



From species distributions to ecosystem structure and function: A methodological perspective



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ABSTRACT

As species biology and ecology is profoundly influenced by climate, any climatic alteration may have severe consequences on marine pelagic ecosystems and their food webs. It remains challenging to estimate the influence of climate on both structural and functional properties of food webs. In this study, we proposed an innovative approach to assess the propagating effects of climate change on ecosystem food web. The approach is based on a sensitivity analysis of a food-web model, a linear inverse model using a *Monte Carlo method coupled with a Markov Chain*, in which changes in the values of parameters are driven by external Ecological Niche Model outputs. Our sensitivity analysis was restricted to parameters regarding a keystone functional group in marine ecosystems, i.e. small pelagic fish. At the ecosystem level, the consequences were evaluated using both structural and functional ecological network indices. The approach is innovative as it is the first time that these three methods were combined to assess ecological network indices sensitivity to future climatic pressure. This coupling method was applied on the French continental shelf of the Bay of Biscay for which a food-web model already exists and where future changes in the distribution of small pelagic fish have already been examined through model building and projections. In response to the sensitivity analysis corresponding to an increase in small pelagics production only, our results suggested a more active system with an intense plankton–small pelagics–seabirds chain and an efficient recycling to maximize detritus use in the system in relation with detritus export. All results combined together seemed to be in favor of a system adapting to sustain the tested increase in production of small pelagic planktivores. Finally, regarding the innovative combination of numerical tools presented, even if further investigations are still necessary to get a more realistic view of cumulative effects resulting from one given pressure (or more) on a food web (e.g. altering different biological compartments at the same time), the Ecological Network Analysis indices values showed a higher variability under the scenarios of change. Our study thus pointed out a promising methodology to assess propagating changes in structural and functional ecosystem properties.

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1. Introduction

The effects of climate change on biological and ecological systems is incontrovertible (Doney and Sailley, 2013; Beaugrand et al., 2015a) and is likely to lead to unexpected modifications in ecosystem functions (Scheffer et al., 2001; Scheffer and Carpenter, 2003; Beaugrand et al., 2009) and associated services for humankind, with strong socio-economic implications (Halpern et al., 2008). In the context of human-driven climate change, these modifications of ecosystem structures, functions, and status are at least partly related to strong alterations of lower trophic levels such as primary producers, primary consumers or planktivorous organisms in aquatic environments (Parmesan and Yohe, 2003; Parmesan, 2006). Different responses have been documented, including physiological effects of climate change on organisms (Arrhenius, 1889; Magnuson et al., 1979), phenological shifts (Edwards and Richardson, 2004) and potential changes in species spatio-temporal distributions (Quéro et al., 1998; Stebbing et al., 2002; Hermant et al., 2010; Alekseenko et al., 2014). However, the propagation of these alterations through the food webs and their consequences on the food-web emerging properties remains poorly understood with only rare examples documented for freshwater and marine systems (e.g. Woodward et al., 2010; Albouy et al., 2013; Chust et al., 2014).

In line with these major issues, our paper proposes a methodology to investigate the propagating effect of climate change on the trophic pathways and the functioning properties of ecosystems. The study case was the Bay of Biscay French continental shelf, with a special emphasis on the consequences of a change in the production of a keystone functional group, i.e. the pelagic planktivorous fish. Here, we proposed for the first time a combination of three numerical methods: (i) an Ecological Niche Model (ENM; Beaugrand et al., 2011; Lenoir et al., 2011) investigating the environmental descriptors driving species distributions to estimate the changes in the production of small planktivorous fish in relation to future climate scenarios; (ii) A Linear Inverse Model using a Markov Chain Monte Carlo method (Kones et al., 2006; Niquil et al., 2012) to determine the consequences of changes in small pelagics production on the carbon flows of the Bay of Biscay French continental shelf food web; and (iii) calculation of Ecological Network Analysis indices (ENA; Ulanowicz, 1992; Patrício et al., 2004; Baird et al., 2012; Saint-Béat et al., 2015) to assess the propagating consequences of changes in

the production of small pelagics on the whole food web. With this ecologically meaningful study case, we are particularly interested in demonstrating whether ENA indices are reflecting the propagating consequences of a change in one compartment balance. Indeed, the recent European directives [e.g. Marine Strategy Framework Directive (MSFD), Water Framework Directive (WFD)] stress the urgent need of development, test, and validation of ecosystem health indicators. This study combining numerical methods allowed exploring the consequences of climate-related changes on the food-web properties and ecosystem status. Moreover, ENA indices (Ulanowicz, 1986) were proposed as ‘candidate’ indicators for the common biodiversity indicators list of OSlo and PARis Convention [OSPAR] (Niquil et al., 2014a), because they capture well the functional and structural properties of ecosystems (Ulanowicz, 1992; Patrício et al., 2004; Baird et al., 2012; Saint-Béat et al., 2015).

This study aims to propose a numerical approach (i) to assess propagating changes in structural and functional ecosystem properties and (ii) test the sensitivity of candidate indicators to the climate change pressure for the common biodiversity indicators list of the OSPAR Convention.

2. Materials and methods

2.1. Study area

The study area considered in this work is the French continental shelf of the Bay of Biscay (between the 30 m- and 150 m-isobaths), a Gulf of the North-East Atlantic Ocean located off the western coast of France and the northern coast of Spain (48.5° N–43.5° N and 8° W–3° W; Fig. 1). This system is hydrodynamically complex, being influenced by upwelling events, coastal run-off and river plumes, seasonal currents, eddies, internal waves, and tidal fronts (Planque et al., 2004). The supply of freshwater is mainly provided by 5 rivers: the Loire, the Garonne–Dordogne, the Adour, the Vilaine, and the Charente. All these hydrodynamic processes are known to affect species populations (Varela, 1996; Lampert, 2001; Hily et al., 2008). Ecosystem dynamics is also driven by anthropogenic pressures, the most important being the multifleet fishery operating in the Bay of Biscay (Hily et al., 2008; Rochet et al., 2012). In this respect, the study area is composed of ICES divisions VIIIa and VIIIb (ICES; www.ices.dk) and has a total surface area of 102,585 km².

2.2. The Bay of Biscay French continental shelf LIM-MCMC model

This study was based on a Linear Inverse Model used to estimate processes difficult to measure in the field, especially for large ecosystems, and, when combined to ENA indices, characterize the ecosystem status of the Bay of Biscay French continental shelf and its associated structural and functional properties (Chaalali et al., 2015) under varying environmental conditions. The structural properties refer to the network of interactions (i.e. presence or absence of pathways and pathway values) linking the species or groups of species, whereas the functional properties correspond to the emergent properties describing how the carbon flows through ecosystem boundaries.

The LIM was built as a combination of mass-balance equations (and potential *in situ* measures of flow expressed as complementary equations) and inequalities which constrain flow values. In most cases, constraints were based on the ecophysiology of the species making up the model compartments (Niquil et al., 2012). LIM food webs are described as linear functions of flows constrained from empirical data. As the system of equalities is underdetermined, infinity of different solutions exists. The Markov Chain Monte Carlo (MCMC) approach coupled with LIM allows retrieving a large set of

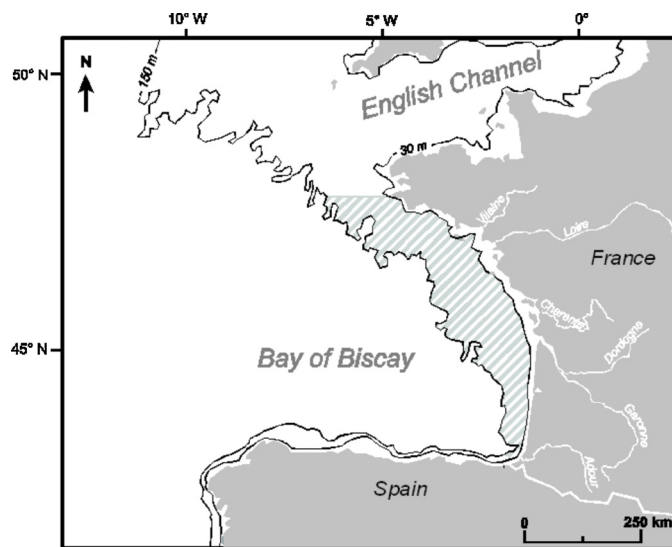


Fig. 1. Study area of the Bay of Biscay continental shelf and locations of the main rivers flowing into it. The shaded area corresponds to the French part of the continental shelf (between 30 m- and 150 m-isobaths), and represents the spatial extent of the LIM-MCMC.

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