



Structural uncertainty in projecting global fisheries catches under climate change



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ABSTRACT

The global ocean is projected to be warmer, less oxygenated and more acidic in the 21st century relative to the present day, resulting in changes in the biogeography and productivity of marine organisms and ecosystems. Previous studies using a Dynamic Bioclimate Envelope Model (DBEM) projected increases in potential catch in high latitude regions and decreases in tropical regions over the next few decades. A major structural uncertainty of the projected redistribution of species and fisheries catches can be attributed to the habitat suitability algorithms used. Here, we compare the DBEM projections of potential catches of 500 species of exploited marine fishes and invertebrates from 1971 to 2060 using three versions of DBEM that differ by the algorithm used to predict relative habitat suitability: DBEM-Basic, DBEM-Maxent and DBEM-Aquamaps. All the DBEM models have similar skill in predicting the occurrence of exploited species and distribution of observed fisheries production. Globally, the models project a decrease in catch potential of 3% to 13% by 2050 under a high emissions scenario (Representative Concentration Pathway 8.5). For the majority of the modelled species, projections by DBEM-Maxent are less sensitive to changes in ocean properties than those by DBEM-Aquamaps. The mean magnitude of projected changes relative to differences between projections differ between regions, being highest (>1 times the standard deviation) in the tropical regions and Arctic Ocean and lowest in three of the main Eastern Boundary Upwelling regions, the eastern Indian Ocean and the Southern Ocean. These results suggest that the qualitative patterns of changes in catch potential reported in previous studies are not affected by the structural uncertainty of DBEM, particularly in areas where catch potential was projected to be most sensitive to climate change. However, when making projections of fish stocks and their potential catches using DBEM in the future, multiple versions of DBEM should be used to quantify the uncertainty associated with structural uncertainty of the models. Overall, this study contributes to improving projection of future changes in living marine resources by exploring one aspect of the cascade of uncertainty associated with such projections.

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1. Introduction

Biogeochemical properties of the oceans have been altered by CO₂ emissions from human activities since the beginning of the 20th century (Gattuso et al., 2015; IPCC, 2013). Particularly, the ocean is becoming warmer, less oxygenated, and (Portner et al., 2014), resulting in changes in the distribution (Cheung et al.,

2013a; Pinsky et al., 2013; Poloczanska et al., 2013), community structure (Beaugrand et al., 2015), trophodynamics (Ainsworth et al., 2011; Kirby and Beaugrand, 2009; Stock et al., 2014a), and productivity of marine organisms and ecosystems (Gattuso et al., 2015; Portner et al., 2014). Consequently, fisheries will be impacted through changes in distribution and potential catches of exploited marine species (Barange et al., 2014; Cheung et al., 2011, 2010). Previous studies using a Dynamic Bioclimate Envelope Model (DBEM) project increases in catch in high latitude regions and decreases in tropical systems by the mid-21st century (Cheung et al., 2010, 2011).

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The DBEM is a numerical approach to project the effect of climate change on exploited species and consists of two main components: (1) predicting species' habitat suitability in each spatial grid; (2) simulating spatial population dynamics of fish stocks that include population growth, movement and dispersal of adult and larvae, as well as the ecophysiological effects of temperature, oxygen and acidity on body size, growth, mortality and reproduction (Cheung et al., 2013b). In addition, DBEM takes into account changes in net primary production (NPP) across space and time that affect an ecosystem's capacity to support fish stocks and alter fisheries catch potential (Fernandes et al., 2013). Thus, the projected redistribution of fisheries catch potential is in part due to poleward shifts in the distributions of exploited fish stocks that result in invasion of warmer-water species into higher latitude regions and local extinction in tropical waters (Jones and Cheung, 2015), and in part to changes in primary productivity (Cheung et al., 2011).

The prediction of species' habitat suitability under changing ocean biogeochemical properties can potentially alter projections of catch potential by DBEM and may be an important source of uncertainty (Jones et al., 2015). Habitat suitability in DBEM is predicted based on species' preferences to environmental conditions, inferred by overlaying current distributions with gridded environmental data (Cheung et al., 2008c). Alternative methods of predicting habitat suitability are available and the application of these methods may generate substantially different projections of biogeography (Elith and Leathwick, 2009). At a regional scale, a case study of projecting future catch potential under climate change scenarios in the UK waters using DBEM and two alternative species distribution models suggests that the projected trends are consistent between models, while the magnitude and finer scale patterns of change may vary substantially (Jones et al., 2015). However, the effects of using different habitat suitability algorithms in projecting global change in fisheries catch under the DBEM framework have not been explored previously.

In this study, we examined the effects of using alternative numerical procedure to predict species' habitat suitability on projected changes in catch of exploited marine fishes and invertebrates under the DBEM framework. Specifically, we compared the DBEM projections using the original habitat suitability algorithm as described in Cheung et al. (2011) with projections that were driven by predicted habitat suitability from Maxent and Aquamaps (Jones and Cheung, 2015). We evaluated the degree of agreement between the predicted potential catch with the total maximum fisheries catches of the modeled species as reported in the *Sea Around Us* dataset (www.seaaroundus.org). We hypothesized that the projected direction of changes in global and regional total potential catch is consistent between alternative algorithms while the projected magnitude of change is more sensitive to alternative habitat suitability predictions. If such hypotheses are supported by this study, it would imply that the general pattern of projected potential catch under climate change showed in previous studies using DBEM projections, e.g., Lam et al. (2014), are robust to alternative structures of DBEM while there is a need to further explore other sources of variability and uncertainties associated with the projections (Cheung et al., 2016).

2. Methods

2.1. Dynamic Bioclimate Envelope Model (DBEM)—Basic structure

We used the DBEM to simulate changes in distribution, abundance and catches of exploited marine fishes and invertebrates. The structure of the DBEM is described in Cheung et al. (2011) and we summarize pertinent aspects of the model here.

2.1.1. Current species distribution

The current distributions of commercially exploited species, representing the average pattern of relative abundance in recent decades (i.e., 1970–2000), were produced using an algorithm developed by the *Sea Around Us* Project (see Close et al., 2006; Cheung et al., 2008b; www.seaaroundus.org). The algorithm estimates the relative abundance of a species on a 0.5° latitude \times 0.5° longitude grid based on the species' depth range, latitudinal range, known Food and Agriculture Organization statistical areas and polygons encompassing their known occurrence regions. The distributions were further refined by assigning habitat preferences to each species, such as affinity to shelf (inner, outer), estuaries, and coral reef habitats. The required habitat information was obtained from FishBase (www.fishbase.org) and SeaLifeBase (www.sealifebase.org), which contains key information on the distribution of the species in question, and on their known occurrence region.

2.1.2. Projecting future habitat suitability

We calculated an index of habitat suitability for each species (P) in each spatial cell i from temperature (bottom and surface temperature for demersal and pelagic species, respectively), bathymetry, specific habitats, salinity and sea ice with 30-year averages from 1971 to 2000 of outputs from Earth System Models (see Supplementary materials). The multiple of these five components resulted in the overall habitat suitability:

$$P_i = P(T_i, TPP) \cdot P(\text{Bathy}_i, \text{MinD}, \text{MaxD}) \cdot P(\text{Habitat}_{i,j}, \text{HAssoc}) \cdot P(\text{Salinity}_i, \text{SAssoc}) \cdot P(\text{Ice}_i, \text{IceP}) \quad (1)$$

where T is seawater temperature, Bathy is bathymetry, Habitat is the proportion of area of the habitat type j relative to the total seawater area of the cell i , Ice is sea ice extent, and Salinity is the salinity class of cell i according to the Thalassic series (hyperhaline, metahaline, mixoeuhaline, polyhaline, mesophaline and oligohaline). For each species, TPP is temperature preference profile, MinD and MaxD are minimum and maximum depth limits, HAssoc is habitat association index, and SAssoc has a value of 1 or 0 indicating whether the species is or is not associated to the specific salinity classes, respectively, and IceP is association to sea ice for polar species.

Specifically, DBEM estimated the temperature preference profile (TPP) of each species by overlaying the estimated species distribution (Cheung et al., 2008b; Close et al., 2006; Jones et al., 2012) with annual seawater temperature and calculated the area-corrected distribution of relative abundance across temperature for each year from 1971 to 2000, subsequently averaging annual temperature preference profiles (TPP). The TPP was calculated from the predicted average relative abundance (R_i) from the estimated current species distribution in temperature class i over the entire range:

$$TPP_i = \frac{R_i}{\sum R_i} \quad (2a)$$

$$R_i = \frac{Q_i}{A_i} \quad (2b)$$

where Q_i and A are the sum of relative abundance and range area from spatial cells within temperature class i .

A species' distribution was also limited indirectly by depth. Thus, there were lower and upper limits of water depth (minD and maxD , respectively) outside of which a species does not occur i.e.:

$$P(\text{Bathy}, \text{minD}, \text{maxD}) = 1 \quad \text{if } \text{Bathy} \geq \text{minD} \text{ and } \text{Bathy} \leq \text{maxD} \quad (3a)$$

$$P(\text{Bathy}, \text{minD}, \text{maxD}) = 0 \quad \text{if } \text{Bathy} < \text{minD} \text{ or } \text{Bathy} > \text{maxD} \quad (3b)$$

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