

Supporting Information: The Regional Effects of Marine Protected Areas

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1 Supporting Information (SI)

SI Text

1.1 Computing environment

All code needed to reproduce our main results and manuscript can be found at <https://github.com/DanOvando/regional-effects-of-mpas>. All analysis were performed in R version 3.6.3 (2020-02-29). Package versions are shown in Table.S1.

Table 1: Package versions and sources used in this paper

	package	loadedversion	date	source
arrayhelpers	arrayhelpers	1.1-0	2020-02-04	CRAN (R 3.6.0)
assertthat	assertthat	0.2.1	2019-03-21	CRAN (R 3.6.0)
backports	backports	1.1.6	2020-04-05	CRAN (R 3.6.2)
base64enc	base64enc	0.1-3	2015-07-28	CRAN (R 3.6.0)
bayesplot	bayesplot	1.7.1	2019-12-01	CRAN (R 3.6.0)
bitops	bitops	1.0-6	2013-08-17	CRAN (R 3.6.0)
bookdown	bookdown	0.18	2020-03-05	CRAN (R 3.6.2)
boot	boot	1.3-24	2019-12-20	CRAN (R 3.6.3)
broom	broom	0.5.6	2020-04-20	CRAN (R 3.6.2)
callr	callr	3.4.3	2020-03-28	CRAN (R 3.6.2)
caret	caret	6.0-86	2020-03-20	CRAN (R 3.6.2)
cellranger	cellranger	1.1.0	2016-07-27	CRAN (R 3.6.0)
class	class	7.3-15	2019-01-01	CRAN (R 3.6.3)

Table 1: Package versions and sources used in this paper (*continued*)

	package	loadedversion	date	source
classInt	classInt	0.4-2	2019-10-17	CRAN (R 3.6.0)
cli	cli	2.0.2	2020-02-28	CRAN (R 3.6.0)
coda	coda	0.19-3	2019-07-05	CRAN (R 3.6.0)
codetools	codetools	0.2-16	2018-12-24	CRAN (R 3.6.3)
colorspace	colorspace	1.4-1	2019-03-18	CRAN (R 3.6.0)
colourpicker	colourpicker	1.0	2017-09-27	CRAN (R 3.6.0)
crayon	crayon	1.3.4	2017-09-16	CRAN (R 3.6.0)
crosstalk	crosstalk	1.1.0.1	2020-03-13	CRAN (R 3.6.2)
data.table	data.table	1.12.8	2019-12-09	CRAN (R 3.6.0)
DBI	DBI	1.1.0	2019-12-15	CRAN (R 3.6.0)
dbplyr	dbplyr	1.4.2	2019-06-17	CRAN (R 3.6.0)
desc	desc	1.2.0	2018-05-01	CRAN (R 3.6.0)
devtools	devtools	2.3.0	2020-04-10	CRAN (R 3.6.3)
dials	dials	0.0.4	2019-12-02	CRAN (R 3.6.0)
DiceDesign	DiceDesign	1.8-1	2019-07-31	CRAN (R 3.6.0)
digest	digest	0.6.25	2020-02-23	CRAN (R 3.6.0)
dplyr	dplyr	0.8.5	2020-03-07	CRAN (R 3.6.2)
DT	DT	0.13	2020-03-23	CRAN (R 3.6.2)
dygraphs	dygraphs	1.1.1.6	2018-07-11	CRAN (R 3.6.0)
e1071	e1071	1.7-3	2019-11-26	CRAN (R 3.6.0)
ellipsis	ellipsis	0.3.0	2019-09-20	CRAN (R 3.6.0)
evaluate	evaluate	0.14	2019-05-28	CRAN (R 3.6.0)
extrafont	extrafont	0.17	2014-12-08	CRAN (R 3.6.0)
extrafontdb	extrafontdb	1.0	2012-06-11	CRAN (R 3.6.0)
fansi	fansi	0.4.1	2020-01-08	CRAN (R 3.6.0)
fastmap	fastmap	1.0.1	2019-10-08	CRAN (R 3.6.0)
forcats	forcats	0.5.0	2020-03-01	CRAN (R 3.6.0)
foreach	foreach	1.4.8	2020-02-09	CRAN (R 3.6.0)
fs	fs	1.4.1	2020-04-04	CRAN (R 3.6.2)
gdtools	gdtools	0.2.2	2020-04-03	CRAN (R 3.6.2)
generics	generics	0.0.2	2018-11-29	CRAN (R 3.6.0)
ggmap	ggmap	3.0.0	2019-02-05	CRAN (R 3.6.0)
ggplot2	ggplot2	3.3.0	2020-03-05	CRAN (R 3.6.2)
ggrepel	ggrepel	0.8.2	2020-03-08	CRAN (R 3.6.2)
ggridges	ggridges	0.5.2	2020-01-12	CRAN (R 3.6.0)
ggsci	ggsci	2.9	2018-05-14	CRAN (R 3.6.0)
ggspatial	ggspatial	1.0.3	2018-12-14	CRAN (R 3.6.0)
ggtext	ggtext	0.1.0	2020-03-19	Github (wilkelab/ggtext@24e9cd0)
glue	glue	1.4.0	2020-04-03	CRAN (R 3.6.2)
gower	gower	0.2.1	2019-05-14	CRAN (R 3.6.0)
GPfit	GPfit	1.0-8	2019-02-08	CRAN (R 3.6.0)
gridExtra	gridExtra	2.3	2017-09-09	CRAN (R 3.6.0)
gridtext	gridtext	0.1.1	2020-02-24	CRAN (R 3.6.0)
gtable	gtable	0.3.0	2019-03-25	CRAN (R 3.6.0)
gtools	gtools	3.8.2	2020-03-31	CRAN (R 3.6.2)
haven	haven	2.2.0	2019-11-08	CRAN (R 3.6.0)

Table 1: Package versions and sources used in this paper (*continued*)

	package	loadedversion	date	source
here	here	0.1	2017-05-28	CRAN (R 3.6.0)
hms	hms	0.5.3	2020-01-08	CRAN (R 3.6.0)
hrbrthemes	hrbrthemes	0.8.0	2020-03-06	CRAN (R 3.6.2)
htmltools	htmltools	0.4.0	2019-10-04	CRAN (R 3.6.0)
htmlwidgets	htmlwidgets	1.5.1	2019-10-08	CRAN (R 3.6.0)
httpuv	httpuv	1.5.2	2019-09-11	CRAN (R 3.6.0)
httr	httr	1.4.1	2019-08-05	CRAN (R 3.6.0)
igraph	igraph	1.2.5	2020-03-19	CRAN (R 3.6.2)
inline	inline	0.3.15	2018-05-18	CRAN (R 3.6.0)
ipred	ipred	0.9-9	2019-04-28	CRAN (R 3.6.0)
iterators	iterators	1.0.12	2019-07-26	CRAN (R 3.6.0)
jpeg	jpeg	0.1-8.1	2019-10-24	CRAN (R 3.6.0)
jsonlite	jsonlite	1.6.1	2020-02-02	CRAN (R 3.6.0)
KernSmooth	KernSmooth	2.23-16	2019-10-15	CRAN (R 3.6.3)
knitr	knitr	1.28	2020-02-06	CRAN (R 3.6.0)
later	later	1.0.0	2019-10-04	CRAN (R 3.6.0)
lattice	lattice	0.20-38	2018-11-04	CRAN (R 3.6.3)
lava	lava	1.6.7	2020-03-05	CRAN (R 3.6.2)
lhs	lhs	1.0.1	2019-02-03	CRAN (R 3.6.0)
lifecycle	lifecycle	0.2.0	2020-03-06	CRAN (R 3.6.2)
lme4	lme4	1.1-23	2020-04-07	CRAN (R 3.6.2)
loo	loo	2.2.0	2019-12-19	CRAN (R 3.6.0)
lubridate	lubridate	1.7.8	2020-04-06	CRAN (R 3.6.2)
magrittr	magrittr	1.5	2014-11-22	CRAN (R 3.6.0)
markdown	markdown	1.1	2019-08-07	CRAN (R 3.6.0)
MASS	MASS	7.3-51.5	2019-12-20	CRAN (R 3.6.3)
Matrix	Matrix	1.2-18	2019-11-27	CRAN (R 3.6.3)
matrixStats	matrixStats	0.56.0	2020-03-13	CRAN (R 3.6.2)
memoise	memoise	1.1.0	2017-04-21	CRAN (R 3.6.0)
mime	mime	0.9	2020-02-04	CRAN (R 3.6.0)
miniUI	miniUI	0.1.1.1	2018-05-18	CRAN (R 3.6.0)
minqa	minqa	1.2.4	2014-10-09	CRAN (R 3.6.0)
ModelMetrics	ModelMetrics	1.2.2.2	2020-03-17	CRAN (R 3.6.2)
modelr	modelr	0.1.6	2020-02-22	CRAN (R 3.6.0)
munsell	munsell	0.5.0	2018-06-12	CRAN (R 3.6.0)
nlme	nlme	3.1-144	2020-02-06	CRAN (R 3.6.3)
nloptr	nloptr	1.2.2.1	2020-03-11	CRAN (R 3.6.2)
nnet	nnet	7.3-12	2016-02-02	CRAN (R 3.6.3)
parsnip	parsnip	0.0.5	2020-01-07	CRAN (R 3.6.0)
patchwork	patchwork	1.0.0.9000	2020-04-21	Github (thomasp85/patchwork@012fb8b)
pillar	pillar	1.4.3	2019-12-20	CRAN (R 3.6.0)
pkgbuild	pkgbuild	1.0.6	2019-10-09	CRAN (R 3.6.0)
pkgconfig	pkgconfig	2.0.3	2019-09-22	CRAN (R 3.6.0)
pkgload	pkgload	1.0.2	2018-10-29	CRAN (R 3.6.0)
plyr	plyr	1.8.6	2020-03-03	CRAN (R 3.6.0)
png	png	0.1-7	2013-12-03	CRAN (R 3.6.0)

Table 1: Package versions and sources used in this paper (*continued*)

	package	loadedversion	date	source
prettyunits	prettyunits	1.1.1	2020-01-24	CRAN (R 3.6.2)
pROC	pROC	1.16.2	2020-03-19	CRAN (R 3.6.2)
processx	processx	3.4.2	2020-02-09	CRAN (R 3.6.0)
prodlim	prodlim	2019.11.13	2019-11-17	CRAN (R 3.6.0)
promises	promises	1.1.0	2019-10-04	CRAN (R 3.6.0)
ps	ps	1.3.2	2020-02-13	CRAN (R 3.6.0)
purrr	purrr	0.3.4	2020-04-17	CRAN (R 3.6.3)
R6	R6	2.4.1	2019-11-12	CRAN (R 3.6.0)
Rcpp	Rcpp	1.0.4.8	2020-04-21	Github (RcppCore/Rcpp@4954e56)
readr	readr	1.3.1	2018-12-21	CRAN (R 3.6.0)
readxl	readxl	1.3.1	2019-03-13	CRAN (R 3.6.0)
recipes	recipes	0.1.10	2020-03-18	CRAN (R 3.6.2)
rEDM	rEDM	1.2.3	2020-03-06	CRAN (R 3.6.2)
remotes	remotes	2.1.1	2020-02-15	CRAN (R 3.6.0)
reprex	reprex	0.3.0	2019-05-16	CRAN (R 3.6.0)
reshape2	reshape2	1.4.4	2020-04-09	CRAN (R 3.6.2)
RgoogleMaps	RgoogleMaps	1.4.5.3	2020-02-12	CRAN (R 3.6.0)
rjson	rjson	0.2.20	2018-06-08	CRAN (R 3.6.0)
rlang	rlang	0.4.5	2020-03-01	CRAN (R 3.6.0)
rmarkdown	rmarkdown	2.1	2020-01-20	CRAN (R 3.6.0)
rpart	rpart	4.1-15	2019-04-12	CRAN (R 3.6.3)
rprojroot	rprojroot	1.3-2	2018-01-03	CRAN (R 3.6.0)
rsconnect	rsconnect	0.8.16	2019-12-13	CRAN (R 3.6.2)
rstan	rstan	2.19.3	2020-02-11	CRAN (R 3.6.0)
rstanarm	rstanarm	2.19.3	2020-02-11	CRAN (R 3.6.2)
rstantools	rstantools	2.0.0	2019-09-15	CRAN (R 3.6.0)
rstudioapi	rstudioapi	0.11	2020-02-07	CRAN (R 3.6.0)
Rttf2pt1	Rttf2pt1	1.3.8	2020-01-10	CRAN (R 3.6.0)
rvest	rvest	0.3.5	2019-11-08	CRAN (R 3.6.0)
scales	scales	1.1.0	2019-11-18	CRAN (R 3.6.0)
sessioninfo	sessioninfo	1.1.1	2018-11-05	CRAN (R 3.6.0)
sf	sf	0.9-1	2020-03-26	Github (r-spatial/sf@69c8d42)
shiny	shiny	1.4.0.2	2020-03-13	CRAN (R 3.6.2)
shinyjs	shinyjs	1.1	2020-01-13	CRAN (R 3.6.0)
shinytan	shinytan	2.5.0	2018-05-01	CRAN (R 3.6.0)
shinythemes	shinythemes	1.1.2	2018-11-06	CRAN (R 3.6.0)
sp	sp	1.4-1	2020-02-28	CRAN (R 3.6.0)
spasm	spasm	1.0.0	2020-04-21	Github (danovando/spasm@bcf6638)
StanHeaders	StanHeaders	2.21.0-1	2020-01-19	CRAN (R 3.6.0)
statmod	statmod	1.4.34	2020-02-17	CRAN (R 3.6.0)
stringi	stringi	1.4.6	2020-02-17	CRAN (R 3.6.2)
stringr	stringr	1.4.0	2019-02-10	CRAN (R 3.6.0)
survival	survival	3.1-8	2019-12-03	CRAN (R 3.6.3)
svUnit	svUnit	1.0.3	2020-04-20	CRAN (R 3.6.2)
systemfonts	systemfonts	0.2.0	2020-04-16	CRAN (R 3.6.2)
testthat	testthat	2.3.2	2020-03-02	CRAN (R 3.6.0)

Table 1: Package versions and sources used in this paper (*continued*)

	package	loadedversion	date	source
threejs	threejs	0.3.3	2020-01-21	CRAN (R 3.6.2)
tibble	tibble	3.0.1	2020-04-20	CRAN (R 3.6.2)
tidybayes	tidybayes	2.0.3.9000	2020-04-18	Github (mjskay/tidybayes@a830130)
tidyr	tidyr	1.0.2	2020-01-24	CRAN (R 3.6.2)
tidyselect	tidyselect	1.0.0	2020-01-27	CRAN (R 3.6.2)
tidyverse	tidyverse	1.3.0	2019-11-21	CRAN (R 3.6.0)
timeDate	timeDate	3043.102	2018-02-21	CRAN (R 3.6.0)
units	units	0.6-6	2020-03-16	CRAN (R 3.6.3)
usethis	usethis	1.6.0	2020-04-09	CRAN (R 3.6.3)
vctrs	vctrs	0.2.4	2020-03-10	CRAN (R 3.6.0)
viridis	viridis	0.5.1	2018-03-29	CRAN (R 3.6.0)
viridisLite	viridisLite	0.3.0	2018-02-01	CRAN (R 3.6.0)
withr	withr	2.2.0	2020-04-20	CRAN (R 3.6.2)
workflows	workflows	0.1.1	2020-03-17	CRAN (R 3.6.2)
xfun	xfun	0.13	2020-04-13	CRAN (R 3.6.2)
xml2	xml2	1.3.1	2020-04-09	CRAN (R 3.6.2)
xtable	xtable	1.8-4	2019-04-21	CRAN (R 3.6.0)
xts	xts	0.12-0	2020-01-19	CRAN (R 3.6.0)
yaml	yaml	2.2.1	2020-02-01	CRAN (R 3.6.0)
zoo	zoo	1.8-7	2020-01-10	CRAN (R 3.6.0)

1.2 PISCO Data

All fish data used in the primary difference-in-difference model were collected by PISCO. The dive transect survey methods are described in Caselle et al. (2015), provided below for ease of reference

“Fish assemblages were surveyed annually as part of a long-term monitoring program conducted by the Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO) using standard underwater visual belt survey methods (www.piscoweb.org9). We analyzed data from 47 PISCO sites at the northern Channel Islands that were sampled annually from at least 2003 to 2012. We also excluded 3 sites on Anacapa where a much older MPA had already been established in 1978. MPAs on each island were sampled annually during June-October and we surveyed multiple sites inside and outside of any individual MPA. Details of MPA characteristics such as size and coastline extent are given in Hamilton et al.9. At each site, we conducted 8 to 12 fish transects that measured 30×2×2m at multiple levels in the water column: benthic, midwater, and kelp canopy (when present). Transects are laid out in a stratified random design, with multiple nonpermanent transects located in fixed strata (i.e., outer, middle, and inner edges of the reef). At each level in the water column, one SCUBA diver per transect counted and estimated the sizes of all fish to the nearest centimeter (total length), excluding small cryptic fishes” - Caselle et al. (2015)

We take a number of steps to translate the raw transect data into the total biomass densities used in this study. For the default run, we only include species that were observed at least once for at least 15 of the 18 years of available data. We also exclude “young of the year” observations due the challenges of correctly identifying and measuring these individuals. We omitted data from 1999 due to changes in the sampling procedures that occurred after 1999. Per recommendations from PISCO staff we omit observations from the canopy level of the transects (leaving the middle, bottom, and middle canopy levels).

PISCO data report positive observations of fish. In order to use these data in our model we need to add in zeros for any transect that could have observed a given species of fish but did not. We assume that a fish could have been observed on a given transect if that species has ever been observed at that site in any time

period in the data (PISCO data are organized by sites, with multiple transect at different locations within the borders of a site). If a species has never been observed at a site we assume that it does not occur at that site.

Once zeros have been introduced to the database, we convert positive observations of fish from numbers to biomass. Each observation in the raw database lists the species, the number of individuals seen, and the size of those individuals (either as one value or as a minimum and maximum size for the group seen). PISCO staff compiled allometric information used to convert lengths to expected weights. For each observation then, we convert the observed lengths to weights per these relationships (accounting for variations in length types such as standard vs. total length). When minimum and maximum ranges were reported, we drew a number of samples equal to the number of observed fish in that group from a uniform distribution spanning the minimum and maximum reported size in that group. We assume all length-to-weight conversions are constant and deterministic.

For each species at each transect, we then calculate the biomass density of that transect as the sum of the observed biomass divided by the transect area. We then average the biomass densities for each species across all the transects at a given site, and lastly sum these mean species biomass densities to achieve the total mean species biomass at the site level.

We include several additional sources of data in our regression analysis. Temperature readings are included from the PISCO data for each transect. We also include PISCO data on the estimated surge and visibility. We augmented these data with information on kelp cover over time from the Santa Barbara Channel Long Term Ecological Research Network (LTER et al. 2017). We used a k-nearest neighbors algorithm to fill in missing kelp observations, and matched the interpolated kelp data to the PISCO data at the resolution of year-month-site (Fig.2). We include a variable capturing the mean cumulative number of observations across all observers conducting transects, in an effort to control for evolving observer skill.

We also included lagged catch totals in the Santa Barbara region for the commercially harvest species in the database, in an effort to control for changes in density caused by changes in fishing pressure. Catches were pulled from the CDFW website (<https://www.wildlife.ca.gov/Fishing/Commercial/Landings>), and extracted using the `tabulizer` package in R (Leeper 2018) (Fig.1).

Table 2: Species included in estimation model

classcode	Common Name	Scientific Name	Targeted?	Stock Status
pcla	kelp bass	<i>Paralabrax clathratus</i>	TRUE	unknown - increasing CPUE
satr	kelp rockfish	<i>Sebastes atrovirens</i>	TRUE	unknown
scau	copper rockfish	<i>Sebastes caurinus</i>	TRUE	Signs of overfishing
ejac	black surfperch	<i>Embiotoca jacksoni</i>	TRUE	unknown
rvac	pile perch	<i>Rhacochilus vacca</i>	TRUE	unknown
rtox	rubberlip seaperch	<i>Rhacochilus toxotes</i>	TRUE	unknown
elat	striped seaperch	<i>Embiotoca lateralis</i>	TRUE	unknown
smys	blue rockfish	<i>Sebastes mystinus</i>	TRUE	Near minimum stock threshold - increasing
spul	California sheephead	<i>Semicossyphus pulcher</i>	TRUE	Below target levels
saur	brown rockfish	<i>Sebastes auriculatus</i>	TRUE	unknown
schr	black-and-yellow rockfish	<i>Sebastes chrysomelas</i>	TRUE	unknown
cpri	ocean whitefish	<i>Caulolatilus princeps</i>	TRUE	unknown
bfre	kelp surfperch	<i>Brachyistius frenatus</i>	FALSE	NA
ocal	senorita	<i>Oxyjulis californica</i>	FALSE	NA
pfur	white seaperch	<i>Phanerodon furcatus</i>	FALSE	NA
hcar	rainbow seaperch	<i>Hypsurus caryi</i>	FALSE	NA
hros	giant kelpfish	<i>Heterostichus rostratus</i>	FALSE	NA
hsem	rock wrasse	<i>Halichoeres semicinctus</i>	FALSE	NA
opic	painted greenling	<i>Oxylebius pictus</i>	FALSE	NA
mcal	halfmoon	<i>Medialuna californiensis</i>	FALSE	NA

Table 2: Species included in estimation model (*continued*)

classcode	Common Name	Scientific Name	Targeted?	Stock Status
cpun	blacksmith	Chromis punctipinnis	FALSE	NA
gnig	opaleye	Girella nigricans	FALSE	NA
hrub	garibaldi	Hypsypops rubicundus	FALSE	NA

1.3 Difference-in-Difference Model

The difference-in-difference (DiD) regression amounts to estimating the pre-post MPA difference in the biomass densities of targeted species minus the same difference for non-targeted species in the Channel Islands.

The simplified form of this model is

$$d_i \sim \text{Gamma}(e^{\beta_0 + \beta_1 T_i + \beta_2 MPA_i + \beta_3 T_i MPA_i + \mathbf{B}^c \mathbf{X}_i + \mathbf{B}^s \mathbf{S}_i}, \text{shape}, \text{scale}) \quad (1)$$

To provide greater detail on this process, we first conduct the data pre-processing described earlier. From there, we aggregated data to the level of total biomass density of targeted and non-targeted species at each site each year. As such, our base model estimates the effect of the MPAs on total biomass density of targeted species, though we also explore the effect on alternative specifications such as mean biomass of targeted species. the model was then fit using the **rstanarm** package in R (5000 iterations, 2500 warmup, 4 chains, adapt_delta = 0.85).

The intercept prior was determined using the **rstanarm autoscale** function. For the non-intercept terms, we manually set a normal(0,2) prior. This implies that coefficients such as the MPA effect have a prior that provides support for an effect size centered on zero with a range of roughly -4 to 4. Since the covariates are centered and scaled, and the dependent variable is on the log-scale, this is an extremely diffuse prior.

The full table of covariates and their posterior means and 89% credible interval can be found in Table.S3.

Table 3: Posterior means and 89th percent credible interval for key model coefficients

term	mean	lower_89th_percentile	upper_89th_percentile
(Intercept)	-2.81	-3.08	-2.55
targeted	0.05	-0.13	0.24
year_bins(2003,2006]	-0.82	-1.06	-0.56
year_bins(2006,2009]	-0.86	-1.18	-0.53
year_bins(2009,2012]	-0.84	-1.18	-0.50
year_bins(2012,2015]	-0.96	-1.29	-0.63
year_bins(2015,2018]	-0.57	-0.92	-0.23
var_tex	0.20	0.05	0.35
var_tex_2	-0.07	-0.18	0.03
var_surge	0.09	0.00	0.17
var_kelp	-0.06	-0.10	-0.01
var_lag_catch	0.06	-0.04	0.18
var_temp	0.26	0.07	0.45
regional_temp_dev	-0.22	-0.38	-0.04
regional_temp_dev_2	0.01	-0.02	0.04
targeted:year_bins(2003,2006]	0.28	0.04	0.52

Table 3: Posterior means and blah percent credible interval for key model coefficients (*continued*)

term	mean	lower_89th_percentile	upper_89th_percentile
targeted:year_bins(2006,2009]	0.51	0.26	0.75
targeted:year_bins(2009,2012]	0.59	0.35	0.84
targeted:year_bins(2012,2015]	0.30	0.04	0.56
targeted:year_bins(2015,2018]	-0.07	-0.34	0.20

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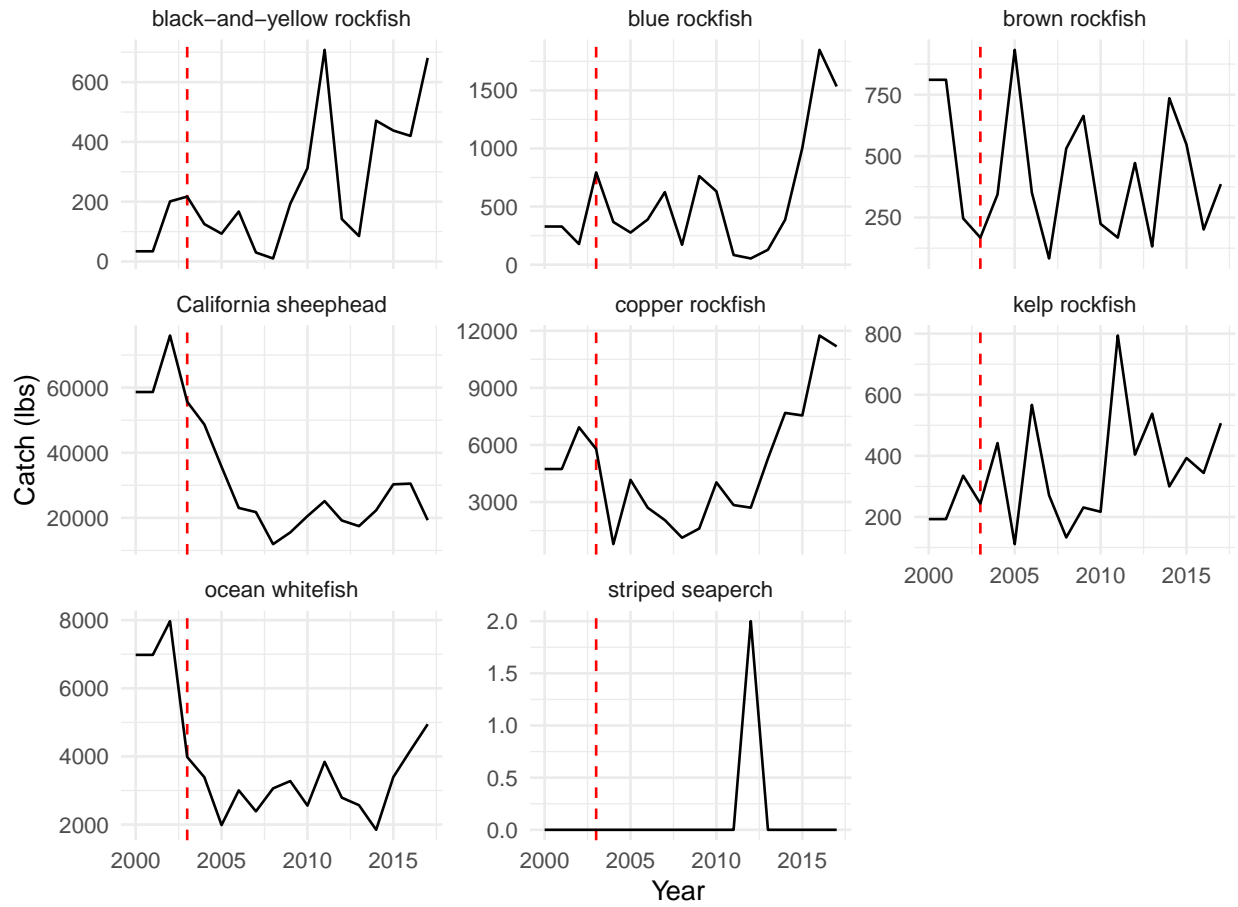


Figure 1: Total CDFW reported commercial catches in the Santa Barbara region

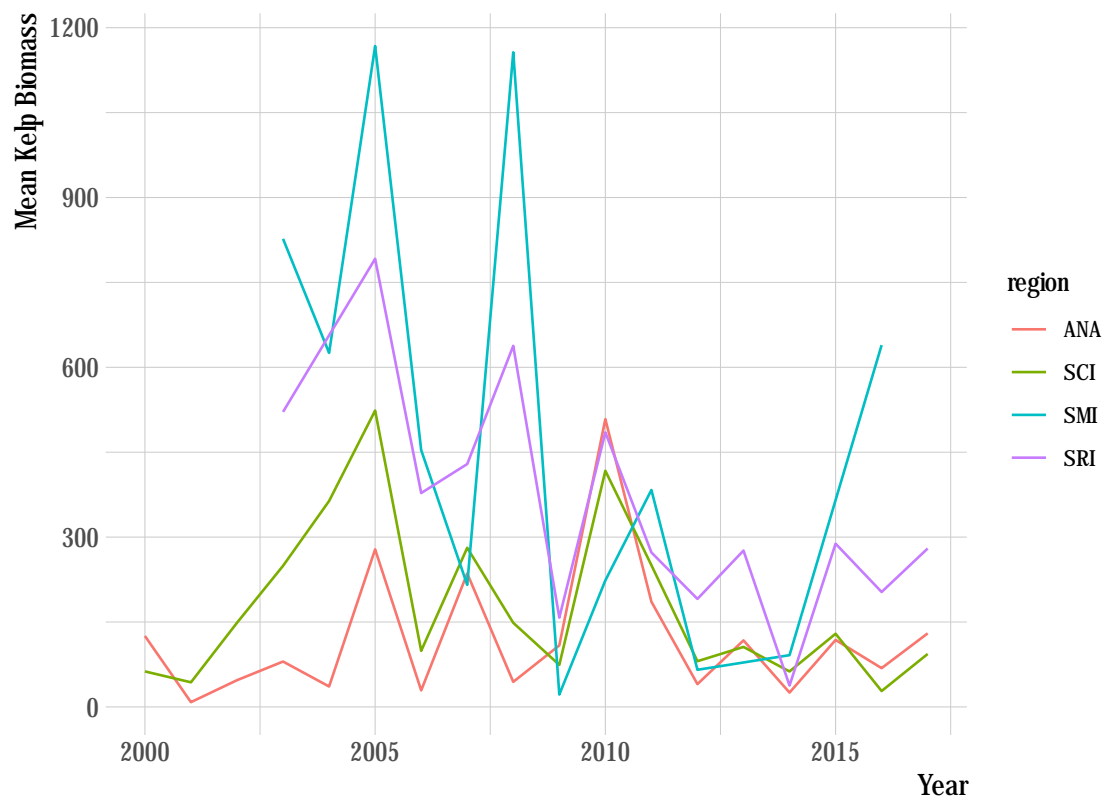


Figure 2: Mean kelp biomass by island over time from SBC LTER

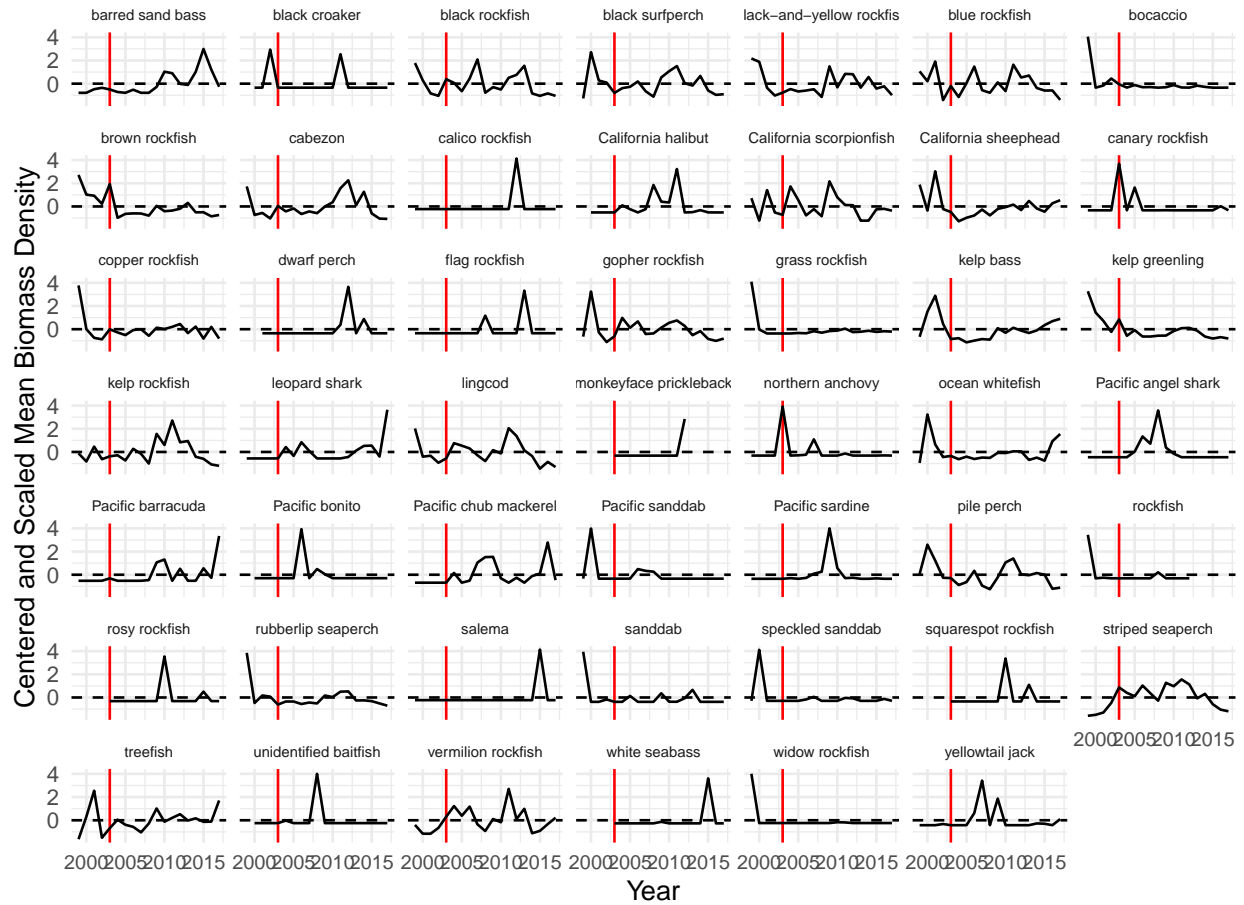


Figure 3: Centered and scaled mean biomass densities of all targeted finfish in analysis before filtering

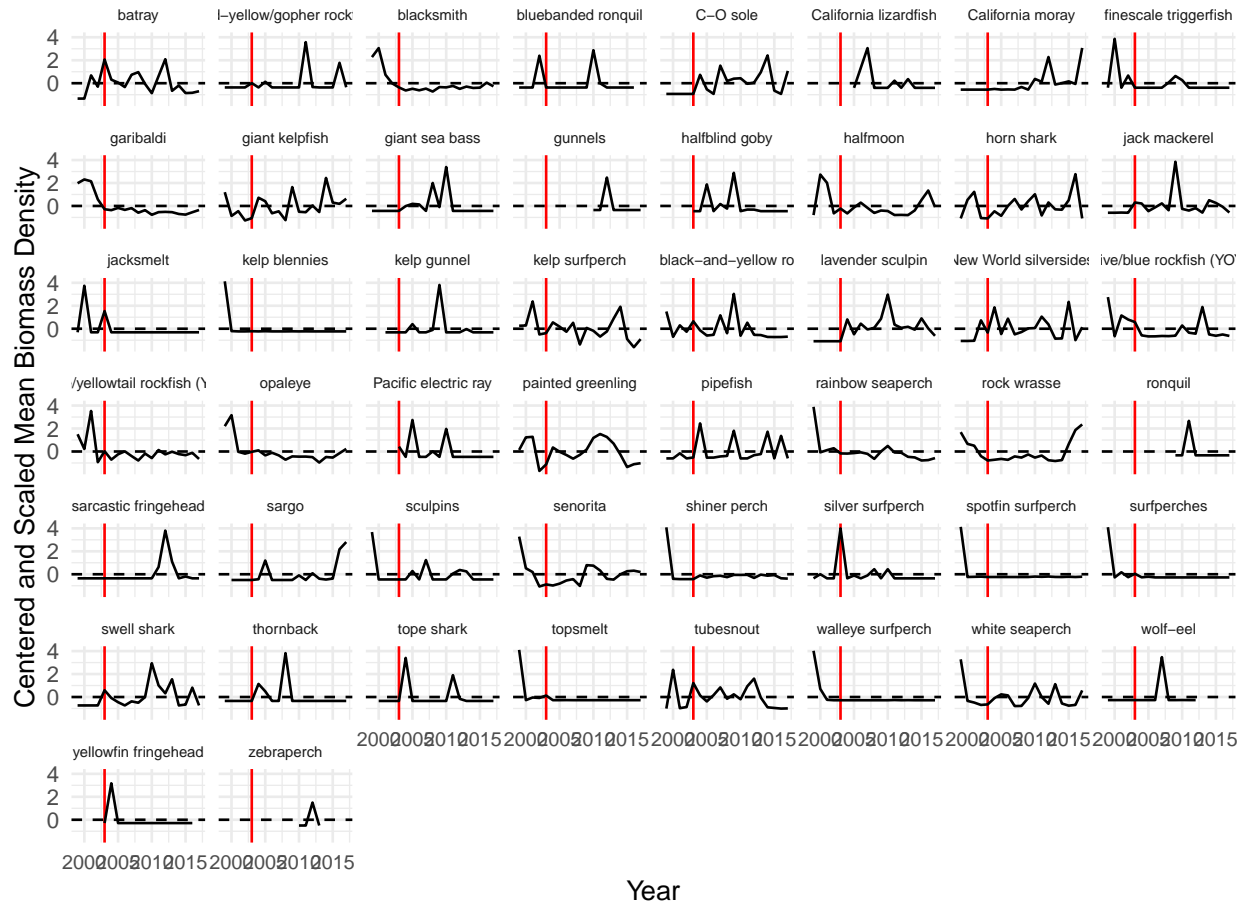


Figure 4: Centered and scaled mean biomass densities of all non-targeted finfish in analysis before filtering