

Reference Points from Stock Smart database

Stock Smart

The NMFS Species Information System is the database where NMFS stock assessment data and metadata are archived at the national scale. Publicly accessible data is available at: <https://apps-st.fisheries.noaa.gov/stocksmart?app=download-data>

I pulled down all the years (2005-2022) for the PFMC “Jurisdiction”, which is the data in “Assessment_Summary_Data_PFMC.xlsx”. The .csv version is just a flattened version of the first page of the Excel Workbook.

Explore the data

I filtered the data to just the Groundfish FMP, and did some data wrangling to get the units of biomass to be comparable across the time series, where possible, and filtered to stocks that have at least 4 assessments over the 17 year period.

There are 13 stocks that have that level of monitoring.

```
ref <- read.csv('data/Assessment_Summary_data_PFMC.csv', header=T)

ref2 <- ref %>%
  filter(FMP == "Pacific Coast Groundfish") %>%
  dplyr::mutate(
    refpt = case_when(
      Bmsy.Basis == "B40%" ~ "40",
      Bmsy.Basis == "Coastwide SPB40%" ~ "40",
      Bmsy.Basis == "SPB40%" ~ "40",
      Bmsy.Basis == "SPB40%\n\n" ~ "40",
      Bmsy.Basis == "SPR40%" ~ "40",
      Bmsy.Basis == "SB40%" ~ "40",
      Bmsy.Basis == "SSB40%" ~ "40",
      Bmsy.Basis == "SPR40% as proxy" ~ "40",
```

```

      Bmsy.Basis == "B25%" ~ "25",
      Bmsy.Basis == "SPB25%" ~ "25",
      Bmsy.Basis == "SSB25%" ~ "25")) %>%
#dplyr::mutate(B.unf = Bmsy / refpt) %>%

group_by(Stock.Name) %>%
select(Stock.Name, Common.Name, Assessment.Year, Estimated.B, B.Unit, B.Basis, Bmsy,
      Bmsy.Basis, B.Bmsy, refpt) %>%
filter(!is.na(Bmsy) & length(Bmsy)>3) %>%
mutate(Bmsy.corr = case_when(
  B.Unit == "10^8 eggs" ~ Bmsy*10^8,
  B.Unit == "billion eggs" ~ Bmsy*10^9,
  B.Unit == "Billion eggs" ~ Bmsy*10^9,
  B.Unit == "trillion eggs" ~ Bmsy*10^12,
  B.Unit == "trillion eggs\n" ~ Bmsy*10^12,
  B.Unit == "Eggs" ~ Bmsy,
  B.Unit == "larvae" ~ Bmsy,
  B.Unit == "million larvae" ~ Bmsy*10^6,
  B.Unit == "million eggs" ~ Bmsy*10^6,
  B.Unit == "Million eggs" ~ Bmsy*10^6,
  B.Unit == "Million Eggs" ~ Bmsy*10^6,
  B.Unit == "Metric Tons" ~ Bmsy,
  B.Unit == "mt" ~ Bmsy,
  B.Unit == "mt\n" ~ Bmsy,
  B.Unit == "mt (female biomass only)" ~ Bmsy*2,
  B.Unit == "mt (female mature biomass)" ~ Bmsy*2,
  B.Unit == "mt (female mature)" ~ Bmsy*2,
  B.Unit == "Million Metric Tons" ~ Bmsy*10^6,)) %>%
ungroup()

refsum <- ref2 %>%
  group_by(Stock.Name) %>%
  summarize(ct = n()) %>%
  ungroup() %>%
  arrange(-ct)
print(refsum)

```

A tibble: 13 x 2

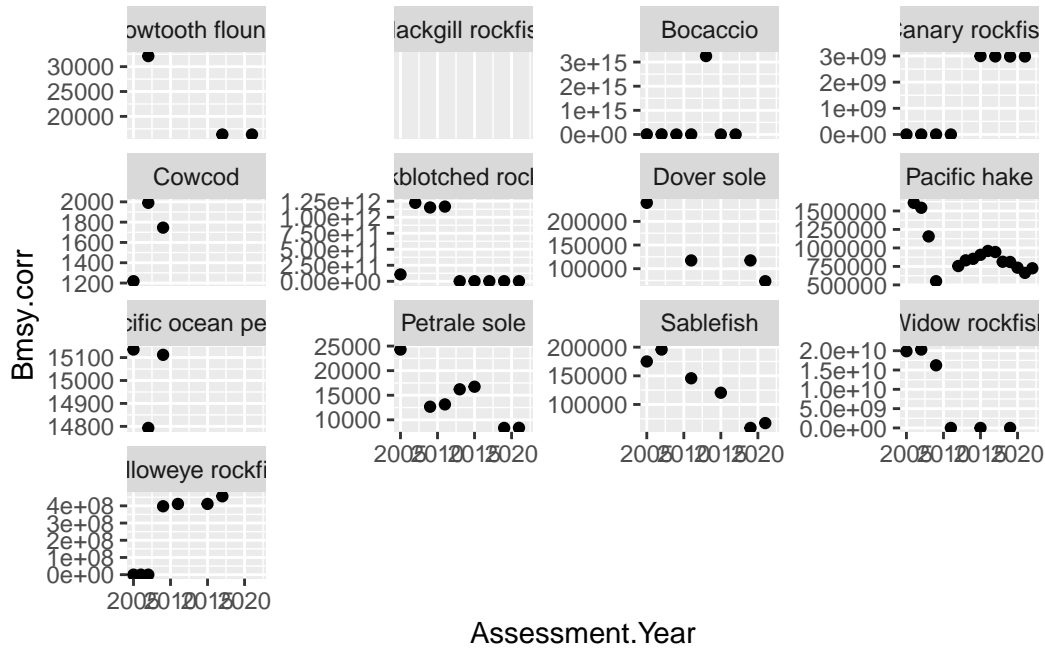
Stock.Name	ct
<chr>	<int>
1 Pacific hake - Pacific Coast	15

2	Darkblotched rockfish - Pacific Coast	9
3	Canary rockfish - Pacific Coast	8
4	Bocaccio - Southern Pacific Coast	7
5	Petrale sole - Pacific Coast	7
6	Yelloweye rockfish - Pacific Coast	7
7	Sablefish - Pacific Coast	6
8	Widow rockfish - Pacific Coast	6
9	Pacific ocean perch - Pacific Coast	5
10	Arrowtooth flounder - Pacific Coast	4
11	Blackgill rockfish - Southern California	4
12	Cowcod - Southern California	4
13	Dover sole - Pacific Coast	4

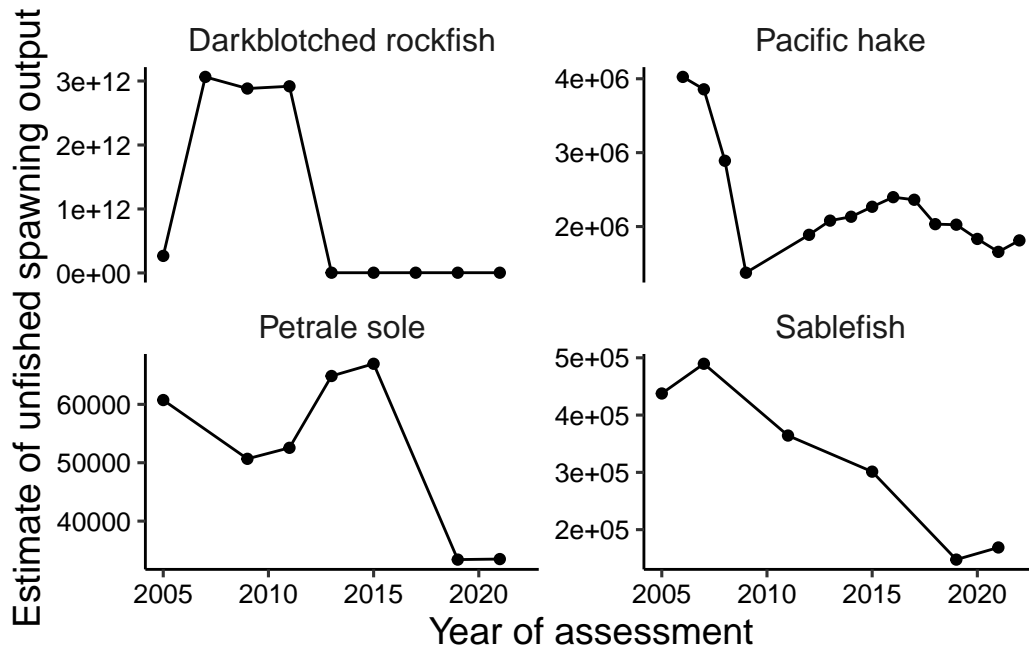
There are a couple of things we could plot to look at productivity/carrying capacity. Here I am choosing Bmsy because unless there is a change in policy about the reference point (e.g., from b40 to b25 for flatfish), it should have a consistent interpretation across the time series (like Bzero).

When I plot all the species, there are some inconsistencies that are coming from changes in the units of biomass for some of the rockfish species, e.g., changing from spawning biomass to eggs to larvae as the measure of spawning output. This might be able to be standardized with a bit more digging into the assessments, or at least the Bzero might be able to be backed out...

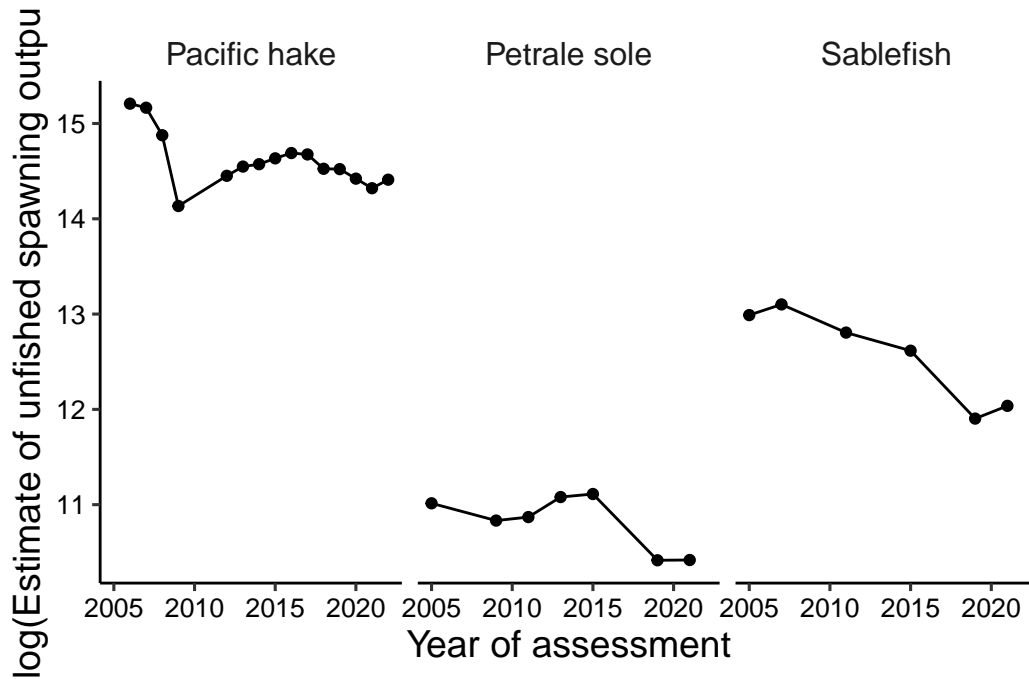
Warning: Removed 8 rows containing missing values (``geom_point()``).



If we just focus on hake, petrale, and sablefish, the plot is a bit cleaner because the units don't change across the time series. At the end of Kristin and Jameal's convo, we decided to move forward with these three for now. Kristin should look into the older values to groundtruth them and/or talk to assessment authors to understand how the assessment model structure may have changed, which could influence our interpretation. For example, we know the hake model has been pretty consistent since 2011, so we might focus just on those more recent years.



Here is the exact 3-panel plot that's in the current version of the manuscript (7/9/24). Note y axis is on a log scale.



Here is a summary table of percent change $((\text{max}-\text{min})/\text{max})$ in estimated spawning output by species over the full time series (not in log-scale) :

```
# A tibble: 3 x 4
```

Stock.Name	B.unf.max	B.unf.min	percent.change
<chr>	<dbl>	<dbl>	<dbl>
1 Pacific hake - Pacific Coast	4025000.	1375000	0.658
2 Petrale sole - Pacific Coast	66952	33406.	0.501
3 Sablefish - Pacific Coast	489594.	147730	0.698

We wanted to add error bars to the plot, but that meant going back to the original assessments and pulling those estimates because they weren't in the stock SMART database, which AB did. This new data frame has the medians and 95% confidence/credible intervals.

