goes against global projections but follows 608 the trend observed in the Bay of Biscay (Chust et al., 2021). However, as the Bay of Biscay is 609 bottom-up controlled (Corrales et al., 2022), it is vital to obtain reliable results on the 610 611 evolution of low trophic levels. Also, our models suggest that fishing mortalities would 612 remain constant until the mid-century. However, fisheries management is likely to be adapted to the situation (Badjeck et al., 2010; Quentin Grafton, 2010), especially since the 613 614 increase in temperature would not impact the stocks in the same way depending on 615 whether the species is stenothermal or eurythermal (Serpetti et al., 2017). Also, our method 616 did not integrate the effects of overfishing of some groups, which can favor NIS to the 617 detriment of native species (Saygu et al., 2020). Furthermore, we assumed that the biomass 618 of native species would decrease proportionally to the reduction of their potential 619 environmental niche, however biomass and environmental niches are not necessarily linked. 620 First, a species will not necessarily use its entire environmental niche: the fact that 621 environmental conditions are favorable in one place does not mean that the species will be 622 present there. Second, biomass does not depend solely on environmental parameters but 623 also on trophic and anthropic factors. Finally, we could not integrate the effects of warming 624 on organism recruitment and spawning, although this has been recorded, for example, on 625 herring in the Celtic Sea (Lauria et al., 2012). Such an effect could indirectly impact biomass 626 and productivity. It is also worth noting that sea temperature affects the organism's length 627 and weight, and the growth coefficient k, which are used in the calculation of P/B (Kielbassa 628 et al., 2010).

629

630

4.2. The Bay of Biscay trophic network in 2050 under the RCP8.5 scenario

In this section, we compare the Current model with the ClimOnly model. Our results 631 632 indicate that such ecosystem alterations could increase the quantity of matter flowing through the food web, as suggested by the 15% TST increase by 2050 under RCP8.5 (+0.77°C 633 at the surface). This can, firstly, be explained by the rise in P/B and Q/B. Indeed, despite an 634 observed decrease in total biomass, increasing P/B and Q/B led to higher flux in the system. 635 With the method used in this study, the decline in biomass is due to the decrease in habitat 636 suitability and the increase in P/B and Q/B is due to the rise in sea temperature. This 637 638 phenomenon is well-known, as marine organisms' metabolic activity is related to

639 temperature (Bruno et al., 2015; Carozza et al., 2019). Warming water is expected to increase P/B and Q/B ratios (Brown et al., 2004). Indeed, respiration and excretion fluxes are 640 641 projected to rise with sea warming, as already modeled for small pelagic fishes in the Bay of Biscay (Chaalali et al., 2016). Moreover, we forced an increase in the phytoplankton P/B in 642 643 our model, leading to a higher net primary production in the Bay of Biscay by the midcentury. Thus a higher quantity of matter supported the whole ecosystem. Although several 644 645 marine biogeochemical models have forecasted a 3.3%.°C⁻¹ mean global loss of net primary production under RCP8.5, associated with lower diatom biomass (Bopp et al., 2005), these 646 647 results are often derived from global climate models and do not take into account local specificities (Chust et al., 2014). Some authors have made an assumption of increased 648 649 primary production. For example, an increase in nutrient concentrations, due to high run-off, 650 would lead to higher primary production (Legge et al., 2020). Moreover, Chust et al. (2021) 651 highlighted an observed increase in primary production in the Bay of Biscay over the last two 652 decades.

653 The intensification of the quantity of matter in the system following temperature increase 654 under RCP8.5 was associated with an increase in recycling index (i.e., FCI), as previously 655 projected by Chaalali et al. (2016), with an increase of 23% in the Bay of Biscay by the end of the century under RCP8.5. A rise in FCI is commonly observed in disturbed ecosystems 656 657 (Saint-Béat et al., 2015). This increase in FCI values (calculated as the ratio between recycled matter and the TST) despite an increase in TST, means a higher amount of recycled matter. 658 659 Fath and Halnes (2007) highlighted that flows to and from the detritus compartment are a 660 major part of total structural cycling and an increasing FCI, therefore, results in an increase 661 in detritivory (Fath et al., 2019). Indeed, an increase in detritivory was projected in the Bay 662 of Biscay, although the D/H ratio decreased due to a greater rise in herbivory. The Bay of 663 Biscay could become more dependent on primary production, despite an increase in detritivory. The drop in D/H ratio is also an indicator of stressed ecosystems (Ulanowicz, 664 665 1997). In our case, the higher rate of herbivory can be explained by the increase in primary production (+2%) and may also be due to the decrease in biomass of some demersal species, 666 667 which could result in a higher biomass of groups responsible for herbivory fluxes. Increased herbivory may therefore be due to a combination of both the increase in primary production 668 669 and the decrease in predation. In addition, the increasing FCI can be explained by the increase of bacterial P/B and Q/B associated with a constant biomass in the future models. 670 671 This supposes that excess bacterial production is consumed, which contributes to the increase of the FCI. Regarding the European landing obligation (i.e., no discards) that was 672 673 applied in our projected models, this change did not show any influence on the trophic 674 network structure at the scale of the whole Bay of Biscay ecosystem because its contribution 675 to the current flow from detritus was only 0.021%.

676

The loss of biomass of some functional groups due to climate change could directly impact the MTL indicators. A constant MTL_2 (TL > 2) associated with an increase in $MTL_{3.25}$ (TL > 3.25) was expected under climate change. This may be explained by the biomass 680 reduction of some trophic groups in intermediate trophic positions, combined with a constant biomass of top predators (TL > 4) such as pelagic fishes (e.g., tunas) and sharks. 681 682 Indeed, demersal piscivorous fishes (TL = 3.7) were projected to lose 18% of their potential environmental niche by the mid-century under RCP8.5 (Le Marchand et al., 2020). As a 683 684 result, we reduced their biomass by 18% between the Current model and the future hypotheses. In the same way, flatfish biomass (TL = 3.4) was reduced by 4%. The decrease of 685 686 these groups' biomass combined with the biomass stability of the top predators (TL > 4), such as pelagic fishes (e.g., tunas) and sharks, led to increased productivity, resulting in a 687 constant MTL₂ associated with an increase in MLT_{3.25} with warming. We should note that this 688 study did not take into account the evolution of fishing pressure, which could alter the 689 community structure. However, the significant increase of the trophic level of demersal 690 691 fishes observed in the Bay of Biscay, associated with the higher biomass of high trophic level predators (Arroyo et al., 2019), corroborates our results. Moreover, although the 692 693 opportunistic predation behavior of fishes and cephalopods cannot be integrated into 694 Ecopath, as the diet matrix is predefined and fixed, omnivory (i.e., SOI) was projected to 695 greatly decrease by the mid-century. This result is probably due to the drop in biomass of some prey as well as of predators. For example, the fall in biomass of demersal benthos 696 feeding fishes could reduce their predation by higher trophic level species and could, thus, 697 decrease the omnivory of their predators (i.e., demersal piscivorous fishes). Indeed, the 698 699 demersal piscivorous omnivory indicator decreased by 44% under the ClimOnly hypothesis (Table S12 in the Supplementary data). Moreover, it is important to note that the omnivory 700 index is calculated based on the trophic level of prey. Thus, all modifications to prey trophic 701 702 levels may alter the omnivory index value. The decrease in omnivory was associated with a 703 rise in the relative ascendency. This suggests that parallel pathways (feeding directly or 704 indirectly on a group) tend to disappear. The fall in the biomass of some functional groups 705 could explain this observation. Indeed, energy was weakly channeled to trophic pathways 706 to/from groups whose biomass was altered. As a consequence, other pathways were favored, causing the increase in A/C. The trend in both these ENA indices (i.e., increase in 707 708 A/C, decrease in SOI) by 2050 under the effect of climate change according to RCP8.5 709 indicates a system becoming simpler by moving towards a chain-like food web.

710

711 Changes with the arrival of NIS

712 The arrival of NIS altered energy circulation in the system. It amplified the impact of 713 climate change (ClimOnly) on the AMI. The impact on other network properties depended 714 on the nature of this arrival. ENA indicators are known to be sensitive to environmental specificities and physical parameters, making it difficult to compare ENA values among 715 716 different ecosystems, but efficient for a "before/after" comparison (Niquil et al., 717 2012). Indeed, ecosystems are distinguished by specific network properties resulting from 718 interactions between organisms and between these organisms and their environment. These properties affect the ecosystem response to a perturbation, hence the diversity of effect on 719 720 invasive species. First, the A/C index was very sensitive to the arrival of NIS. The arrivals in

721 the NISPel and NISEqual models could lead to higher A/C and AMI values. This means that 722 these two models could increase the full food-web organization and favor direct pathways to 723 reach higher trophic levels with potentially greater efficiency. Concerning FCI, the variations between the NIS hypotheses highlighted the effects of community composition. Indeed, FCI 724 725 is strongly correlated with the type of community (Baird et al., 2007). It is worth noting that high biomass of pelagic species (i.e., the NISPel and NISMax hypotheses) induce lower 726 727 cycling rates. In contrast, higher biomass of demersal species (i.e., the NISEqual model) showed high rates of cycling. Finally, the NISInt model with a low biomass change for both 728 729 pelagic and demersal species does not seem to affect the cycling rates. It is worth noting that the P/B and Q/B values of NIS were different from those of their mirror groups (Table S5 730 731 in the Supplementary data), as they were calculated separately for the study. There was no trend in the values. The largest contributors to the flow to detritus under the ClimOnly 732 733 model were microzooplankton (41%), although this proportion is highly dependent on the structure of the trophic network. The major predator of microzooplankton is 734 735 mesozooplankton. High consumption of mesozooplankton by planktivorous fishes induces a 736 decrease in predation on microzooplankton. This lessens the flow to detritus by small 737 phytoplankton that are the diet of microzooplankton.

The arrival of NIS could amplify the effect of warming on the trophic network 738 739 structure in the Bay of Biscay due to changes in predation controlled by fish biomass. The MTL of both low trophic level consumers (TL > 2) and predators (TL > 3.25) could be affected 740 741 by changes in trophic composition. For example, NISPel is characterized by a drop in MTL₂ (-3% compared with ClimOnly), due to a massive arrival of planktivorous pelagic fishes such as 742 743 Sardinella aurita and Trachurus tracae with a low trophic level (respectively 2.5 and 3.3). It should be noted, however, that the amount of zooplankton consumed by Sardinella aurita 744 745 may have been underestimated in our model, giving it a lower trophic level than other planktivorous pelagic fishes such as Sardina pilchardus and Engraulis encrasicolus. On the 746 747 contrary, the $MTL_{3,25}$ was very high (+2% compared with ClimOnly), indicating the arrival of top predators such as tunas. The MTL₂ could increase due to a massive arrival of demersal 748 749 piscivorous species. The significant decrease in the SOI index suggested that the arrival of NIS could amplify the effect of climate change on changes to the trophic network structure. 750 751 In the Baltic Sea, the arrival of a new predator, an invasive crab (*Rhithropanopeus harrisii*), in 752 a bottom-up controlled ecosystem, has been known to deeply impact both lower trophic 753 levels (by a drop in species richness) and pelagic phytoplankton (by a greater biomass) (Kotta et al., 2018). The NISEqual hypothesis proved that a simple change in marine communities 754 755 could greatly affect trophic functioning. In the Barents Sea, the observed borealization of Arctic marine communities due to the climate-driven expansion of boreal species is 756 757 reportedly inducing a deep change in the structure of the current Arctic trophic network (Frainer et al., 2017; Pecuchet et al., 2020; Frainer et al., 2021). In Norway, community 758 759 changes in the sublittoral area due to kelp expansion induced a change in the trophic 760 structure and its associated flows (Paar et al., 2019). Our results highlighted the issue of NIS,

which should be considered more frequently in ecosystem modeling. Indeed, not considering this question may affect ecosystem model projections (Bentley et al., 2017).

763

764 *Combined effects and implications for the trophic network*

We expected that a decrease in total biomass and trophic functions due to 765 766 potentially reduced environmental niches under climate change could be offset by the arrival of NIS. However, our results indicate that whatever the biomass and species arriving 767 768 in the Bay of Biscay with sea temperature rise, some effects could be observed on the 769 trophic networks. Even in the case of NISEqual, in which the functional groups' losses were 770 replaced in terms of quantity, the trophic network was not projected to return to the current 771 structure. The effects of climate change in the marine realm are often studied individually, 772 whereas these effects are more likely to occur in combination, which could have a more 773 profound impact on ecosystems and fisheries (Ainsworth et al., 2011; Halpern et al., 2015). 774 In terms of the combination of different consequences of climate change, our results support the idea that the ecosystem response is more complex when two or more stressors 775 776 are associated. The case of the NISEqual hypothesis showed that the arrival of NIS of the same trophic function and in the same proportion could not compensate for the effects of 777 778 the increase in sea temperature.

779 The cumulative effects of both sea warming and the arrival of NIS could lead to less 780 resistant and less resilient ecosystems in the Bay of Biscay. Even though the interpretation of 781 ENA indicators is often complex (Saint-Béat et al., 2015), our results illustrate major trends. 782 According to Saint-Béat et al. (2015), FCI, SOI, and A/C can be used to estimate the response 783 of a system to a perturbation. In our case, the increase in FCI in the projected models is typical of stressed ecosystems. The disruption of initial recycling has a strong impact on the 784 ecosystem due to the large number of indirect effects associated with cycling (Fath and 785 Halnes, 2007). By indirect effects, the authors referred to paths between two compartments 786 787 of a length greater than 1. As a consequence, changes in cycling can alter pairwise relations leading to a potential impact on ecosystem response to perturbation such as species 788 789 invasion, extinction as well as climate change. Omnivory enables the system to adapt to a 790 perturbation by shifts in predator diet. Our results show a large decrease in the omnivory 791 index in the future. The ecosystem could thus be most impacted by the decrease or loss of a 792 species or trophic group, as the ability of a consumer to modulate its diet according to the 793 prey present falls. A decrease in omnivory reduces the flexibility of the system and, 794 therefore, makes it more vulnerable to the disappearance or reduction of biomass of a 795 trophic group. In this way, the consequences for the trophic cascade could have a greater 796 impact (Spiers et al., 2016). However, the combined interpretation of omnivory and A/C 797 shaded this conclusion. The future increase of A/C observed brings the system to a state 798 closer to the "window of vitality" of ecosystems, which defines the optimal range of A/C 799 where the ecosystem is the most sustainable (Fath, 2015). A stress in an ecosystem induces 800 a change in its structure and functioning. In our case, the stress induced by the increase in sea water temperature and the arrival of NIS changes the structure of the trophic network
and the way energy enters it. It decreases the capacity of the system to absorb new stresses.
The multiplication of pressures on an ecosystem accentuates the consequences of each
pressure taken separately (Halpern et al., 2007; Wernberg et al., 2011).

805 5. Conclusion

806 This study is timely and important because the cumulative impacts of climate change and non-indigenous species arrivals have rarely been studied in the marine realm. Given 807 808 uncertainties about non-indigenous species arrivals, simulation through several models was relevant. Indeed, we cannot predict when and which species will enter the area from 809 southern regions under climate change. The models we developed in this study could all 810 represent future realities occurring at different times in the near future. It is possible that 811 NISPel may happen first, then the arrival of demersal with NISEqual and finally the 812 813 establishment of NIS with high biomass: NISMax. ENA indicators are increasingly used to quantify changes in ecosystems in order to adapt management strategies (Safi et al., 2019). 814 815 They make it possible to compare a single ecosystem at different levels of change and to compare trends with other ecosystems. The ENATool routine (Guesnet et al., 2015) allowed 816 817 us to make up for lacking data, especially concerning organism biomass. Our results revealed a negative impact of sea warming on the current trophic network due to the loss of 818 819 functional group biomass, despite an increase in productivity. The arrival of NIS could imply changes in communities, restructuring the trophic network. Finally, the cumulative effects of 820 821 both these influences could accentuate trophic network degradation.

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