Global Effects of Marine Protected Areas

on Food Security Are Unknown

Supplementary Information

Daniel Ovando   Owen Liu   Renato Molina   Ana Parma   Cody Szuwalski

This document presents methods and sensitivity analyses for "Global Effects of Marine Protected Areas on Food Security Are Unknown".

1   Methods

1.1   Summary

The food-provision results of Sala et al. (2021) are based on the methods described in Cabral et al. (2020) (see Ovando et al. (2021) for a summary of issues with this model), which are in turn based on estimates of stock status and life history from Costello et al. (2016).

In the steps between Costello et al. (2016) and Sala et al. (2021), Sala *et al.* made a number of changes to the model and new assumptions. This analysis tests the effects of these changes and assumptions on projections of the impacts and design of a global network of marine protected areas for food security.

Projections of the impacts of fisheries reform (in this case, implementation of no-take MPAs) require some estimate of fishing mortality rates and expected stock status in the absence of the policy (in this case Marine Protected Areas, MPAs). The challenge here is the vast majority of the world's fisheries, and roughly 50% of global catch (Hilborn et al. 2020), come from "unassessed" fisheries that lack formal estimates of stock status.

To fill this gap, Costello et al. (2016), based on Costello et al. (2012), utilized a catch-based data-limited assessment method to provide estimates of stock status, as measured by biomass relative to biomass at

1

maximum sustainable yield (MSY), B/B_{MSY}, and the fishing mortality rate relative to the fishing mortality rate that would produce MSY at equilibrium (F/F_{MSY}).

The core methods of Costello et al. (2016) are:

- Assume that for each unassessed taxonomic group, separate stock units exist within a specific country's waters within an FAO major statistical area, except for highly migratory unassessed stocks, which are assumed to be well-mixed within FAO major statistical areas.

- Given the catch history for that "stock" (generally defined by the intersection of taxa, country, and FAO statistical area), generate informative priors on B/B_{MSY} using an updated version of the panel regression model described in Costello et al. (2012). Critically, Costello et al. (2012) estimates B/B_{MSY} as a function of traits of the catch history including maximum catch volume, the number of years to peak catch, the ratio of catch in a given year to max catch, and others (See Table S1 of the supplementary materials for Costello et al. (2012)).

- Use these priors on B/B_{MSY} in a modified version of Catch-MSY (Martell and Froese 2013), in the manner of Anderson et al. (2017). The modified version of Catch-MSY utilizes a Pella-Tomlinson (Pella and Tomlinson 1969) population model to estimate B/B_{MSY}, F/F_{MSY}, and parameters such as MSY, carrying capacity K, and the Pella-Tomlinson growth parameter g, conditional on the shape of the catch history and the priors derived from the panel regression from Costello et al. (2012).

- Based on these estimates of current stock status and life history, Costello et al. (2016) then applied a "business as usual" fishing mortality policy, based in F/F_{MSY} for each stock (generally, bionomic equilibrium for unassessed stocks). This provides estimates of stock status and fishery catches over time around the globe.

Sala et al. (2021) utilize some of the life history parameters and the "business as usual" stock status from Costello et al. (2016) to make their projections. However, they make two key modifications:

1. They aggregate **all** of the individual unassessed stocks assumed by Costello et al. (2016) into one global stock per species.

2. They use a Schaefer (logistic) population model rather than a Pella-Tomlinson model, borrowing some parameters estimated under the Pella-Tomlinson for their Schaefer model.

These choices introduce two related statistical problems, as well as two strong and unrealistic assumptions. As noted, Costello et al. (2016) based their estimates of stock status on the attributes of individual stocks'

catch histories. Sala et al. (2021) assume instead that each unassessed stock is one global population, with stock status a function of the MSY weighted mean stock status of individual stocks from Costello et al. (2016). However, to the extent that the trends and magnitude of the sum of the catch histories differ from the individual catch histories, the stock status estimated for the "global" stock by the methods of Costello et al. (2016) will not be the same as the MSY weighted average of the individual stocks; i.e., changing the assumed trajectory and volume of catches by aggregating from individual stocks to a global stock would change the estimate of stock status used for projections. It is not clear how different the results will be, but they will be different.

The second is the conversion to a Schaefer model. Estimated life history traits such as *MSY* are not intrinsic attributes of a population, but rather are a function of data and assumed model structure and resulting covariances across parameters. So, the MSY estimates produced by Costello et al. (2016) would have been different had those estimates been produced by a Schaefer model rather than a Pella-Tomlinson model, and as such, Pella-Tomlinson derived MSY values cannot simply be plugged into a Schaefer model framework as done by Sala et al. (2021).

Beyond these methodological issues, we also felt it was important to test the implications of two assumptions of Sala et al. (2021): that unassessed stocks are comprised of one global population, and the spatial scale of density dependence. To examine the effect of these issues, we developed a parallel version of the Sala et al. (2021)'s methods, allowing us to compare the estimates of the impacts and design of a global network of marine protected areas for food security under i) variations of the population dynamic model used, ii) the assumed stock structure, and iii) the nature of density dependence. Below, we detail the methods used to make these comparisons.

1.2 Creating Comparable Stocks

The stocks utilized in Sala et al. (2021) are built out of the values reported in Costello et al. (2016). It should be possible then to re-run the global MPA network prioritization used in Sala et al. (2021) but instead using the component stocks from Costello et al. (2016). However, the "global" unassessed stocks do not consistently reflect the sum of their constituent unassessed stocks, and there are some discrepancies in the actual listed stocks themselves.

The food provision analyses used in Sala et al. (2021) depend on results from Cabral et al. (2020), in particular an object called `MegaData_Ray`, which contains the estimates of life history parameters and BAU stock status for each of the stocks included in Sala et al. (2021) (https://github.com/rencabral/pnas-

3

MegaData_Ray was produced as a correction to errors made in the BAU fishing mortality rates for assessed (in the RAM Legacy Stock Assessment Database, RLSADB) stocks in the original version of Cabral et al. (2020). However, examination of MegaData_Ray found some inconsistencies in their methods. As such, in order to ensure we were able to create stocks that were as identical as possible in every way except for the assumptions tested here, we rebuilt the set of candidate stocks using the original MegaData_Ray object provided by Sala *et al.* (called MegaData from now on).

Running the methods of Sala et al. (2021) requires habitat layers from Kaschner et al. (2019). These layers were provided for Cabral et al. (2020), but not for Sala et al. (2021). However, there were 65 stocks with a total MSY of 1.2 MMT, listed in Sala et al. (2021) that were not present in the version of Cabral et al. (2020) for which carrying capacity estimates were made available. We could not use these stocks as we did not have access to the required carrying capacity estimates.

In order to compare differences in outcomes based only on core assumptions, we needed to have exact matches between the stocks used in the "Global" assumptions set representative of the assumptions used in Sala et al. (2021) and those used in the "Regional" assumptions based on Costello et al. (2016). However, there are 48 species reported as used in Sala et al. (2021) that are not present in the the estimates from Costello et al. (2016) that we have access to. There are also 40 species listed as "assessed" by Costello et al. (2016) that are listed as unassessed by Sala et al. (2021).

Given these challenges then, it was not possible for us to generate alternative scenarios for each of the exact stocks listed in Sala et al. (2021). As such, we focus on the subset of stocks for which we can make comparisons across the different sets of assumptions, i.e. for which we were able to make exact matches with Costello et al. (2016), totaling 1011 out of the 1150 reported by Sala et al. (2021). With this subset of matching stocks we can then ask, how sensitive are the outcomes and design of global MPA networks to the assumptions presented in Sala et al. (2021)?

1.2.1 Assessed Stocks

For assessed stocks, we restricted our analyses to stocks with exact stock ID matches between Sala et al. (2021) and Costello et al. (2016). We then updated the business as usual fishing mortality rates based on the F/F_{MSY} values reported in RLSADB version v4.495 (https://zenodo.org/record/4824192) in the UdivUmsypref entry, which per the official RLSADB documentation and personal communication with RLSADB staff is the preferred estimate of fishing mortality rates relative to MSY based reference points for

¹¹¹ use in food-security style questions [1]. These then provide the business as usual F/F_{MSY} values for assessed

¹¹² stocks that are held constant across all scenarios.

¹¹³ The model used in Sala et al. (2021) is based on exploitation rates, not F/F_{MSY} values. In order to compare

¹¹⁴ outcomes under both Pella-Tomlinson and Schaefer population models, we calculated the exploitation rate

¹¹⁵ that would produce the desired F/F_{MSY} values conditional on the life history parameters and the population

¹¹⁶ models.

¹¹⁷ For the Pella-Tomlinson (PT) model used in the "Regional" assumptions, $F_{MSY} = g$ (Costello et al. 2016),

¹¹⁸ with g being the Pella-Tomlinson growth coefficient. For each assessed stock, we pulled g from Costello et

¹¹⁹ al. (2016), and then calculated the business as usual exploration rate for those assessed stocks as

$$F_{BAU}^{PT} = \frac{F}{F_{MSY}} g.$$

¹²⁰ To ensure internal consistency with the MSY values used in Sala et al. (2021) and the Pella-Tomlinson

¹²¹ structure, we then adjust the carrying capacity K following Costello et al. (2016) as:

$$K = \frac{MSY(\phi + 1)^{1/\phi}}{g}.$$

¹²² For the assessed stocks under the Schaefer assumption, we calculated F_{BAU} as

$$F_{BAU}^{SHF} = (\frac{F}{F_{MSY}})r/2.$$

¹²³ Where r is the logistic growth rate reported in Sala et al. (2021) and (with $F_{MSY} = r/2$ under the Schaefer

¹²⁴ model).

¹²⁵ In summary then, for the assessed stocks, we filtered down the assessed stocks to those with matches in

¹²⁶ Costello et al. (2016), used the same MSY values as Sala et al. (2021), adjusted the F/F_{MSY} values based

¹²⁷ on current values in the RLSADB, and calculated the correct F_{BAU} for each stock given these parameters

¹²⁸ and selected population dynamics model, adjusting K as needed. This then gives us a set of assessed stocks

¹²⁹ with the same MSY and business as usual F/F_{MSY} but different underlying population models that are

¹³⁰ internally consistent with the methods that create the parameters/data used by Sala et al. (2021).

---

[1] `UdivUmsypref` uses either the discrete or instantaneous fishing mortality rate relative to the MSY based reference point, whereas `FdivFmsy` only contains the instantaneous fishing mortality rates.

1.2.2 Constructuing Unassessed Stocks

The unassessed stocks required a different set of steps to create a comparable set of stocks between the "Regional" and "Global" assumptions. First, there are numerous stocks listed as species level unassessed (i.e. not the RAM Legacy Stock Assessment Database) stocks by Sala et al. (2021) but which are not listed as such in the Costello et al. (2016) estimates. Inspection suggests that some of these species are listed as "unassessed" by Sala et al. (2021) but "assessed" by Costello et al. (2016). However, it is beyond the scope of this analysis to attempt to diagnose the reasons for these discrepancies. Second, for the stocks that do match, according to the methods from Cabral et al. (2020) the "unassessed" stocks for a given species are constructed based on the sum of the individual MSY values for each individual unassessed stocks within that species. When comparing the global stock MSY values used in Sala et al. (2021) to the sum of the individual stock MSY's reported in Costello et al. (2016) for projection under the business as usual - conservation concern policy (on which Sala et al. (2021) is based), while the totals match up for most stocks, for many the total MSY used in Sala et al. (2021) greatly exceeds the sum of the MSYs reported in Costello et al. (2016) (Fig.S1). The reason for this discrepancy is not clear to us.

To create the "Regional" version of the unassessed stocks, we used all the life history parameters from Costello et al. (2016) (MSY, K, g, business as usual F/F_{MSY}). We then needed to match the spatial proportions of carrying capacity used in Sala et al. (2021) to the stock definitions used in Costello et al. (2016). To do this, for a given stock from Costello et al. (2016), we clipped the shapefile for the FAO statistical area of the stock in question to the exclusive economic zone (EEZ) of the country of the stock in question (except for multinational stocks such as tunas in Costello et al. (2016) which were only clipped to the FAO statistical area). We then clipped the habitat layer used in Sala et al. (2021) to the Costello et al. (2016) stock structure, and normalized the habitat values in the new clipped stock structure to sum to 1 for each stock.

We provide an illustration of this below. The largest unassessed stock, by MSY, used in Sala et al. (2021) is largehead hairtail (*Trichiurus lepturus*). Under the stock structure used in Sala et al. (2021), largehead hairtail is a pan-global stock (Fig.S2-A). However, according to the FAO catch statistics and by extension the stock structure used in Costello et al. (2016), largehead hairtail are caught in a large number of countries, but far fewer than those assumed by Sala et al. (2021), and critically, the distribution of the catch is much different, with nearly all of the reported catch coming from the Northwest Pacific by China (Fig.S2-B).

So, under the "Regional" assumption, we match the stock structure of Costello et al. (2016), which in this case assumes that every polygon is an independent stock, i.e. MPAs off of Florida, USA have no impact on stock status of largehead hairtail off of China. Under the "Global" assumption used by Sala et al. (2021),
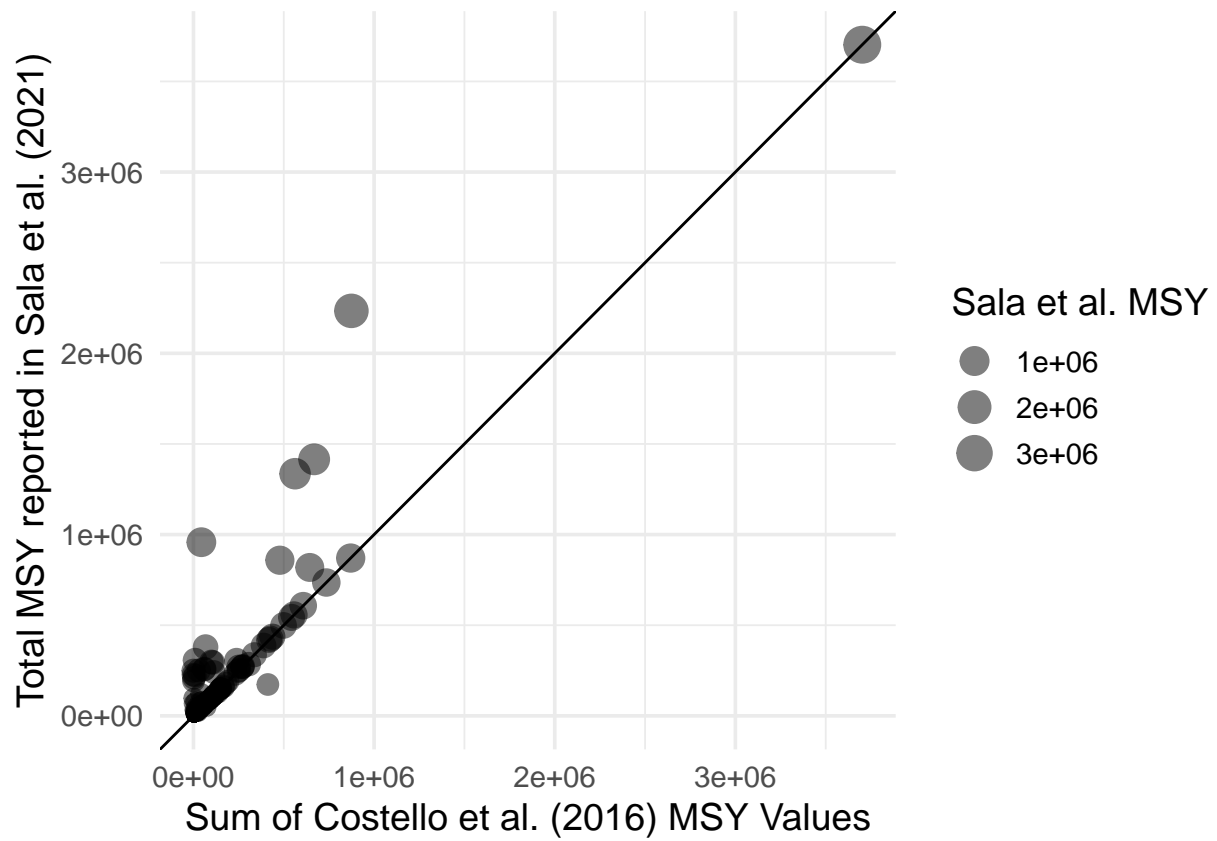
Figure S1: Comparison of total MSY for unassessed species reported in Sala et al. (2021) (y-axis) to sum of MSY values per species used in Costello et al. (2016) projections. Each point represents one unassessed stock from Sala et al. (2021).

as there is only one global largehead hairtail stock, MPAs protecting equivalent amounts of habitat off of Florida can have just as large of an impact on largehead hairtail as those off of China.

Once we had created the divided unassessed stocks for the "Regional" assumptions, we had to ensure that the total MSYs matched up between the "Regional" and "Global" assumptions, since in the raw data provided from Sala et al. (2021) the total MSYs for many unassessed stocks do not match their constituent parts (Fig.S1). For each unassessed species, we summed the MSYs for each individual stock used in the "Regional" assumptions, and then set the total MSY for that species in the "Global" assumption to that value, correcting the Schaefer carrying capacity K accordingly

$$K = \frac{4MSY}{r}.$$

We chose to downscale to the MSY values reported in Costello et al. (2016) in order to preserve the covariance across the other parameters needed for projection; had we "upscaled" to the total MSY reported in Sala et al. (2021) a) we would not have known how to distribute the almost universally higher (Fig.S1) MSY values across the constituent stocks, and b) existing values for growth rate and carrying capacity needed for projection would be inconsistent with this new MSY. The resulting MSY values represent 76% of the total MSY values reported in Sala et al. (2021).

1.3 Population Models

Sala et al. (2021) converted the methods of Costello et al. (2016) into a Schaefer model, which provides an analytical solution to the equilibrium state of their model. We modified their methods to construct a numerical simulation model for the biomass dynamics of fished populations with MPAs that a) can handle two different options for spatial scale of density dependence and b) subs in a Pella-Tomlinson model for the growth dynamics.

1.3.1 "Pooled" vs. "Local" density dependence

Density dependence at one or more life stages is a key part of population dynamics, and takes many different forms in different population models. The exact functional form and life history timing of density dependence will vary depending on the biology and ecology of the species in question. One key question for this analysis is whether density dependence is a function of the biomass in a specific area (say inside vs. outside of an MPA) or across the entire population. Neither is inherently right; as pointed out by Hastings and Botsford (1999) and illustrated in Babcock and MacCall (2011) (See Table 1 therein), a wide range of combinations of timing and location of density dependence are possible when considering spatial dynamics.

9

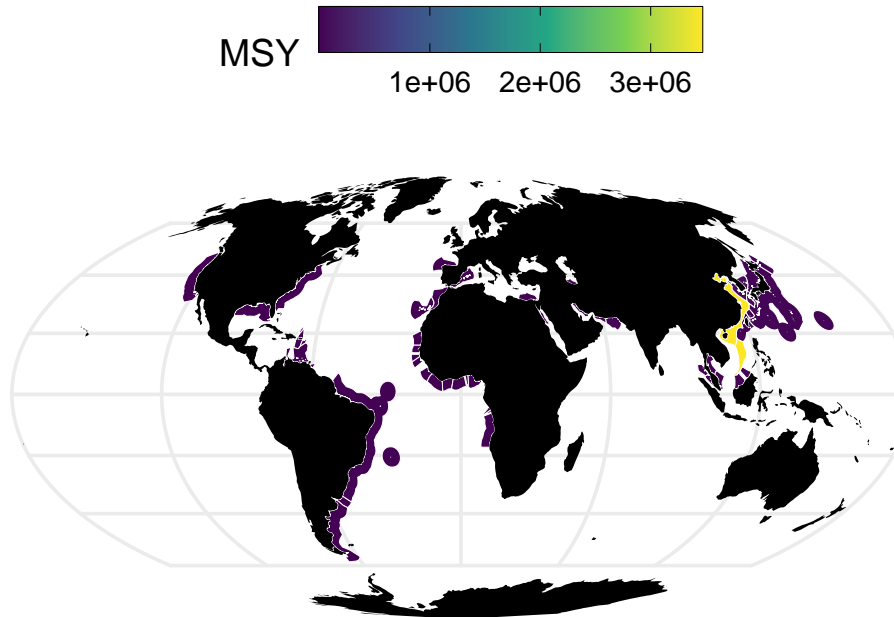# a) Global Stock Structure
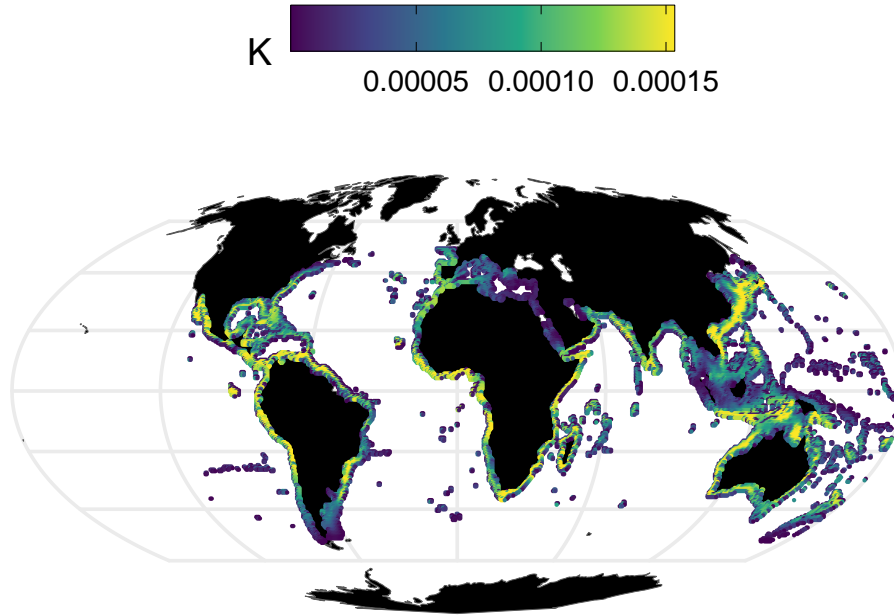
B) Regional Stock Structure

Figure S2: Comparison of stock structure for largehead hairtail (*Trichiurus lepturus*) under the A) assumptions of Sala *et al.* (2021) (*Global*) and B) Costello et al. (2016) (*Regional). In A), color shows fraction of global carrying capacity per cell. In B), color shows MSY estimated for each stock by Costello et al. (2016), with each polygon representing a separate stock.

Sala et al. (2021) assumes a form of density dependence in which density dependence is a function of the total biomass in the population, defined as the sum of biomass insides and outside of the MPAs. Whether in Pella-Tomlinson mode or Schaefer mode, within the context of a biomass dynamics model, this implies that density dependent growth is a function of

$$f\left(\frac{B_{inside} + B_{outside}}{K_{global}}\right).$$

In contrast, "local" density dependence function implies that density dependent growth is a function of the biomass within a specific location, while local biomass may still benefit from production elsewhere (i.e., through immigration)

$$f\left(\frac{B_{inside}}{K_{inside}}\right).$$

Both forms can be applicable in different circumstances, and each has advantages and disadvantages within the limiting constraints of a two-patch biomass dynamics model. We would note that the "local" set of assumptions are widely used in MPA modeling, including in papers authored by members of Sala *et al.* . Sala et al. (2013) (equation 6) and by extension Sala et al. (2016) assume that density dependence is a function of local spawning biomass, not pooled, as does Cabral et al. (2019) (equations 4 and 5). Hastings and Botsford (1999) as well as Rassweiler, Costello, and Siegel (2012), and Rassweiler et al. (2014) (used in tactical modeling of MPAs in the Channel Islands, USA) all use forms of local density dependence. Each of them makes different assumptions about *dispersal*, but conditional on dispersal, in each of these papers density dependence is a function of some local attribute in a given patch, not a sum across all patches in the model.

Both local and global density dependence can be justified under different circumstances. It is important to consider though, that there is no such thing as isolated "larvae" or "recruits" in a surplus production model: Models such as the logistic one used in Sala et al. (2021) or the Pella-Tomlinson model used here and in Costello et al. (2016) both model the **total biomass** of the population at one time. Under these models density dependent growth represents the total change in biomass resulting from the sum of recruitment, survival, and somatic growth across all age groups. As such, assuming "pooled" density dependence is not equivalent to only assuming global larval dispersal, density dependence, and the reallocation to home patches; it is also assuming that all the density dependent growth and mortality of the adult portions of the population are also a function of pooled, rather than local, biomass, and similarly distributed then

11

216 reallocated.

1.3.2 Pella-Tomlinson Model Structure and Local vs. Pooled Density Dependence

218 We follow the same Pella-Tomlinson structure used in Costello et al. (2016) although modified to allow for
219 the kinds of two-patch MPA dynamics used in Sala et al. (2021). Population model was written in C++
220 with the `Rcpp` package (Eddelbuettel and Balamuta 2018). Under "local" density dependence, the equations
221 are as follows, where B is biomass, t is time, ϕ scales the shape of the production curve (set to 0.188 per
222 Costello et al. (2016), such that $B_{MSY}/K = 0.4$, g is the growth rate, K is the carrying capacity, R is the
223 proportion of the total carrying capacity inside the MPA ([0,1]), and m is the movement rate:

$$B_{t+1,MPA=1} = B_{t,MPA=1} + \frac{\phi+1}{\phi} g B_{t,MPA=1} \left(1 - \left(\frac{B_{t,MPA=1}}{K \times R} \right)^{\phi} \right)$$
$$- m(B_{t,MPA=1} - \frac{R}{1-R} B_{t,MPA=0}).$$

$$B_{t+1,MPA=0} = (1 - u_t) \times (B_{t,MPA=0} + \frac{\phi+1}{\phi} g B_{t,MPA=0} \left(1 - \left(\frac{B_{t,MPA=0}}{K \times (1-R)} \right)^{\phi} \right)$$
$$+ m \left(B_{t,MPA=1} - \frac{R}{1-R} B_{t,MPA=0} \right)).$$

224 Under "pooled" density dependence

$$B_{t,Total} = B_{t,MPA=1} + B_{t,MPA=0},$$

$$B_{t+1,MPA=1} = B_{t,MPA=1} + R \frac{\phi+1}{\phi} g B_{t,Total} \left(1 - \left(\frac{B_{t,Total}}{K} \right)^{\phi} \right)$$
$$- m \left(B_{t,MPA=1} - \frac{R}{1-R} B_{t,MPA=0} \right).$$

$$B_{t+1,MPA=0} = (1 - u_t) \times (B_{t,MPA=0} + (1-R) \frac{\phi+1}{\phi} g B_{t,Total} \left(1 - \left(\frac{B_{t,Total}}{K} \right)^{\phi} \right)$$
$$+ m \left(B_{t,MPA=1} - \frac{R}{1-R} B_{t,MPA=0} \right)).$$

225 Note that both the "local" and "pooled" density dependence forms allow for movement between the fished
226 and MPA patches. The difference is whether density dependent growth occurs locally and is then dispersed
227 (local), or whether density dependent growth of all kinds occurs as a total pool and then is redistributed to
228 each patch in proportion to its size.

1.4 MPA Design Algorithm

Sala et al. (2021) assigns MPA by iteratively calculating the marginal food provision effects of converting each individual fished cell in their model to an MPA, adding the top ranked cell to the MPA network, and then repeating the process with the remaining fished cells until all cells are placed inside an MPAs.

This process is feasible given the analytical solutions used in Sala et al. (2021). However, the *Regional* set of assumptions requires numerical simulations, which make the MPA design process used in Sala et al. (2021) cumbersome. We created a modified version of their MPA design process using a version of a Sampling Important Resampling (SIR) algorithm.

In the first phase of the process, the algorithm calculates the marginal food provision value of every cell in the model, assigning the top ranked cell as its first MPA. For subsequent steps, the model samples 2,500 cells (or the number of cells remaining, whichever is lower) out of the total possible, with sampling weighted by the marginal food provision values in the last iteration. The marginal food provision values of each of the sampled cells is calculated, and the top ranked cell is added to the MPA network. The 2,499 cells not selected are returned to the pool, and their prior marginal food provision values are updated. In this way, the algorithm searches over a smaller space for the next MPA cell, concentrating on cells that had close to the best performance in the last iteration, while updating the value of non-selected cells. This process continues until all the cells are placed inside an MPA network. This process also allows us to pick MPAs at a finer resolution of 25 cells at a time rather than the 100 cells at a time reported in Cabral et al. (2020).

2 Sensitivity Analyses

Table S1: Summary of assumption sets run. "Unassessed Range" refers to the assumed stock structure use for unassessed stocks, with Costello et al. (2016) indicating that the same assumptions as Costello et al. (2016) is used.

Assumption Set Name	Unassessed Range	Population Dynamics	Density Dependence
Global	Global	Schaefer	Pooled
Regional	Costello et al. (2016)	Pella-Tomlinson	Local
Regional-Pooled	Costello et al. (2016)	Pella-Tomlinson	Pooled

2.1 Country-Level Stocks, Global Density Dependence

In order to test the sensitivity of our results to the choice of "local" vs "pooled" density dependence, we re-ran our analysis keeping everything constant except for the spatial scale of density dependence, turning it to "pooled" instead of "local". Results differ somewhat from those produced with "local" density dependence presented in the main paper, but present the same general findings of lower potential upside, smaller proportion of carrying capacity protected, and a fundamentally restructured global prioritization map (Fig.S3, Fig.S4)
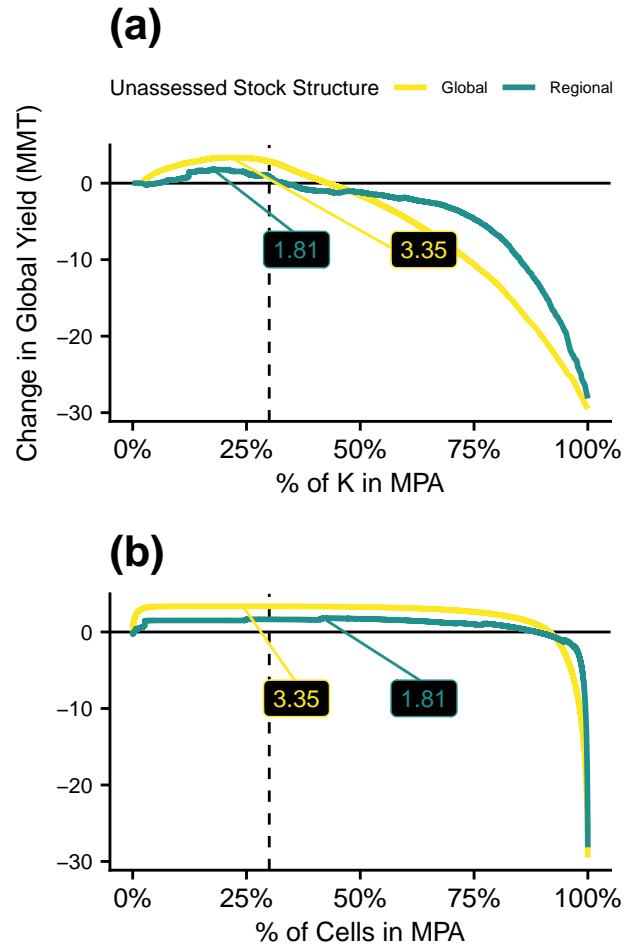
14

Figure S3: Change in global yield as a function of percent of global carrying capacity (K) in MPAs (a) and percent of global ocean surface in MPAs (b). *Global* indicates that both stocks and density dependence are assumed to occur at global scales, following Sala et al. (2021) . *Regional* indicates that stocks are modeled in the same manner as Costello et al. (2016) with pooled density dependence in this sensitivity analysis
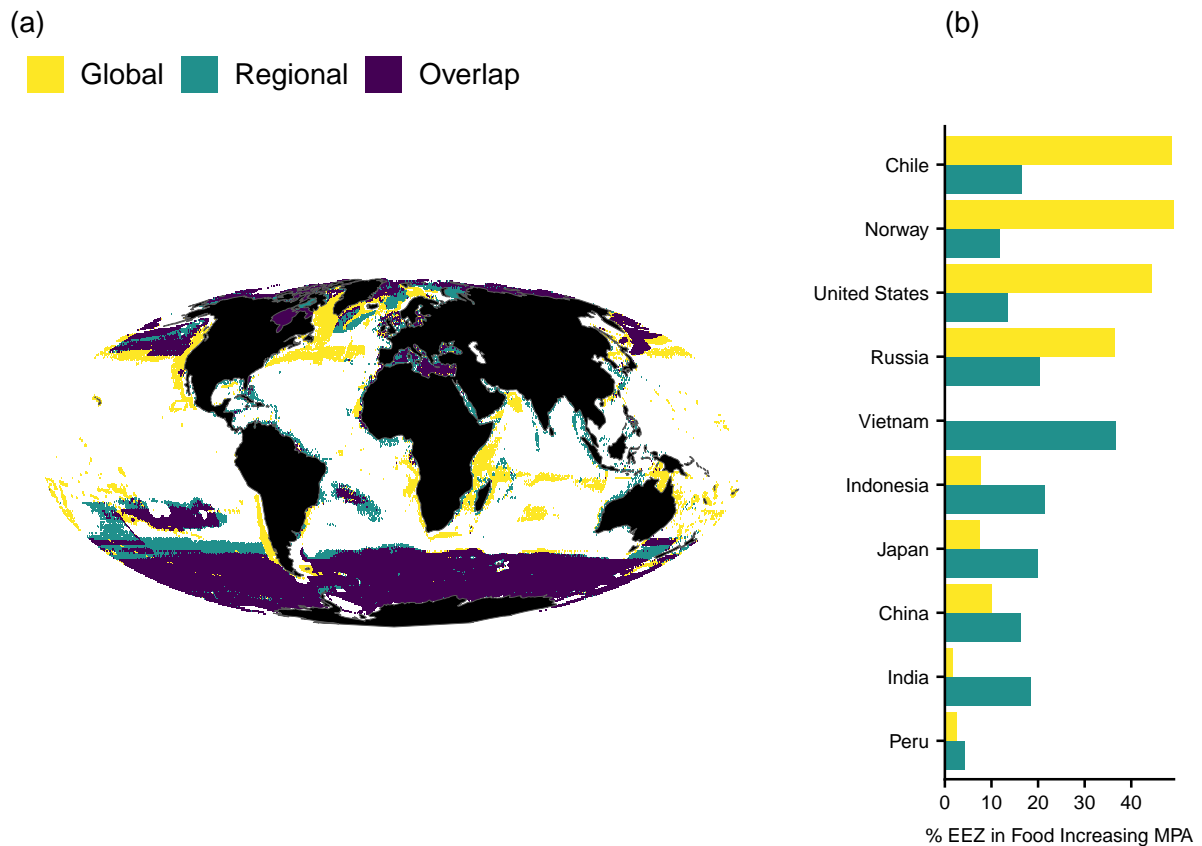
Figure S4: Spatial differences in MPA outcomes between alternative assumptions. Map (a) shows cells identified in the top 30% of MPAs, where color indicates which set of assumptions produced which cells, with overlapping cells indicated by the 'Overlap' color. Bars (b) indicate the percent of the top-ten countries' by recent FAO reported catches EEZs each assumption set projects could be placed inside food increasing MPAs. Existing MPAs omitted as these are automatically included by the model. *Global* assumes one global stock per unassessed species and pooled density dependence, following Sala et al. (2021) . *Regional* indicates that stocks are modeled in the same manner Costello et al. (2016) with pooled density dependence in this sensitivity analysis.

2.2 Fishing Causes Increase in MPA Biomass Under Global Density Dependence

One of the unusual features of the pooled density dependence and movement models used in Sala et al. (2021) is that under these dynamics, it is possible for fishing outside of MPAs to actually increase fish biomass inside the MPA relative to the biomass in the MPA in the absence of any fishing anywhere.

We demonstrate this using a Schaefer model with the same density dependence and movement dynamics used in Sala et al. (2021) (Fig.S5)
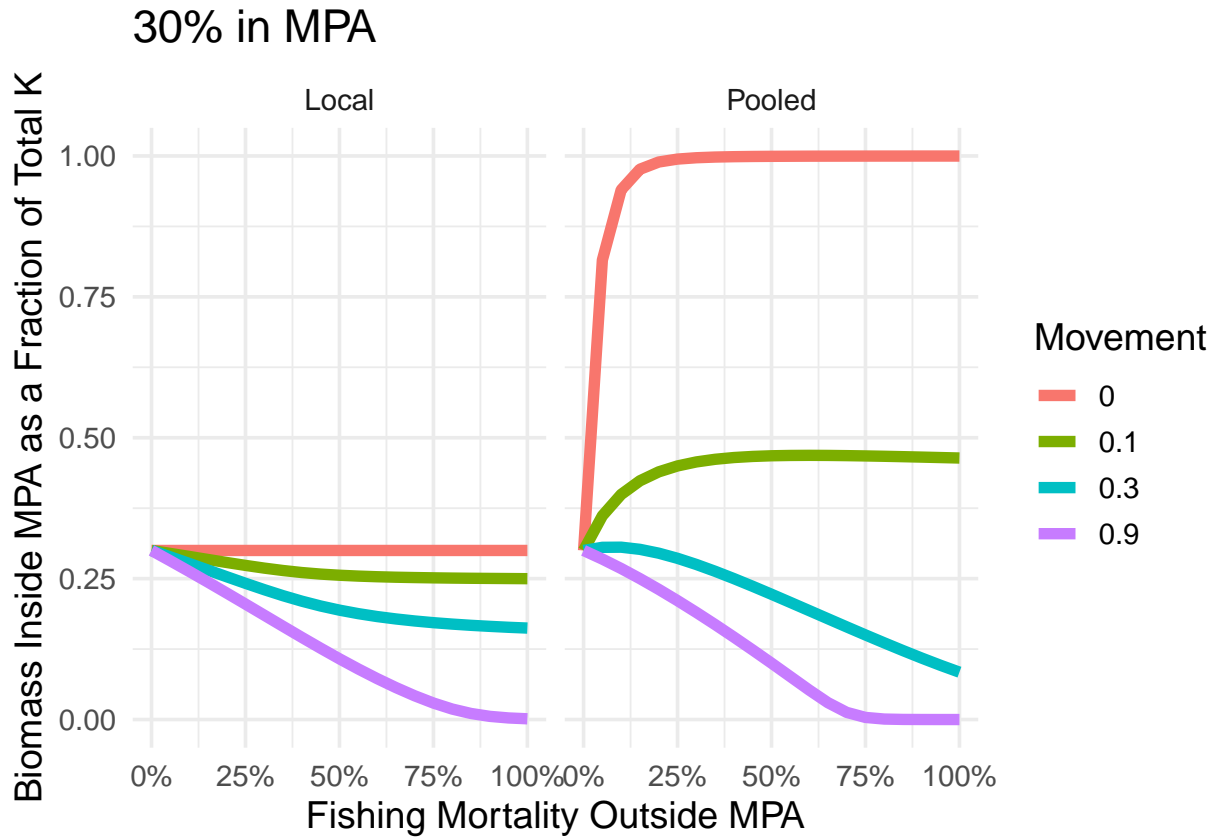

Figure S5: Equilibrium depletion (biomass divided by carrying capacity K) inside a marine protected area covering 30% of a region as a function of the fishing mortality rate outside the MPA. Color represents movement rate, panel indicates which form of density dependence is used, with the 'Pooled' implying that density dependence is a function of biomass inside and outside the MPA, while the 'Local' implies that growth inside the MPA is a function of biomass inside the MPA.

3 Stock Footprint Size

We can compare the size of the stock footprint for the assessed stocks used in Sala et al. (2021), that uses the spatial footprints created by Free et al. (2019) for each of the assessed stocks, to those for the "unassessed" stocks that use the Aquamaps species distribution model (SDM) as the footprint. While the RAM footprints are not definitive, they provide a sense of what experts have judged to be the range of a connected biological stock.

Sala et al. (2021) assumes that proportion of K is proportional to the Aquamaps SDM. So, rather than simply summing the number of cells with "K" > 0 for each species, we calculate a K-weighted footprint as

$$footprint_s = \sum_{i=1}^{I} \frac{k_{i,s}}{max(\boldsymbol{k_s})}.$$

where k is the "carrying capacity" for species s in cell i from KprotectedPerCell_Library. So, for a species where k_i is equal in every patch, *footprint* will equal the number of cells. But, if the k_i are much greater in some patches than in others, the k-weighted footprint will be smaller.

Implementing this measure shows that there are stark differences between these two footprints: the median unassessed fishery has a k-weighted footprint roughly 14 times greater than the median assessed stock, with many unassessed stocks having order of magnitude greater spatial footprints than assessed stocks (FigS6).
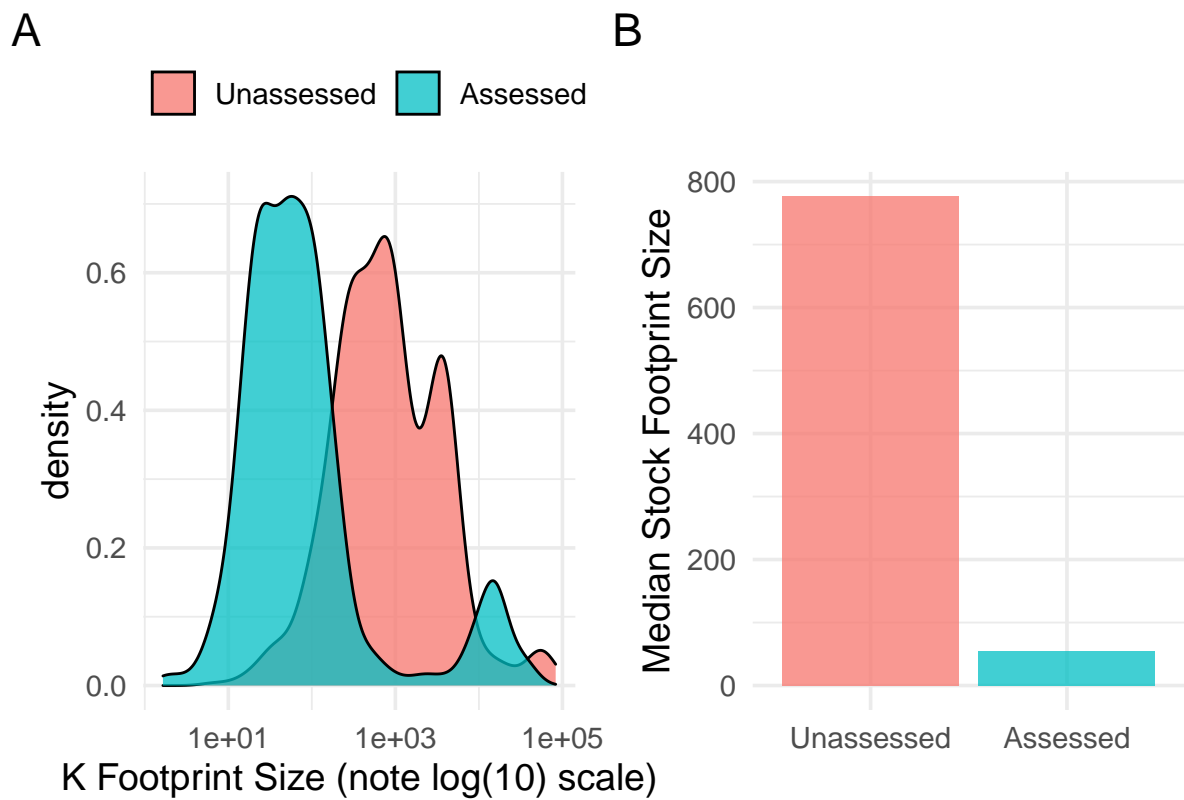
Figure S6: Comparison of K-weighted spatial footprint size between unassessed and assessed stocks. A) Distribution of individual stocks (Note Log(10) scale of axis) B) difference in median K-weighted footprint size
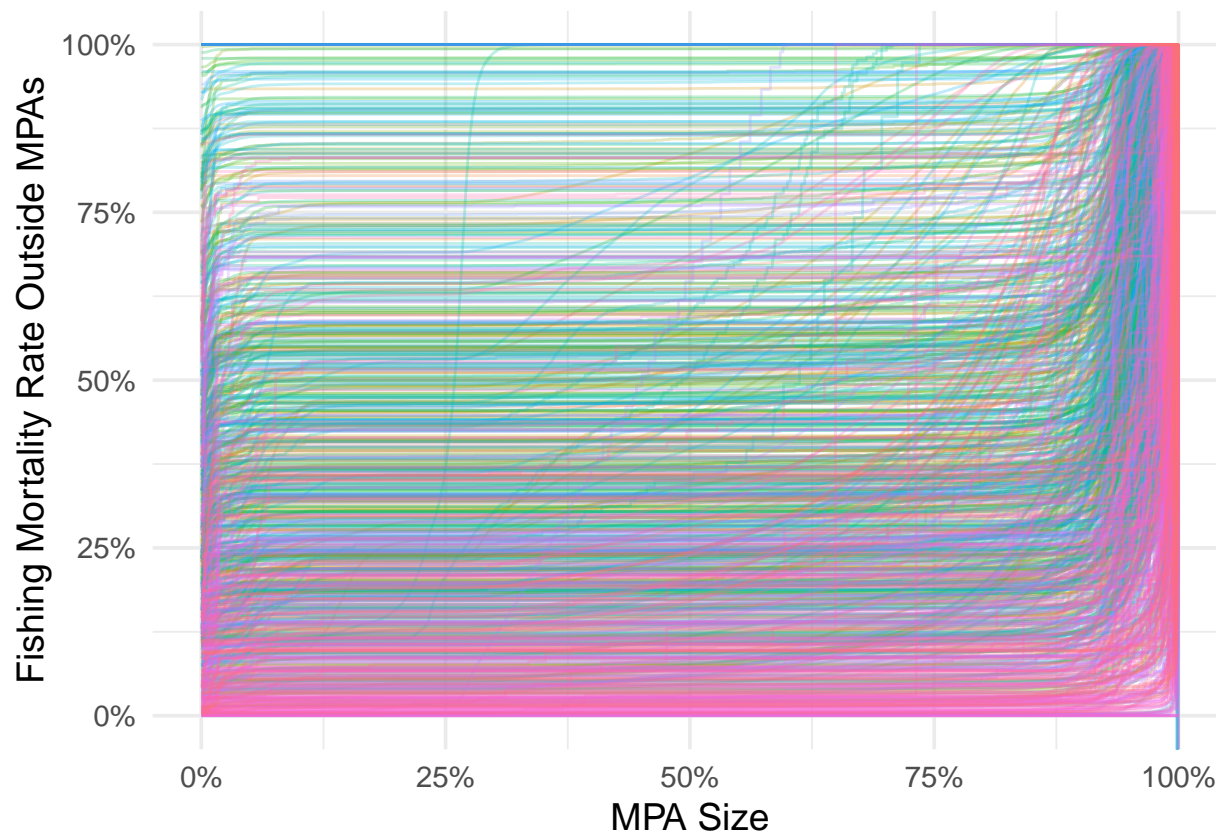
4 Fished Area Exploitation Rates

Figure S7: Trajectory of fishing mortality rates in fished areas as a function of increasing percent of cells inside an MPA. Each line represents an individual stock.
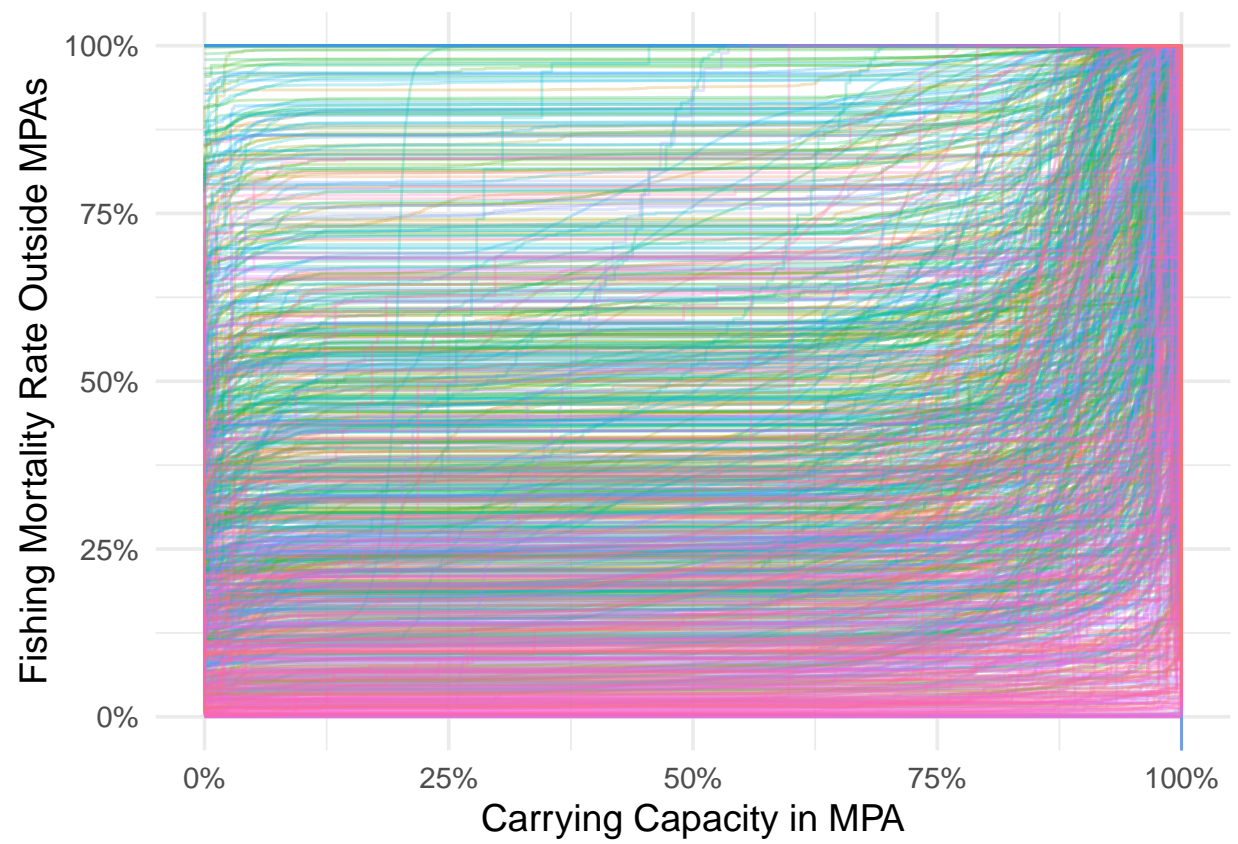
Figure S8: Trajectory of fishing mortality rates in fished areas as a function of increasing percent of carrying capacity (K) inside an MPA. Each line represents an individual stock.

5 References

Anderson, Sean C., Andrew B. Cooper, Olaf P. Jensen, Cóilín Minto, James T. Thorson, Jessica C. Walsh, Jamie Afflerbach, et al. 2017. "Improving Estimates of Population Status and Trend with Superensemble Models." *Fish and Fisheries* 18 (4): 732–41. https://doi.org/10.1111/faf.12200.

Babcock, Elizabeth A., and Alec D. MacCall. 2011. "How Useful Is the Ratio of Fish Density Outside Versus Inside No-Take Marine Reserves as a Metric for Fishery Management Control Rules?" *Canadian Journal of Fisheries and Aquatic Sciences* 68 (2): 343–59. https://doi.org/10.1139/F10-146.

Cabral, Reniel B., Darcy Bradley, Juan Mayorga, Whitney Goodell, Alan M. Friedlander, Enric Sala, Christopher Costello, and Steven D. Gaines. 2020. "A Global Network of Marine Protected Areas for Food." *Proceedings of the National Academy of Sciences* 117 (45): 28134–39.

Cabral, Reniel B., Benjamin S. Halpern, Sarah E. Lester, Crow White, Steven D. Gaines, and Christopher Costello. 2019. "Designing MPAs for Food Security in Open-Access Fisheries." *Scientific Reports* 9 (1): 8033. https://doi.org/10.1038/s41598-019-44406-w.

Costello, Christopher, Daniel Ovando, Tyler Clavelle, C. Kent Strauss, Ray Hilborn, Michael C. Melnychuk, Trevor A. Branch, et al. 2016. "Global Fishery Prospects Under Contrasting Management Regimes." *Proceedings of the National Academy of Sciences* 113 (18): 5125–29. https://doi.org/10.1073/pnas.1520420113.

Costello, Christopher, Daniel Ovando, Ray Hilborn, Steven D. Gaines, Olivier Deschenes, and Sarah E. Lester. 2012. "Status and Solutions for the World's Unassessed Fisheries." *Science* 338 (6106): 517–20. https://doi.org/10.1126/science.1223389.

Eddelbuettel, Dirk, and James Joseph Balamuta. 2018. "Extending extitR with extitC++: A Brief Introduction to extitRcpp." *The American Statistician* 72 (1): 28–36. https://doi.org/10.1080/00031305.2017.1375990.

Free, Christopher M., James T. Thorson, Malin L. Pinsky, Kiva L. Oken, John Wiedenmann, and Olaf P. Jensen. 2019. "Impacts of Historical Warming on Marine Fisheries Production." *Science* 363 (6430): 979–83. https://doi.org/10.1126/science.aau1758.

Hastings, Alan, and Louis W. Botsford. 1999. "Equivalence in Yield from Marine Reserves and Traditional Fisheries Management." *Science* 284 (5419): 1537–38. https://doi.org/10.1126/science.284.5419.1537.

Hilborn, Ray, Ricardo Oscar Amoroso, Christopher M. Anderson, Julia K. Baum, Trevor A. Branch, Christopher Costello, Carryn L. de Moor, et al. 2020. "Effective Fisheries Management Instrumental in Improving Fish Stock Status." *Proceedings of the National Academy of Sciences*, January. https://doi.org/10.1073/pnas.1909726116.

Kaschner, K, K Kesner-Reyes, C Garilao, J Segschneider, J Rius-Barile, T Rees, and R Froese. 2019. "AquaMaps: Predicted Range Maps for Aquatic Species." World wide web electronic publication.

Martell, Steven, and Rainer Froese. 2013. "A Simple Method for Estimating MSY from Catch and Resilience." *Fish and Fisheries* 14 (4): 504–14. https://doi.org/10.1111/j.1467-2979.2012.00485.x.

Ovando, Daniel, Owen Liu, Renato Molina, and Cody Szuwalski. 2021. "Models of Marine Protected Areas Must Explicitly Address Spatial Dynamics." *Proceedings of the National Academy of Sciences* 118 (23). https://doi.org/10.1073/pnas.2025958118.

Pella, Jerome J., and Patrick K. Tomlinson. 1969. "A Generalized Stock Production Model." *Inter-American Tropical Tuna Commission Bulletin* 13 (3): 416–97. http://aquaticcommons.org/3536/.

Rassweiler, Andrew, Christopher Costello, Ray Hilborn, and David A. Siegel. 2014. "Integrating Scientific Guidance into Marine Spatial Planning." *Proceedings of the Royal Society B: Biological Sciences* 281 (1781): 20132252. https://doi.org/10.1098/rspb.2013.2252.

Rassweiler, Andrew, Christopher Costello, and David A. Siegel. 2012. "Marine Protected Areas and the Value of Spatially Optimized Fishery Management." *Proceedings of the National Academy of Sciences* 109 (29): 11884–89. https://doi.org/10.1073/pnas.1116193109.

Sala, Enric, Christopher Costello, Jaime De Bourbon Parme, Marco Fiorese, Geoff Heal, Kieran Kelleher, Russell Moffitt, et al. 2016. "Fish Banks: An Economic Model to Scale Marine Conservation." *Marine Policy* 73 (November): 154–61. https://doi.org/10.1016/j.marpol.2016.07.032.

Sala, Enric, Christopher Costello, Dawn Dougherty, Geoffrey Heal, Kieran Kelleher, Jason H. Murray, Andrew A. Rosenberg, and Rashid Sumaila. 2013. "A General Business Model for Marine Reserves." *PLoS ONE* 8 (4): e58799. https://doi.org/10.1371/journal.pone.0058799.

Sala, Enric, Juan Mayorga, Darcy Bradley, Reniel B. Cabral, Trisha B. Atwood, Arnaud Auber, William Cheung, et al. 2021. "Protecting the Global Ocean for Biodiversity, Food and Climate." *Nature*, March, 1–6. https://doi.org/10.1038/s41586-021-03371-z.