Geoscientific
Model Development

A protocol for the intercomparison of marine fishery and ecosystem models: Fish-MIP v1.0

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Abstract. Model intercomparison studies in the climate and Earth sciences communities have been crucial to building credibility and coherence for future projections. They have quantified variability among models, spurred model development, contrasted within- and among-model uncertainty, assessed model fits to historical data, and provided ensemble projections of future change under specified scenarios. Given the speed and magnitude of anthropogenic change in the marine environment and the consequent effects on food security, biodiversity, marine industries, and society, the time is ripe for similar comparisons among models of fisheries and marine ecosystems. Here, we describe the Fisheries and Marine Ecosystem Model Intercomparison Project protocol version 1.0 (Fish-MIP v1.0), part of the Inter-Sectoral Impact Model Intercomparison Project (ISIMIP), which is a cross-sectoral network of climate impact modellers. Given the complexity of the marine ecosystem, this class of models has substantial heterogeneity of purpose, scope, theoretical underpinning, processes considered, parameterizations, resolution (grain size), and spatial extent. This heterogeneity reflects the lack of a unified understanding of the marine ecosystem and implies that the assemblage of all models is more likely to include a greater number of relevant processes than any single model. The current Fish-MIP protocol is designed to allow these heterogeneous models to be forced with common Earth System Model (ESM) Coupled Model Intercomparison Project Phase 5 (CMIP5) outputs under prescribed scenarios for historic (from the 1950s) and future (to 2100) time periods; it will be adapted to CMIP phase 6 (CMIP6) in future iterations. It also describes a standardized set of outputs for each participating Fish-MIP model to produce. This enables the broad characterization of differences between and uncertainties within models and projections when assessing climate and fisheries impacts on marine ecosystems and the services they provide. The systematic generation, collation, and comparison of results from Fish-MIP will inform an understanding of the range of plausible changes in marine ecosystems and improve our capacity to define and convey the strengths and weaknesses of model-based advice on future states of marine ecosystems and fisheries. Ultimately, Fish-MIP represents a step towards bringing together the marine ecosystem modelling community to produce consistent ensemble medium- and long-term projections of marine ecosystems.

1 Introduction

The ocean provides nearly half of global primary production (Field et al., 1998), hosts 25 % of eukaryotic species (Mora et al., 2011), provides 11 % of global animal protein consumed by humans (FAO, 2014), and is a source of livelihoods for millions (Sumaila et al., 2012). Yet the pace and magnitude of projected climate change over the coming century, in combination with fisheries exploitation and a raft of other human impacts, suggests that marine ecosystems will remain under considerable pressure in the midterm to long term (Pörtner et al., 2014; UN, 2016). Identification of the potential future effects of these pressures, even with high uncertainty (Payne et al., 2016), is required to anticipate the impacts of environmental change on ecosystem resilience (Bernhardt and Leslie, 2013), biodiversity conservation (Cheung et al., 2016a; Queirós et al., 2016), socio-economics (Fernandes et al., 2017), and food security (Barange et al., 2014; Merino et al., 2012). Marine ecosystem models give us an approach to meeting this goal by providing scenario-driven projections of future fisheries production (e.g. Blanchard et al., 2012; Fernandes et al., 2016, 2017; Lehodey et al., 2015; Mullon et al., 2016), marine ecosystem structure and functioning (Jennings and Collingridge, 2015), and species compositions and distributions (Jones and Cheung, 2015) under global change.

The scientific understanding of the physical climate system and its response to anthropogenic perturbation has profited enormously from model intercomparison efforts like the Coupled Model Intercomparison Project (CMIP; Taylor et al., 2012) and the Ocean Model Intercomparison Project

(OMIP; Griffies et al., 2016). CMIP and other efforts have highlighted differences among models, provided ranges of potential climate change responses and ensemble projections for end users, and allowed the outputs of individual analyses to be interpreted in a broader context. They have also provided a quantification of the relative contributions of different sources of uncertainty to projected uncertainties in climate responses (Hawkins and Sutton, 2009; Payne et al., 2016).

In addition to model intercomparison experiments for the climate and ocean system, a systematic intercomparison and assessment of *impact* models – including the marine realm – is similarly essential for understanding the impacts of (and associated uncertainty around) climate change on important biological and human systems (Barange et al., 2014). Such impact models typically use the outputs of scenario-driven Earth system models (ESMs), individually or as ensembles, as inputs to project the effects of these on sectors such as agriculture or energy. The Inter-Sectoral Impact Model Intercomparison Project (ISIMIP; www.isimip.org) was set up to enhance consistency among climate impact studies across different sectors, including food production, ecosystems and biodiversity, freshwater availability, and human health among others (Huber et al., 2014; Schellnhuber et al., 2013). It does so chiefly through providing common climate and socio-economic input data and defining a common set of simulation experiments (Warszawski et al., 2013).

Although there have been prior intercomparisons of fisheries and marine ecosystem models, they have been limited to a few models applied to local or regional case studies (Coll et al., 2008; Fulton and Smith, 2004; Jones et al., 2013; Shin et al., 2004; Smith et al., 2011; Travers et al., 2010) or to lower trophic levels of the global ocean rather than the whole ecosystem (see the Marine Ecosystem Model Intercomparison Project MAREMIP at pft.ees.hokudai.ac.jp/maremip/index.shtml; Bopp et al., 2013). Here, we describe the Fisheries and Marine Ecosystem Model Intercomparison Project (Fish-MIP) protocol v1.0, which intends to standardize to the extent possible input variables to fisheries and marine ecosystem models and to analyse, compare, and disseminate outputs from multiple models to assess climate and fisheries impacts on marine ecosystems and the services they provide, such as potential future fisheries catches. The Fish-MIP protocol has been designed in coordination with the other ISIMIP sectors and forcings, which will enhance consistency when looking at synergistic impacts and considering multisectoral aspects such as global food security and economic impacts. This article describes the Fish-MIP protocol and provides background on the range of existing ecosystem models, including the resolved processes, theoretical approaches, and specifications, and provides the foundation for forthcoming studies under the umbrella of this project. We emphasize here that Fish-MIP is continuously ongoing in terms of development and refinement: see www.isimip.org/gettingstarted/

marine-ecosystems-fisheries/forupdates. While many Fish-MIP model runs for the v1.0 protocol (ISIMIP simulation round 2A) have been completed, some are still in progress or under analysis, and results will be published once runs are complete (see Blanchard et al., 2017, though).

The scope of Fish-MIP v1.0 is global and regional using fisheries and marine ecosystem models able to make historical ($\sim$ the 1950s onwards) and medium- to long-term (defined here as $\sim$ 2030–2100) projections of ecosystem structure, dynamics, and function using the same set of scenarios and reanalyses of climate change and variability. Single-species and multispecies tactical models for fisheries stock assessment and management are therefore excluded; a complementary initiative presently underway under the auspices of the intergovernmental organizations ICES (www.ices.dk) and PICES (www.pices.int), the Strategic Initiative on Climate Change effects of Marine Ecosystems (SICCME), aims to fill this gap. The long time horizon of Fish-MIP means that outputs are most likely to inform those focusing on long-term changes in the global and regional environment and future policy development, such as the Intergovernmental Panel on Climate Change (IPCC), the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES), and the United Nations Regular Process of work on the Sustainable Development Goals (SDGs). Results may also be of interest to national bodies and management authorities interested in scenarios or species distribution shifts (ICES, 2016). Questions of interest include the effect of climate impacts on the distribution, diversity, and productivity of fishes and fisheries, exploration of global fisheries scenarios and projections and their implications for food security (Béné et al., 2015), and the conservation status of marine fauna and their role in biogeochemical cycles.

The development of marine ecosystem models, which aim to simulate the structure, dynamics, production, and functional role of marine biota interacting with each other and their environment across multiple trophic levels, was initiated at least 4 decades ago (Andersen and Ursin, 1977; Polovina, 1984; Sheldon et al., 1977) and somewhat earlier for efforts with less-resolved biology (Hamblin, 2005). More recently, to support ecosystem-based fisheries management, marine ecosystem models have been applied to assess changes in ecosystem structure and function under fisheries and environmental drivers (Fulton, 2010). Unlike in the physical and chemical sciences, where there is often clarity about fundamental representations and processes driven by underlying theory or experimentation, the development of marine ecosystem models has been approached from many perspectives, reflecting differences in scientific and management objectives, theoretical frameworks, modelling structures and parameterizations, input data needs, resolutions (spatial, temporal, vertical, process, and taxonomic), and process complexity. They include differing assumptions of top-down, bottom-up, or mixed trophic control, the role of species as opposed to trophic groups, functional groups, or

body size classes, and the characterization of growth, mortality, recruitment, and movement.

Applying such a range of different model types will provide useful insights into the effects of climate variability and change on marine ecosystems and fisheries, but also makes intercomparisons challenging. Unsurprisingly, the inputs to and outputs from such models are diverse and difficult to standardize, with no common set of defined output metrics that can be used for comparison purposes. Here we review the models participating in the first round of Fish-MIP simulations (using CMIP5 ESM output), describe our intercomparison protocol, highlight the challenges that have arisen in developing this protocol, and detail the approaches that we have used to resolve these difficulties. We also identify future pathways for Fish-MIP, including the use of CMIP6 output and refined fisheries scenarios. The lessons learned here also apply to other marine model comparisons and will help to guide the development of new models to investigate patterns of change in the future oceans.

2   Marine ecosystem models participating in Fish-MIP

The last 3 decades have seen a profusion of marine ecosystem models being developed, with many emerging during the last decade (Fulton and Link, 2014; Nielsen et al., 2017; Peck et al., 2016). Fish-MIP is open to all developers and users of marine ecosystem models who are willing to run consistent scenarios to facilitate comparisons. All models in the intercomparison must be documented in appropriate venues, such as the peer-reviewed literature, to ensure that descriptions of the model are widely available and that key features and parameterizations are codified and model runs repeatable. Here we introduce the model types that have been included in Fish-MIP to date, recognizing that these are a subset of the many available and extensively reviewed elsewhere (Fulton and Link, 2014; Hollowed et al., 2000; Plagányi, 2007; Plagányi et al., 2011, 2014; Townsend et al., 2008; Travers et al., 2007).

2.1   Model heterogeneity

The diversity of model types participating in Fish-MIP and some of their unique characteristics are summarized in Table 1. One constant feature across all the participating models is the inclusion of multiple species or functional groups (typically an aggregation of species or food web elements) and environmental drivers. These minimum specifications are in line with the need to characterize the transfer of biomass from primary producers to mid- and upper trophic level organisms, which are often those impacted or used by society or of conservation interest. Among the key differences therein, the spatial resolution of participating models ranges from simple 0-D boxes encompassing model parameters averaged over a large area, to irregularly shaped polygons cor-

responding to depth and bathymetric features, to regional models gridded at $0.1 \times 0.1°$, to global models gridded at resolutions typically around $0.5 \times 0.5°$ to $1 \times 1°$. Some models are fully or partially vertically resolved, while others consider depth implicitly through food web interactions and habitat preference patterns or do not model the vertical dimension at all. The movement of fish can be ignored, defined by discrete rules between adjacent grid cells, driven by climate niche models, or expressed through formal advection–diffusion systems of equations. Fisheries are elaborated to differing degrees, from complete absence, to a simple fishing mortality term, to more elaborate fishing effort allocation formulations.

The wide array of modelling approaches leads to a wide array of input data requirements (Table 2). Some models use a single forcing variable, often a primary production anomaly or estimate derived from the output of a regional ocean-biogeochemistry or a global Earth system model (ESM), while others use multiple variables directly. While all the global Fish-MIP models use temperature as an input variable, some use fully vertically resolved 3-D data, others use temperature averaged over a near-surface layer such as the mixed layer, a few wide layers (e.g. epipelagic, upper mesopelagic, and lower mesopelagic layers), sea-surface and sea-bottom temperature, or sea-surface temperature only (Table 2). Some models require or can use additional inputs other than primary production and temperature, such as total alkalinity, nutrients, light (photosynthetically active radiation), or a turbulent mixing parameter. In terms of temporal scales, most models run on monthly or yearly time steps, though others run on very fine timescales of a day or less, creating another axis of variation when considering model differences and input requirements.

In terms of model outputs, all current Fish-MIP models can produce a measure of biomass density for all consumers and for particular size classes (which itself may require translation from functional groups to sizes classes or classification of species under a particular class if body length is not tracked; Table 3). Most models also consider some measure of fisheries production (e.g. catches, fisheries landings, mortality rates). It is worth highlighting the difference between models that predict catch from effort and fish biomass versus those that are forced using catch data: in the former, catch is an output, while in the latter, it is an input, and measures of fisheries production cannot thus be calculated. Further, some models enable statistical fitting to catch or effort data in which case other parameters are estimated (such as fishing mortality rates).

The great heterogeneity in input data requirements presented a large challenge when developing the Fish-MIP protocol and constrained the set of ESM outputs (from CMIP v5) that could be used. Forcing using identical ESM outputs is not feasible as the requirements and options for each Fish-MIP model differ (Table 2). Instead, participating models are forced using standardized inputs for those variables that are

Table 1. A taxonomy of marine ecosystem models taking part in the Fish-MIP project. See also Tables 2 and 3 for the degree of heterogeneity in inputs and outputs that also exists across the model types.

Fish-MIP model	Brief model description	Domain	Defining features and key processes	Spatial and temporal scale and vertical resolution	Taxonomic scope	Key reference
Species distribution models – statistical relationships between species and environment; focus on role of habitat change and population dynamics						
DBEM	The DBEM defines a bioclimatic envelope for each species and simulates changes in abundance and carrying capacity under a varying environment.	Global	Carrying capacity is a function of the environment and species' preferences for these factors. Movement of adults is driven by a gradient of habitat suitability and density. Larval dispersal is dependent on currents and temperature. Growth, reproduction, and mortality are dependent on oxygen, pH, and temperature.	$1/2 \times 1/2°$; model outputs are annual average. Vertical dimension implicit through species niche preferences.	Fish and invertebrate species (primarily commercial).	Cheung et al. (2011)
SS-DBEM	SS-DBEM is based on the DBEM and the macroecological model, projects changes in species distribution, abundance, and body size, and includes population dynamics, dispersal, and competition.	Global	Key processes include ecophysiology, population dynamics, dispersal, trophic interactions, fishing mortality, and habitat suitability.	$1/2 \times 1/2°$ and yearly. Often aggregated into management or ecological meaningful units (e.g. EEZ, LMEs, or ICES areas). Vertical dimension implicit through species niche preferences.	All trophic levels of fish and invertebrates.	Fernandes et al. (2013)
Trophodynamic models – structured based on species interactions and transfer of energy across trophic levels						
Ecopath with Ecosim (EwE)	Ecopath with Ecosim is a mass-balance food web model that accounts for the flow of biomass between trophic groups.	Regional	Includes a mass-balance component (Ecopath), a temporal dynamic component (Ecosim), and a spatial–temporal dynamic component (Ecospace). Typically resolved to a mix of functional groups and key species.	Spatial resolution varies from local to global, gridded configuration. Flexible, typically running in monthly time steps. Depth dimension is considered implicitly through food web interactions and habitat preference pattern.	All trophic levels and taxonomic groups can be included as biomass pools or age-structured life history stanzas.	Christensen and Walters (2004)
EcoOcean	EcoOcean is a global food web model based on the EwE framework designed to evaluate the impact of climate change and human pressure on marine ecosystems.	Global	Atmosphere–ocean circulation model (COBALT); EwE food web model with Ecosim and Ecospace habitat capacity model; fisheries effort global gravity model.	Global model. Spatial resolution is $1/2 \times 1/2°$ and outputs are annual or monthly averages. Depth dimension is considered implicitly through food web interactions and habitat preference pattern.	All trophic levels and taxonomic groups included as biomass pools (51 groups).	Christensen et al. (2015)
Size-based models – developed from food web, macroecological, and life history theory for exploration of community size spectra						
Macroecological model	A static model, which uses minimal inputs together with ecological and metabolic scaling theory to predict mean size composition and abundance of animals (including fish).	Global	Provides a simple size-based characterization of marine ecosystems. Relies on estimates of predator–prey mass ratios, transfer efficiency, and changing metabolic demands with body mass and temperature to predict body mass distributions and abundance of marine consumers from phytoplankton primary production and environmental temperature. Ignores non-phytoplankton production and animal movement.	Static equilibrium model, typically applied at scales from $0.5 \times 0.5°$ grids to large marine ecosystems; forced with annual or monthly mean environmental variables. Single vertical (surface-integrated) layer.	Species are not resolved, only body mass classes.	Jennings and Collingridge (2015)
Dynamic Pelagic–Benthic Model (DPBM)	A functional trait-based size spectrum model that joins a pelagic predator size spectra model with a benthic detritivore size spectrum; can include herbivores or other groups that do not feed according to size and unstructured resources.	Global or regional	Individual processes of predation, food-dependent growth, mortality, and reproduction give rise to emergent size spectra for each functional group. Can be linked to GCMs, regional models, or observations via parameterizing phytoplankton and zooplankton size spectra, detritus, and/or temperature.	Spatial scale of grid is flexible and dependent on inputs; temporal scale daily or weekly; two vertical layers (sea surface and sea floor).	Broadly represents "pelagic" fish predators and "benthic" invertebrates but can include herbivorous fish; flexible functional groups.	Blanchard et al. (2012)
BOATS	Combines size-based ecological theory and metabolic constraints to calculate the production of fish, is resolved across multiple size spectra, and applies a coupled economic model to determine effort and harvest based on economic boundary conditions.	Global or regional	Applies empirical parameterizations to describe phytoplankton community structure, trophic transfer of primary production from phytoplankton to fish, growth rates, and natural mortality. Model parameters are calibrated against observed using a Monte Carlo technique. Explicitly models the evolution of effort and harvest. Recruitment is dependent on stock size and the environment, and simple life history features are resolved.	Flexible spatial scale; typically global at $1 \times 1°$; monthly timestep; single vertical (surface-integrated) layer.	All commercial species represented by three groups, defined in terms of the asymptotic mass.	Carozza et al. (2016)

Table 1. Continued.

Fish-MIP model	Brief model description	Domain	Defining features and key processes	Spatial and temporal scale and vertical resolution	Taxonomic scope	Key reference
POEM	A mechanistic ecosystem model that uses body size as the basis of interaction. Offline coupled to an Earth system model using zooplankton biomass and mortality fields to force ecosystem dynamics.	Global	Simple size-based relationships defined by empirical allometric relationships are used to model ecological interactions.	Spatial scale $1 \times 1°$; daily timestep; single vertical layer representing upper 200m.	One or two "ecotypes", e.g. a piscivore or a planktivore.	Watson et al. (2015)
Composite (hybrid) models – including multiple (e.g. size, age, trophic, physical, and other) model formulations in system representation						
Atlantis	Atlantis is a whole ecosystem model taking a transport model derived from hydrodynamic or GCM output that sets the conditions for a full representation of the food web and human users.	Regional	Modular (multiple options per process). Includes age structure and major ecological processes such as full life history closure, gape-limited predation, habitats, movement, biogeochemical nutrient cycling, and a range of effort allocation options.	3-D spatial polygons matched to biophysical features; vertically resolved using "slab" layers (with finer layers and the surface and thicker at depth). Timestep is flexible, typically 6–24 h.	All trophic levels and taxonomic groups can be represented using a mix of biomass pools and age-structured populations. Typically resolved to a mix of functional groups and key species.	Fulton et al. (2011)
OSMOSE	The higher-trophic-level model OSMOSE (Object-oriented Simulator of Marine ecOSystems Exploitation) is a spatial multispecies and individual-based model which focuses on fish species. Its current structure embeds a coupling with hydrodynamic and biogeochemical models.	Regional	Trophic interactions are size-based so the modelled food webs are dynamic. The whole life cycle of the modelled species is represented (migration, food-dependent growth, reproduction, and mortality), with tracking of all life stages (from eggs to terminal age) in space and time. Provides size-, age-, species-, and trophic-level-based indicators in output.	Flexible. Typically, resolution of $1/6°$ and a weekly time step. Spatially resolved in 2-D; the vertical distribution of species is handled through a matrix of accessibility.	Fish and invertebrate species and functional groups.	Travers et al. (2009)
SEAPODYM	SEAPODYM is an Eulerian modelling framework including functional groups of lower and mid-trophic levels and population dynamics of target species; developed for investigating spatial pelagic fish population dynamics under the influence of fishing and environment.	Regional or global	Functional groups of zooplankton and micronekton are simulated and used with physical and biogeochemical variables to define the habitats, movements, and key population dynamic processes of targeted fish species. Fishing impact is simulated through catch and effort data. A statistical optimization approach uses all available data (catch by size, tagging data, larvae density, acoustic estimates) to estimate model parameters.	Flexible; typically $1/12°$ grid and daily timestep, or 1–2° grid × monthly time step. Three vertical layers of epipelagic and mesopelagic ocean.	One zooplankton and several micronekton functional groups defined based on their vertical behaviour and one to several targeted species with their fisheries.	Lehodey et al. (2008, 2010)
APECOSM	A 3-D dynamic energy budget-based Eulerian model of size-structured marine populations and communities based on environmentally driven individual bio-energetics, trophic interactions, and behaviours that are upscaled to populations and communities.	Regional or global	Includes light- and temperature-driven size-based predation, food- and temperature-driven growth, reproduction and senescence, and the impact of the environment on vertical and horizontal movements and schooling.	Can be run on any 3-D spatial grid from regional to global scale, with a daily timestep distinguishing day and night; no vertical resolution but vertical movements explicitly parameterized.	Generic size-based communities are explicit (typically epipelagic, migratory, mesopelagic, and bathy-pelagic) and focus species.	Maury (2010)
Madingley	A global, mechanistic, spatially explicit "general ecosystem model" of terrestrial and marine ecosystems used to explore changes in ecosystem structure and function.	Regional or global	Models functional groups and multispecies "cohorts"; millions of cohorts in model. Includes spatially explicit dispersal driven by ESM outputs, food-dependent growth, starvation, and senescence mortality. Allows for complete extinction of functional groups, and dynamic changes in ecosystem structure. Food web links are dynamic; cohorts can be prey or predator depending on size. Unlike many models, is not "mass balanced". Predators can switch between prey groups based on densities and preferences.	Any (typically 1–2° and monthly), with no vertical resolution at present	All (marine and terrestrial), excluding microbes, modelled as functional groups.	Harfoot et al. (2014)

included (Table 3). These variables are used on the spatial, temporal, and vertical scale appropriate to each model, but with a minimum monthly time step; e.g. models with a daily time step had to use monthly forcing data, taking the average value for that month and applying it daily (without the day-to-day variability typical of finer-scale forcing). This pri-

marily reflects the limitations imposed by the available ESM output.

Across the diversity of participating models, we recognize four broad classes: those focusing on species distribution, trophodynamic structure, size- or age-based structure, and composite (hybrid) models. This simple classification is

Table 2. Selected Earth system model outputs that are required or optional for individual Fish-MIP models. Fish-MIP models can require surface values, a mean or summed surface layer value (e.g. top 100 m), surface and sea-floor values, or fully three-dimensional values. Note that this list is correct at the time of writing, but that models are continuously in development with new components and requirements being added. Units follow CMIP5 standard output (http://cmip-pcmdi.llnl.gov/cmip5/data_description.html).

	Common variables used by at least 50 % of Fish-MIP models (provided for all Fish-MIP simulations)							Selected variables used by a small proportion of models				
	u and v current speed (m s^{-1})	Sea temperature or potential temperature (K)	Dissolved O$_2$ concentration (mol m^{-3})	Primary organic carbon productivity (mol m^{-3} s^{-1})	Zooplankton carbon concentration (mol m^{-3})	pH (unitless)	Salinity (psu)	Total alkalinity (mol m^{-3})	Phytoplankton carbon concentration (mol m^{-3})	Turbulent mixing (m^2 s^{-1})	Ice coverage (fraction)	Mixed-layer depth (m)
DBEM	●	●	●		●	●	●				●	
SS-DBEM	●	●	●	●		●	●				●	(●)
Ecopath With Ecosim	(●)	(●)	(●)	●	●	(●)	(●)		●			
EcoOcean	(●)	●	(●)	●	(●)	(●)	(●)		●		(●)	
Macroecological model		●		●	(●)				(●)			●
DPBM		●		(●)	(●)				(●)			●
BOATS		●		●								
POEM	●	●			●	●	●				●	●
Atlantis	●	●	●	[2]	[1]	●	●	●	[2]	●	●	
OSMOSE		●	●	●	●[3]		●		●[3]			
SEAPODYM	●	●	●	●					●			
APECOSM	●	●	●		●[3]	●			●[3]	(●)		
Madingley	●	●			●	[1]	●					

● Used by model. (●) Can optionally be used by model. [1] Not used for forcing, but can be used for cross-validation. [2] Not used directly, but in combination with hydrodynamic flows is used to set boundary conditions and sub-grid-scale processes to allow for similar primary productivity shifts as in ESM outputs to be realized. [3] Separated into large and small size classes.

used to structure this summary of models contributing to the Fish-MIP project.

2.1.1 Model classes: species distribution based models

Species distribution models (Cheung et al., 2016b; Fernandes et al., 2013; Jones and Cheung, 2015; Pearson and Dawson, 2003) use statistical, empirical, and theoretical relationships between a species and its environment to explore the implications of shifting environmental conditions and resulting habitat suitability distributions on the biomass and spatial range of species. Recent development has integrated this class of models with a mechanistic representation of ecophysiology and population dynamics and hence potential fisheries production (Cheung et al., 2011; Fernandes et al., 2013) and

fishing scenarios (Fernandes et al., 2016, 2017). For instance, the Dynamic Bioclimate Envelope Model (DBEM; Table 1) was applied to a suite of over 1000 species to examine shifts in distribution, abundance, and productivity under climate change scenarios and resultant global patterns of local extinction, invasion, biodiversity, and catch (Cheung et al., 2016b; Jones and Cheung, 2015). A version of DBEM that has incorporated size-based trophodynamics to mimic ecological interactions has also been applied to model a number of ecosystems (Fernandes et al., 2013, 2016, 2017). Typically, this class of models includes a large number of primarily commercially valuable fishes and invertebrates.

Table 3. Forcing variables derived from Earth system models and provided as input for global and regional marine fisheries models. Names and units follow CMIP5 standard output (https://cmip.llnl.gov/cmip5/data_description.html).

Variable	Name	Unit (assuming depth resolved)	Frequency	Comments
u current	uo	$m\,s^{-1}$	Monthly	
v current	vo	$m\,s^{-1}$	Monthly	
Temperature	t	K	Monthly	
Dissolved oxygen concentration	o2	$mol\,m^{-3}$	Monthly	
Primary organic carbon productivity	intpp	$mol\,m^{-3}\,s^{-1}$	Monthly	Sum of primary productivity by all primary producers (three groups – lphy, sphy, diaz – for GFDL reanalysis and GFDL-ESM2M, two groups – lphy, sphy – for IPSL)
Phytoplankton carbon concentration	phyc	$mol\,m^{-3}$	Monthly	Sum of small and large phytoplankton (including diazotrophs)
Small phytoplankton carbon concentration	sphyc	$mol\,m^{-3}$	Monthly	Picophytoplankton and nanophytoplankton
Large phytoplankton carbon concentration	lphyc	$mol\,m^{-3}$	Monthly	Diatoms, large non-diatoms, and diazotrophs
Zooplankton carbon concentration	zoo	$mol\,m^{-3}$	Monthly	Sum of small and large zooplankton
Small (micro)zooplankton carbon concentration	szoo	$mol\,m^{-3}$	Monthly	Post-diagnosed by normalizing to phytoplankton where unavailable
Large (meso)zooplankton carbon concentration	lzoo	$mol\,m^{-3}$	Monthly	Post-diagnosed by normalizing to phytoplankton where unavailable
pH	ph	unitless	Monthly	
Salinity	so	psu	Monthly	

2.1.2 Model classes: trophodynamic-based models

Trophodynamic models are typically structured based on species interactions and the transfer of energy across trophic levels. Ecopath with Ecosim (EwE), one of the oldest and most widely used marine ecosystem modelling approaches (Christensen and Walters, 2004), focuses explicitly on trophodynamics, as does its global offshoot EcoOcean (Christensen et al., 2015). EwE has been extensively used to explore potential fisheries impacts on and management options for aquatic ecosystems, to assess the impact of other human activities and climate variability and change (Niiranen et al., 2013), and to analyse and compare ecosystem structural and functional traits (Colleter et al., 2015). More recent applications include cumulative human impacts, marine *conservation*, environmental impact assessments, and end-to-end modelling (Coll et al., 2015). EwE models typically include demersal and pelagic species from primary producers

up to top predators, both commercial and non-commercial. Ecospace, the spatial–temporal model run in Ecosim in conjunction with the food web and fisheries dynamics components, has been further developed to spatially derive the foraging capacity of individual species from physical, oceanographic, and environmental drivers such as depth, temperature bottom type, oxygen concentrations, and primary production (Christensen et al., 2014). This development, in combination with the recently added spatial–temporal framework module (Steenbeek et al., 2013), has bridged the gap between environmental envelope models and food web models (Christensen et al., 2014, 2015). EwE models are typically structured by species or functional groups and can also include the age- or size- based representation of species.

2.1.3 Model classes: size- or age- based models

Contemporary models in this class build on size-based conceptualizations of marine ecosystems (Boudreau et al., 1991;

Dickie et al., 1987; Platt and Denman, 1978; Sheldon et al., 1972; Sheldon and Parsons, 1967) to characterize the flux of energy from primary producers to higher predators. Size-based approaches are predicated on the substantial role of body size in structuring food webs, which results from the dominance of small primary producers, size-based predation, and ontogenetic increases in trophic level when many predators grow 5–6 orders of magnitude in body mass from egg to adult (Jennings et al., 2012). The size-based models with the lowest parameter demands rely on empirical relationships that link body mass, temperature, and biological rates to support parameterization (e.g. Benoît and Rochet, 2004; Blanchard et al., 2009; Borgmann, 1987; Jennings and Collingridge, 2015; Watson et al., 2015). More complex size-based approaches describe some of the differences among species in a size-structured community by incorporating information on traits such as species maximum (asymptotic) size (e.g. Andersen and Beyer, 2006; Carozza et al., 2016; Pope et al., 2006). Life history theory can be used to estimate parameters such as size at maturity and reproductive output from maximum size. Other size- and species- based models may incorporate some species-specific information directly (Blanchard et al., 2014; Maury et al., 2007; Maury and Poggiale, 2013; Shin and Cury, 2004), but use general size-based relationships to describe other components of the system such as predator–prey relationships. As a variant of a size-based approach, time of development (i.e. age) to reach a critical life stage can be used to model the dynamics of species or functional groups (Lehodey et al., 2010). This approach can help to represent the effects of key environmental influences (e.g. temperature) in a different way. As well as being used for assessing the effects of fishing and environmental variation on marine ecosystems (e.g. Fu et al., 2013; Shin and Cury, 2004), size- or age-based ecosystem models have been used to underpin linked analyses of the effects of climate change on fisheries and society (Barange et al., 2014), including marine commodity trade (Mullon et al., 2016).

2.1.4 Model classes: composite (hybrid) models

The final class of models uses multiple formulation types to create representations of entire systems. Until recently, these models were distinct from other classes due to the breadth of processes covered; convergent evolution means that this is becoming less the case. Nevertheless, this class of models still tends to feature a broader set of ecological processes (including movement, feeding, reproduction, habitat use), the major biophysical drivers (e.g. temperature and salinity), a more complete food web, and often nutrient dynamics and cycles. This is achieved through composite (hybrid) end-to-end approaches that bring together multiple modelling methods either by coupling component models (which may be from the classes above) or via direct integration in a single unified framework. They resolve the food web to at least

functional group and in some cases the species level (or a mix of the two approaches). An example is Atlantis (Fulton et al., 2011), which uses a transport model to characterize three-dimensional current flows, a size-resolved biomass pool-based representation of the plankton food web, patch dynamic representation of demersal habitats, colonization-based representation of bacterial groups, and a fully age-structured representation of the vertebrate groups. On top of this is an effort allocation, and fisheries management model, and an ability to capture biogeochemical processes.

Many of the composite models (e.g. OSMOSE; Travers et al., 2009) are age or size structured, allowing them to capture the size-based feeding and ontogenetic shifts found in the size-based approaches discussed above. Aspects of the size-based approach are also used to represent the bulk of the food web in some composite models such as for the mid-trophic levels of SEAPODYM (Lehodey et al., 2008, 2010) and APECOSM (Maury, 2010), with more detailed elaboration applied to a subset of the system of particular interest (e.g. target species and higher trophic level species, such as tunas). Most composite (hybrid) process-based models have had a regional focus, in part due to data and computational requirements. An exception is the Madingley model (Harfoot et al., 2014), which although not designed specifically for fisheries (or indeed only marine) studies, can be applied to those questions nonetheless. It takes an agent- and process-based approach and by representing broad functional groups rather than individual species has somewhat mitigated computational constraints. As with the other classes of models there has been a broad range of motivations for the development of these types of models. Nevertheless, their most common uses to date have been to explore ecosystem dynamics (Harfoot et al., 2014; Travers-Trolet et al., 2014), consider fisheries management options (Fulton et al., 2014) and climate change scenarios (Lehodey et al., 2015), and test the performance of ecosystem indicators (Fulton et al., 2005; Travers et al., 2006).

3 Forcing data: Earth system models and fisheries

The fundamental goal of Fish-MIP is to compare the response of marine ecosystem models to common external forcings, including anthropogenic change. This is achieved by forcing the fisheries and marine ecosystem models with ocean hindcasts and scenario-driven projections from general circulation models (GCMs) that include coupled biogeochemistry modules. At present, this has been limited to global-scale ESMs following CMIP5 protocols, though in principle regional GCMs (e.g. using the ROMS framework) could also be used. For participating Fish-MIP models that allow it, the simulations also include spatially explicit estimates of fishing effort or catch. A completely standardized forcing cannot be used as the broad range of ecosystem models require different sets of inputs. Excluding all models ex-

cept those with common inputs would have removed many well-established and widely used marine ecosystem models from the Fish-MIP project and substantially reduced the inclusivity and utility of the comparisons. Consequently, Fish-MIP decided to force all models with the specific inputs they needed, but to draw these from a consistent set of ESM simulations (subsampled at different spatial and temporal resolutions).

The first round of Fish-MIP was conducted with CMIP5 output, as detailed here. This is because model outputs from CMIP6 in formats suitable for marine ecosystem models were not available to the ISIMIP and Fish-MIP communities at the time the Fish-MIP v1.0 simulations were started. However, the Fish-MIP project has participated in the Vulnerability, Impacts, Adaptation and Climate Services (VIACS) advisory board for CMIP6 (Ruane et al., 2016), specifically to communicate the requirements for marine ecosystem models, in particular the need for archiving full three-dimensional depth-resolved monthly biogeochemical outputs. We therefore anticipate that CMIP6 output (Eyring et al., 2016) will be utilized in a future round of Fish-MIP (likely in ISIMIP phase 3, planned for the end of 2018) and in addition that the number of ESMs providing suitable forcings to Fish-MIP models will increase.

3.1 Environmental drivers from Earth system models

We reviewed the 10 CMIP5 models considered by Bopp et al. (2013) that included projections for a suite of potential physical and biogeochemical stressors (warming, deoxygenation, acidification, and changes in ocean productivity). The models we determined suitable for Fish-MIP were GFDL-ESM2M and IPSL-CM5A-LR, with CESM1-BGC also likely to be incorporated in the future. Four key criteria were used to select ESM model outputs for use in Fish-MIP.

Availability. At minimum, representative concentration pathway (RCP) simulations with lowest and highest impact scenarios (RCPs 2.6 and 8.5) to 2099 are available and accessible, and ideally RCPs 4.5 and 6.0 as well. Historical runs are available from at least 1960. All physical and biogeochemical oceanic forcing fields needed to drive all the Fish-MIP marine ecosystem models (i.e. all "common" variables listed in Table 2) are ideally available at 3-D spatial and monthly mean temporal resolution.

Quality control. ESMs vary widely in the complexity of their biogeochemical formulations, with some including minimalist representations aimed at the efficient representation of carbon cycling and others featuring more resolved representations of plankton dynamics aimed at both biogeochemical and marine resource applications. While the ESMs are robustly correlated with SST, oxygen, CO_2, and 3-D-resolved pH, they vary widely in their correlation with satellite-based NPP estimates (Bopp et al., 2013), likely in large part a result of differences in the scope of objectives.

Globally, we did not select models for which the correlation coefficient (r) with NPP fell below 0.4.

Future response. The selected ESMs spanned a significant fraction of the cross-ESM range in the future projections of physical and biogeochemical fields, especially in primary production and plankton biomasses. This allows the Fish-MIP models to be tested across a wide range of plausible future scenarios. In this regard, IPSL-CM5A-LR features a relatively strong surface warming and global NPP decline, GFDL-ESM2M has relatively small changes, and CESM1-BGC, though not incorporated in the first round of model runs, is an intermediate case.

Model drift. The model drift of the ESM outputs, as diagnosed from the control simulation (i.e. no climate forcing), is negligible.

Interestingly, the "availability" criterion imposed the greatest limitation on the choice of ESMs. Of the more than 30 ESMs participating in CMIP5, only a subset (10) included necessary marine biogeochemical ocean model components (temperature, pH, dissolved oxygen, and NPP; Bopp et al., 2013). Furthermore, only one model (IPSL-CM5A-LR) currently produces the full set of ESM outputs required to drive all marine ecosystem models included in the Fish-MIP project (i.e. met the full "availability" criterion and had full three-dimensional depth-resolved monthly data). Many modelling groups at the time of protocol development had either not uploaded their full biogeochemical fields to the CMIP5 Earth System Grid Federation (ESGF) archive or did not output the variables at the full 3-D spatial and monthly time resolution required by some Fish-MIP marine ecosystem models, possibly due to a lack of time and/or funding. As a result, ESM modelling groups were approached individually to obtain access to the full biogeochemical fields at the required temporal and spatial resolution. "Quality control" also eliminated several models from our ESM selection. Since ESMs have not been specifically designed to force ecosystem models, some outputs such as planktonic biomass and productivity may have spurious or unrealistic values for some regions and/or depths and needed to be checked before use. Although "availability" and "quality control" mostly acted to limit our ESM selection, fortuitously the models selected for these attributes also span a range of potential "future response" trajectories in ocean temperature, NPP, dissolved oxygen, and pH (Bopp et al., 2013). For ease of use, all data were converted into the same units and re-gridded onto a common $1 \times 1°$ grid. For examples of ESM forcing data see Figs. S1 and S2 in the Supplement.

The number and type of phytoplankton and zooplankton groups represented in ESMs vary substantially (Bopp et al., 2013) and an explicit differentiation into large and small planktonic groups, as needed by some of the ecosystem models, was not always available. For the purpose of forcing Fish-MIP models, "large" and "small" phytoplankton groups were defined in such instances. In the ESM outputs, we defined the large phytoplankton functional group (lphy) to in-

clude diatoms, large non-diatoms, and the diazotrophs; although small diazotrophs exist, it was generally not possible to separate them out, and ESMs tend to parameterize diazotrophs as larger, *Trichodesmium*-like organisms (Capone et al., 1997). Primary production associated with nitrogen fixation is much less than total primary production (Gruber and Galloway, 2008), allaying concerns over this simplification. The small phytoplankton group (sphy) included the picophytoplankton and nanophytoplankton groups. Only the IPSL-CM5A model explicitly represented size-differentiated zooplankton groups (szoo and lzoo). For other ESMs for which these were unavailable, the zooplankton size classes were post-diagnosed by normalizing to phytoplankton biomass such that $lzoo = zoo \times lphy / (sphy + lphy)$ and $szoo = zoo \times sphy / (sphy + lphy)$. This simple approach makes the assumption that the small zooplankton and large zooplankton biomass residence times are the same.

For the first round of Fish-MIP, all modellers were encouraged to force their models with the ESM inputs that made sense biologically and ecologically, as determined by the mechanisms and assumptions specific to individual models (the "optimized" simulation), enabling us to examine outputs based on ideal (from the perspective of the individual marine ecosystem model) forcings. For subsequent rounds, we will also specify a "standardized" ESM input simulation to better distinguish differences in marine ecosystem model outputs due to ESM forcings from those due to ecosystem model structure. As an example, some modelling groups preferred to remove the diazotroph contribution from their primary productivity or planktonic biomass input fields because it was assumed that this material is not efficiently transferred up the food chain. Removing the diazotrophs is the "optimized" simulation, while the "standardized" simulation would include the diazotrophs in the biomass and primary productivity input fields.

Downscaling to regional domains

Fish-MIP aims to compare temporal and spatial outputs between global and regional models. Output from global models can be subsampled over the areas considered by regional models, such as the North Sea, and the regional models can be forced with ESM output averaged over the grid cells included in the regional model domain. In this way, the global and regional model responses to common environmental variations can be directly compared. Regional marine ecosystem models often have highly resolved survey, stock assessment, and/or fishing effort data as inputs, and therefore this direct comparison can help to test and contextualize biases in the global models. Furthermore, regional marine ecosystem models have often been previously integrated with higher-resolution ocean and biogeochemical simulations, providing comparisons with resolution of fine-scale structure in space and time.

At this point in ESM development, it is important to note that regional downscaling remains problematic. The ESMs in CMIP5 have ocean resolutions of ~ 1–$2°$ and are thus only capable of resolving circulation features on the order of 300 km or larger. This leads to a limited representation of coastal ocean and marginal sea currents and upwelling and, in some cases, substantial regional biases in ecosystem drivers (Holt et al., 2016; Stock et al., 2011). In addition, ESMs struggle to represent iron limitation well (Tagliabue et al., 2015), which can add an additional potential source of bias, especially when simulating primary production in iron-limited ecosystems such as the Southern Ocean (Moore et al., 2013) or sub-Arctic Pacific. They also struggle to represent the extent of tropical oxygen minimum zones (Cabré et al., 2015), which represents a limitation for marine ecosystem models using dissolved O_2 as an input variable. More generally, confidence in climate change projections is greatest at continental scales and above (Randall et al., 2007). Thus, while the Fish-MIP protocol is developed to enable the consideration of both global and regional applications, the limitations of present tools suggest an emphasis on forecasted large-scale changes (e.g. shifting and evolving ocean biomes, latitudinal contrasts) coupled with a more cautious consideration of the regional implications of large-scale drivers (such as CO_2) resolved by ESMs.

To date, some regional ecosystem models have used the downscaling of global-scale model outputs or high-resolution shelf seas models (Barange et al., 2014; Stock et al., 2011). The concerted development of high-resolution global climate and Earth system models with improved resolution of coastal processes (e.g. Saba et al., 2016) should ease this limitation moving forward. Alternatively, growing suites of regionally downscaled solutions (e.g. Holt et al., 2016) may provide a basis for region-specific implementations of the Fish-MIP protocol. Although it is likely that these biases will be reduced over the coming years and decades, they must be borne in mind as inescapable shortcomings of the current state-of-the-art in ESM models.

3.2 Fishing scenarios

Fishing is an important human driver of changes in marine ecosystems and is represented in most marine ecosystem models as a spatially and temporally varying term that removes biomass and production from the system. This term is typically applied in one of two ways within marine ecosystem models. It can be imposed as a biomass removal rate per unit of time based on empirical or modelled catches (or landings) and removed directly from the system biomass for specific functional groups, ages, and size classes. Alternatively, it can be applied as a mortality rate, which removes a fraction of the existing biomass per unit of time. This mortality rate can be applied directly or calculated from a fishing effort term which considers both "nominal effort" (total resources devoted to fishing) and the catchability of fish to give

an "effective" fishing effort (Jennings et al., 2001). Nominal effort reflects human involvement in fishing (e.g. number and engine power of fishing boats and time spent fishing). Catchability, defined as the proportion of biomass that can be caught per unit of fishing effort, can be affected by both ecological and human factors. For example, the aggregation behaviour of some fish stocks can increase their catchability (Arreguin-Sanchez, 1996). Improvements in fishing technology or changes in gear configuration (e.g. changes in the mesh size of nets) can also affect catchability.

There are important differences between models forced with catch and those forced with effort that make the consistent representation of fisheries impacts in the Fish-MIP project challenging when bringing such disparate approaches together. Models forced with catch can drive ecosystem components extinct if the forced catches are incompatible with biomass dynamics and can be used to see if observed historical catches can be maintained given model dynamics. Models forced with effort or mortality produce emergent catches derived from available modelled biomass. These catches can be compared to historically observed data to assess confidence in the model's forcing and ability to reproduce observations. Fish-MIP models also vary in the complexity and degree of linkages and feedbacks to other biophysical and human components of the ecosystems that they represent. In some models, fishing effort, catch, or mortality rates are parameters or forcing variables with no feedback from the biological systems to the socio-economic systems. However, some hybrid and trophodynamic models fully couple these systems.

Individual Fish-MIP models use various data sources for their fisheries impact forcing, which reflects variation in model purpose, development history, functional group representation, spatial scale and resolution, inclusion of illegal, unregulated, and unreported (IUU) fisheries, and other factors. Modelled fishing mortality rates, catches, or effort can vary over time and space and can be spatially explicit or applied at local, regional, or basin scales. Most databases on global fishing catch or effort can be spatially disaggregated to match the scales represented in (global) marine ecosystem models. The difference between such data sources may be considerable; see Fig. S3 for an example of the difference in global catches over time between two databases.

As examples of approaches taken by individual Fish-MIP models, the EcoOcean model applies fishing as an effort term based on the Sea Around Us Project (SAUP) effort database (Anticamara et al., 2011; Christensen et al., 2015; Watson et al., 2013), the DBEM model uses an alternate catch reconstruction database (Watson, 2017), BOATS has a dynamic bioeconomic approach using SAUP catch price data to simulate spatially resolved changes in fishing effort over time based on individual fishers attempting to optimize their outcomes (Carozza et al., 2017), and SS-DBEM represents maximum sustainable yield without explicitly calculating fishing mortality (Fernandes et al., 2016, 2017; Mullon et al., 2016) using SAUP data

supplemented by other sources (the ICES data collections at www.ices.dk/marine-data/dataset-collections/Pages/Fish-catch-and-stock-assessment.aspx and the RAM legacy stock assessment database at www.ramlegacy.org). This last example further demonstrates how fishing impacts may be modelled implicitly. Regional models have typically used yet different data sources, which are often finely resolved observer-derived local datasets with highly taxonomically resolved information.

In the first round of Fish-MIP, to maximize the participation of marine ecosystem models, we decided to allow models to implement fishing according to their own standard method to produce realistic historical transients, followed by constant fishing impacts for future scenarios. That is, models continued to use their specific catch, effort, or other forcing data (often but not always SAUP data for global models), but with simple standardized scenarios imposed.

For historical simulations (to 2005), biomass removal based on reported catches or historical effort levels was imposed to reconstruct the historical level of fishing (Christensen et al., 2015) or assumptions were made about average fishing mortality in historical periods (Cheung et al., 2016b). As above, this was based on each Fish-MIP model's specified fishing database. In addition to the standardized scenario, an optional scenario was suggested with no fishing (zero effort or mortality or fisheries-induced). Some models included no representation of fishing and thus only ran this optional scenario of zero fishing. For future projection simulations, in the current absence of operationalized spatially explicit scenarios of effort or catch, the standardized model run was to keep fishing constant at 2005 rates (from their specified data source), while the optional scenario was again zero fishing. Our scenarios therefore imposed a fishing impact (in fished model runs) while maintaining consistency among each model's fit to historical data. Given the simplicity of this approach, we focus on climate impacts for Fish-MIP 1.0 and plan to explore the impacts of fishing in more detail following the development of specified future fisheries scenarios.

Improving the inter-model consistency of fisheries forcings remains a substantial challenge for the marine ecosystem modelling community. In subsequent iterations of Fish-MIP, we will aim to reconcile the various historical input data streams to further quantify their effects on results and, if possible, further standardize prescribed input sources. Developing more sophisticated future scenarios of fisheries remains challenging. Formally developed global qualitative storylines depicting future fishing activity, management, and technological change are beginning to be designed (e.g. Maury et al., 2017), but need to be "operationalized" in terms of translating them into a spatially and temporally explicit form to enable them to force marine ecosystem models. The development of such global projections of fishing pressure over the 21st century will be necessary to better understand the consequences of interactions between climate and fisheries effects

Table 4. Selected outputs produced by individual models. Note that this list is correct at the time of printing, but that models are continuously in development with new components and requirements being added. This table lists a range of potential outputs from models participating in Fish-MIP; for the list of requested and optional model outputs, see Table 5.

Model	Fish species and functional group carbon	Biomass density (g m^{-3} month^{-1})	Fisheries metrics (various)	Relative species and functional group abundances (unitless)	Trophic level (unitless)	Production of carbon (g m^{-3} month^{-1})	Production and biomass ratio (unitless)	Mortality rate (month^{-1})	Species and functional group diversity (unitless)	Individual-based metrics (e.g. growth rates; various)	Food web interaction metrics (various)
		Common outputs produced by at least 50 % of models							Optional outputs produced by a small proportion of models		
DBEM			•[4]	•							
SS-DEBM		•[1]	•[5]	•							
Ecopath with Ecosim		•	•[6]	•	•	•	•	•	•		•
EcoOcean		•	•[7]	•	•	•	•	•	•		•
Macroecological model		•			•	•	•	•			
DPBM		•[1]	•[6,8]	•	•	•	•	•		•	•
BOATS		•[1]	•[6]	•		•	•	•		•	
POEM		•				•					
Atlantis		•	•[6]	•	•	•	•	•	•	•	•
OSMOSE		•	•[6]	•	•	•	•	•	•	•	•
SEAPODYM		•[2]	•[9]			•	•	•			
APECOSM		•[3]	•[10]	•				•	•[10]	•	
Madingley		•		•	•			•	•	•	•

[1] As a size spectrum. [2] Tunas and associated species; age structured. [3] Size spectrum for epipelagic, migratory, mesopelagic, and bathypelagic communities, together with focus species (e.g. tunas). [4] Relative functional group abundances. [5] Catch rates. [6] Catch and fishing mortality. [7] Seafood production. [8] Potential catch. [9] Catch and size frequency for tunas. [10] Commercial landings.

on ecosystems and resultant yields. Deriving projections that recognize the complexities of fisheries management remains particularly challenging, even at regional scales which may more naturally map to specific existing management units. Such projections would need to account for the significance of many drivers and feedbacks which influence mortality rates and the catches that result. These include economic drivers of fleet capacity, effort, and distribution; environmental and fisheries policies and associated management targets, the extent to which targets are met and their responsiveness to changes in the environment, fisheries, and society; the selectivity and efficiency of fishing operations; fishery and species interactions; and external modifiers of demand for and access to wild fish for food (e.g. growth of aquaculture, marine conservation, certification, ethics). A further challenge is to develop comparable projections for different fish production models, for example with appropriate assumptions necessary to translate between species- and size-based projections of mortality and selection. The underlying difficulty with developing all such projections is that yield is not a stable construct, but changes dynamically in relation to the species and sizes targeted, with feedbacks, and with the evolution of the fished ecosystem. When future fishing scenarios do become operationalized, they will be used to replace the standardized run with constant 2005 catch or effort in future model experiment protocols.

Table 5. Common output variables to be provided by global and regional marine fisheries models.

Output variable	Variable name	Temporal resolution	Unit	Comments
Total system carbon biomass	tsb	Monthly	$\mathrm{g\,m^{-2}}$	All primary producers and consumers
Total consumer carbon biomass density	tcb	Monthly	$\mathrm{g\,m^{-2}}$	All consumers (trophic level > 1, vertebrates and invertebrates)
Carbon biomass density of consumers $> 10\,\mathrm{cm}$	b10	Monthly	$\mathrm{g\,m^{-2}}$	If asymptotic length (L_{inf}) is $> 10\,\mathrm{cm}$, include in $> 10\,\mathrm{cm}$ class
Carbon biomass density of consumers $> 30\,\mathrm{cm}$	b30	Monthly	$\mathrm{g\,m^{-2}}$	If asymptotic length (L_{inf}) is $> 30\,\mathrm{cm}$, include in $> 30\,\mathrm{cm}$ class
Total catch (all commercial functional groups or size classes)	tc	Monthly	g wet biomass $\mathrm{m^{-2}}$	Catch at sea (commercial landings plus discards), fish and invertebrates; fished runs only
Total landings (all commercial functional groups or size classes)	tla	Monthly	g wet biomass $\mathrm{m^{-2}}$	Commercial landings (catch without discards), fish and invertebrates; fished runs only

4 Output data

The broad range of marine ecosystem and fisheries models (Sect. 2) leads to an equally broad range of potential model outputs (Table 4). To compare outputs from Fish-MIP models, we selected six common output variables that most models would be able to produce (total system biomass, total consumer biomass, biomass of consumers > 10 and $> 30\,\mathrm{cm}$, and, for models forced by fishing effort, catches and landings; see Table 5). We also developed a list of additional optional outputs that some models are capable of producing (e.g. biomass and catch of individual species or trophic group); see Table S1. This dual approach was adopted to achieve a balance between having common outputs that all models could produce and producing comparisons across as broad an array of outputs as possible. Some output variables were not native to individual models (such as biomass by size classes) and required post-processing; however, this appeared to be the only way to compare the outputs of size-based models with those from species- or trophic-group-structured models.

Some models output biological state variables (e.g. biomass) as wet weight and some as carbon, so different factors were used when converting from one to the other, sometimes differing between functional groups. Another issue is the conversion of biomass density to or from size classes, functional groups, and species. There appeared to be no universal approach that was meaningful across all ecosystem model types, so we settled on model outputs for all sizes, as well as size bins of maximum length > 10 and $> 30\,\mathrm{cm}$. This meant that mass–length conversions were handled differently in different models. All of these details matter when we are seeking to develop effective and informative compar-

isons and were not all readily documented or accessible at the outset. However, our comments should not be taken to imply that every detail needs to be harmonized among models; in fact, for equitable comparison, it may be desirable to retain much of the diversity of model specifications. In any case, carefully specified information must be shared on those aspects that are harmonized – be it variable names and definitions, scenarios, or datasets – and those aspects that necessarily remain idiosyncratic. For example, 3-D models can use oceanic depth profiles that differ from ESM outputs. Ultimately, modellers used their specific depth profile and we accepted this as a potential confounding factor (in the same way as having 2-D and 3-D models). Another important contrast is the inclusivity of the species represented, which in some cases is all species (e.g. macroecological model), in others all commercial species (e.g. BOATS), and in others only a subset of commercial species (e.g. SEAPODYM). Thus, at this point, for quantities such as fish catch the relative trends can be compared readily between models and observations, but the absolute values need to be considered carefully.

It was agreed that output data should be depth column integrated on a $1 \times 1°$ grid at a monthly (where possible) resolution, with "no data" values set to $1.0\mathrm{e} + 20\mathrm{f}$ and variable names as in Table 5. Time series requested were 1971 to 2004–2005 (depending on ESM forcing) for historical models runs and 2006–2099 for future scenarios. For an example of model output, see Fig. S4. All files were to be saved in netcdf format with a .nc4 extension (a conversion script for .csv files was made available at http://vre2.dkrz.de). Full details on outputs, including the conventions for file naming, were made available in the ISIMIP 2A simulation protocol at https://www.isimip.org/protocol/#isimip2a, and the instruc-

Table 6. All experiments (historical and future, standardized, and optional) for the global and regional fisheries and marine ecosystem models participating in the first round of Fish-MIP. Runs in bold are prioritized (Tier 1), those in roman preferred but optional (Tier 2), and those in italics optional (Tier 3); this is to allow modellers with limited computational resources to participate and prioritize. Note that the CMIP5-based runs (non-reanalysis) are continuous from historical into the future, reducing the total number of runs.

Earth system model forcing	Scenario	Time period	Fishing effort	Ocean acidification	No. of runs
GFDL ESM2M (reanalysis)	historical	1971–2005	**unfished (zero effort or mortality)** time-varying effort or mortality	default (time-varying pH)	2
IPSL-CM5A-LR	historical	1971–2005	**unfished (zero effort or mortality)** time-varying effort or mortality	default (time-varying pH)	2
GFDL ESM2M	historical	1971–2005	**unfished (zero effort or mortality)** time-varying effort or mortality	default (time-varying pH)	2
IPSL-CM5A-LR	2.6 (rcp2p6) 8.5 (rcp8p5)	2006–2099	**unfished (zero effort or mortality)** keep constant at 2005 levels	default (time-varying pH)	4
IPSL-CM5A-LR	*4.5 (rcp4p5) 6.0 (rcp6p0)*	*2006–2099*	*unfished (zero effort or mortality) keep constant at 2005 levels*	*default (time-varying pH)*	*4*
GFDL ESM2M	2.6 (rcp2p6) 8.5 (rcp8p5)	2006–2099	**unfished (zero effort or mortality)** keep constant at 2005 levels	default (time-varying pH)	4

tions are at https://www.isimip.org/protocol/isimip2b-files/ (see also the Supplement for this paper).

Commercial species were defined as all potentially harvested fish > 10 cm. All modelling groups used their own size classes and functional groups when running the model and provided the name and definition of size classes and functional groups used for total catch and landings. For common standard equations and mass–length conversion, models that did not have their own conversions were referred to FishBase (www.fishbase.org). It was also requested that the conversion values from wet weight to carbon should be specified.
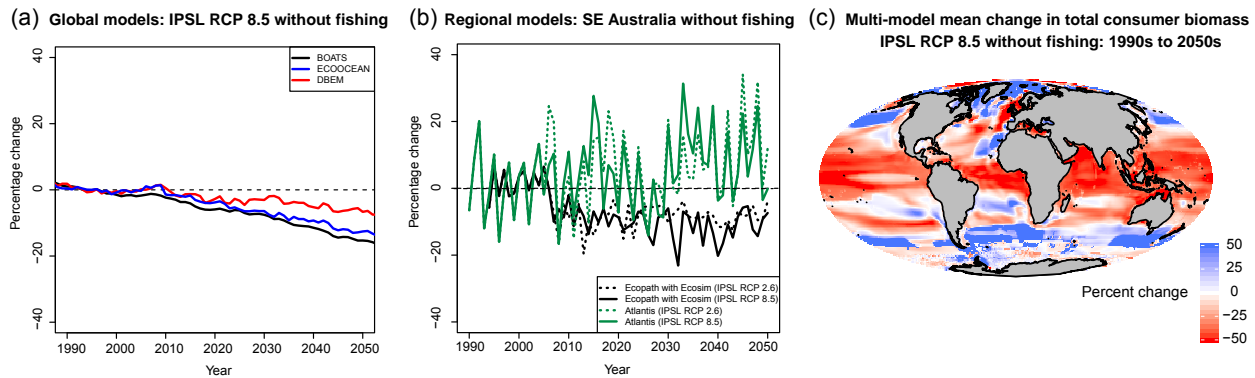
5   Core simulations in the Fish-MIP v1.0 protocol

As the first marine sector included within ISIMIP, the Fish-MIP protocol was developed to align with the aims and scope of the overall ISIMIP project and to harmonize forcing simulations and scenarios whenever feasible. However, we also needed to balance this approach with the need to allow the effective intercomparison of marine ecosystem models given currently available modelling platforms and forcing data (see previous Section) and to consider the relative roles of climate and fishing. For historical (hindcasting) model runs, we used a GFDL-reanalysis product (Cheung et al., 2013) as our common "observational" climate input set of time series (Table 6). For future projections, we used GFDL and IPSL products (see Sect. 3), with priority on the RCP 2.6 and 8.5 scenarios, to span a range of alternate futures (Table 6). Thus,

it should be possible to compare the effects of a climate signal based on a given ESM across ecosystem models, with differences among models reflecting a combination of their sensitivities to different aspects of climate change linked to differences in model structure and parameterization (as well as any other differences in forcing variables).

Depending on the ecosystem model complexity, times required for a defined simulation can differ by orders of magnitude. We therefore decided on a multi-tier hierarchy of standardized and optional climate- and fisheries-forced simulations (see Table 6) that ensured we could do the following: (i) compare many marine ecosystem model outputs across a few top priority ESMs and reanalysis product historical runs; (ii) assess the spread of future projections by comparing outputs for at least one ESM (IPSL) across all four RCPs (2.6, 4.5, 6.0, 8.5), as well as for at least one RCP (8.5) across the selected ESMs; (iii) separate the climate from the fishing signal by including simulations with and without fishing in historical and future runs; (iv) and for regional models, separate the effect of running the model with local data (key run, which may use statistically downscaled inputs) compared to a data subset from a global ESM. The core simulations from the initial round are as follows.

Historical runs. For historical runs for both global and regional models, the top priority (Tier 1) was one run each with all the climate datasets (reanalysis based, CMIP5 based) with no fishing (zero effort or mortality) and ocean acidification (time-varying pH). The lower priority (Tier 2) was to run the

Figure 1. Example outputs from the Fish-MIP v1.0 protocol core simulations. **(a)** Global model time series output. Percentage change in global spatially averaged total consumer carbon biomass density (g m^{-2}) from 1990 to 2050. All values are relative to the 1990–1999 mean. Values are shown for three marine ecosystem models: a size-based model (BOATS), a trophodynamic model (EcoOcean), and a species distribution model (DBEM). Output only shown for IPSL RCP 8.5 model runs without fishing imposed. For definition of total consumer carbon biomass, see Table 5. **(b)** Regional model time series output. Percentage change in spatially averaged total consumer carbon biomass density (g m^{-2}) from 1990 to 2050. All values are relative to the 1990–1999 mean. Values are shown for two regional marine ecosystem models in southeast Australia: a trophodynamic model (Ecopath with Ecosim) and a composite (hybrid) model (Atlantis). The spatial extent of models is overlapping but non-identical. Output only shown for IPSL RCP 2.6 and IPSL RCP 8.5 model runs without fishing imposed. **(c)** Global spatial model output runs (models as per panel **a**) for IPSL RCP 8.5 with no fishing imposed. Ensemble model mean percentage change in total consumer carbon biomass density (originally in g m^{-2}) from the 1990s to the 2050s; a positive value indicates an increase over time. Percentage changes in each grid cell for the three models in panel **(a)** over this time period were averaged.

same set of climate data with time-varying fishing effort or mortality (see Table 6).

Future runs. For future runs with both global and regional models, the top priority (Tier 1) was one run each with all the climate datasets (CMIP5 based) with no fishing (zero effort or mortality) and ocean acidification (time-varying pH) for both the RCP 2.6 and 8.5 scenarios. The second priority (Tier 2) was to run the same set of climate data with default fishing effort or mortality (kept constant at 2005 levels) (see Table 6). The third priority (Tier 3) was the full set of experiments for RCP 4.5 and 6.0 scenarios where available (at present, only the IPSL-CM5A-LR model).

For all runs, it was requested that all non-specified external forcings (e.g. habitat modification) should be kept at default settings (time varying until 2005, constant at 2005 levels into the future). Input data were provided from 1951–1959 to 2004–2005, with a request that years until 1970 should be replicated as needed and used for spin-up (spin-up to be decided individually by each modelling group). Historical reporting was from 1971–2005 or whenever the model started if later.

Figure 1 shows example outputs from regional and global model runs for a subset of the Fish-MIP models. Note that results can be visualized either spatially or as time series, as absolute values or relative changes, and can be represented as individual simulation outputs for specific models, and/or averages across multiple models. While we refrain from discussing results and specific values as only a subset of models and simulations are shown here, we do note that there is substantial temporal variation in the magnitude and direction of

trends between models and spatial variation in the ensemble model mean. Separate papers from the Fish-MIP project will provide an analysis of the full suite of results. Furthermore, all simulation results are being made publicly available (see the "Code and data availability" section) to enable the whole community to analyse and interpret results.

While we did not have any overlap in terms of different modelling groups using the same model or software framework in a specific region (or at global scales), to tackle this situation in future Fish-MIP protocols, specifically the potential for different modelling groups to make differing configuration decisions, we plan to update our documentation associated with each simulation run to include the full configuration of choices that were made. The Fish-MIP v1.0 protocol will necessarily be revised and revisited, as new climate and fishing data become available as new ecosystem models are included within Fish-MIP (which is encouraged), as the shared understanding of approaches to marine ecosystem modelling increases, and as existing models evolve. The most recent protocol for ISIMIP simulation round 2A is available at https://www.isimip.org/protocol/#isimip2A.

6   Conclusions

We believe that the broad intercomparison of marine ecosystem models facilitated by Fish-MIP provides a useful step towards improving our understanding of the future of the marine realm and catalysing the development and uptake of these models. The wide diversity of marine ecosystem mod-

els provides a healthy spread of perspectives on what are ultimately very complex biological and ecological systems and may provide insight into critical processes that may be incorporated in only a subset of models. We expect that, as in other sectors, model intercomparison will help identify processes that are under-represented or misrepresented in individual models or model types and spur model improvement. Here we have described the Fish-MIP project and protocol in preparation for forthcoming model comparisons at multiple scales. We hope that material compiled for Fish-MIP will inform other intercomparison projects and drive interactions between marine ecosystem modellers and those working in other disciplines. Several marine ecosystem models included in Fish-MIP have already supported projections of the future state of the seas and climate impacts on fisheries. The Fish-MIP intercomparison will add to this by systematically highlighting the uncertainty associated with different model structures and assumptions. This will ultimately improve our capacity to convey the limitations of any advice on future states of marine ecosystems and fisheries and to quantify the benefits and risks associated with alternate management, adaptation, or mitigation options.

Code and data availability. The experimental protocol has no code associated with it. The protocol is described in this paper, the Supplement, and can also be downloaded from https://www.isimip.org/protocol/#isimip2a (for simulation round 2A). The Fish-MIP website is https://www.isimip.org/gettingstarted/marine-ecosystems-fisheries/. Forcing data from CMIP5 used for the Fish-MIP simulation round 2A are available on the ISIMIP servers (https://www.isimip.org/gettingstarted/#how-to-join-isimip); fisheries forcing data for specific fished model runs and models are available by contacting individual Fish-MIP modelling groups. Fish-MIP results from simulation round 2A are publicly available for regional (Eddy et al., 2018) and for global (Tittensor et al., 2018) model outputs.

The Supplement related to this article is available online at https://doi.org/10.5194/gmd-11-1421-2018-supplement.

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