

FIS Status and Trend calculation cheat sheet

LAYERS USED BY THE TOOLBOX

fis_b_bmsy
fis_meancatch
fis_proparea_saup2rgn
fp_wildcaught_weight

DESCRIPTION OF THE LAYERS

fis_b_bmsy

for species: B/Bmsy estimate (either from formal stock assessment, or from a data-poor method such as CMSY)

for genus/family/broader taxa: the toolbox will use median B/Bmsy from species in that region + a penalty for not reporting at species level. In order for the code to assign the correct penalty, the taxa need to include a numerical code of 6 digits, where the first digit behaves like an ISSCAAP code (the standardized species codes used by FAO): 6 means species, 5 means genus, 4 to 1 are increasingly broad taxonomic groups

data source (for CMSY): catch time-series (at least 10 years of catch >0), species resilience (if available)

fis_meancatch

average catch across all years, per species, per region

data source: catch time-series (at least 10 years of catch >0), with a unique identifier for each population that you want to assess separately

(NOTE: if a species that is present in different regions belongs to the same population, you don't want to split the catch among regions, instead, you want to calculate B/Bmsy and mean catch for the whole population)

Example data:

##	fao_saup_id	taxon_name_key	year	mean_catch
## 1	37_8	Aristeus antennatus_690051	2014	14.24398116
## 2	37_8	Atherinidae_400218	2014	27.30120156
## 3	37_8	Balistes capriscus_607327	2014	3.247883895

fis_proparea_saup2rgn:

a conversion file that, for each region for which catch is reported, tells us what proportion of that region falls within each of the final OHI reporting regions. Example data:

##	saup_id	rgn_id	prop_area
## 1	166	1	1.0
## 2	162	2	1.0
## 3	574	3	0.7
## 4	37	4	0.8

only if catch is reported for different regions than the ones used for the OHI assessment: this should be calculated using spatial analyses of overlap of the spatial units at which catch is reported with the spatial units at which the OHI assessment will be reported. The global data was reported by subregions (saup_id) and in some cases multiple subregions were part of the same, larger EEZ. Since for OHI we wanted results by EEZ (rgn_id), in those cases we needed to combine results from the subregions to get the final score, based on their size relative to the total EEZ size (prop_area).

If catch is reported for the same areas for which OHI is calculated: then all the 'prop_area' are = 1. *If catch is reported for the whole area of the assessment, but you want to calculate a separate OHI score for different sub-regions:* for each OHI reporting region (rgn_id) you'll repeat the same region in the saup_id column, and

prop_area will be =1. This effectively means all the reporting regions will get assigned 100% of the catch and will have the same final status and trend score for the fisheries goal (but may have different pressures and resilience scores, if those layers are different in each sub-region).

fp_wildcaught_weight

only needed if there is mariculture: for each region, this represents the relative proportion of catch coming from wild caught fisheries versus mariculture. The layer is used to weight how much the fisheries score influences the final food provision score, the higher the fisheries catch, the more the food provision score will reflect the fisheries score, and vice-versa if mariculture has a higher catch.

(NOTE that, before all mariculture harvest from all species gets summed, the mariculture harvest for each species is smoothed and then multiplied by the resilience score).

SAMPLE DATA TO RUN CMSY

##	id	stock_id	res	ct	yr
## 1	6	Acanthistius brasilianus_41	Medium	100	1950
## 2	23	Acanthurus dussumieri_61		0.059250269	1950
## 3	24	Acanthurus dussumieri_71		0.190749971	1950
## 4	25	Acanthurus lineatus_61	Low	12.74821966	1950

HOW TO

1. Include resilience in the CMSY code

In the CMSY R script, in the PARAMETERS section, replace the following:

```
start_r <- c(0.01,10) ## disable this line if you use resilience
with
```

```
if(res == "Very low"){ start_r <- c(0.015, 0.1) } else { if(res == "Low"){ start_r <- c(0.05,0.5) } else {
if(res == "High"){ start_r <- c(0.6,1.5)
} else { start_r <- c(0.1,1) } } }
```

2. Make assumptions about fisheries regulations

If you assume that fisheries are depleted and there isn't very much fisheries regulation, and you are using the CMSY method to assess B/Bmsy, the original model may work well. If, however, the catch of a species declined because fisheries regulations have closed or limited the fishery, the model may be too pessimistic and underestimate B/Bmsy. In that case it may be best to use a version with a uniform prior on final biomass, instead of the constrained prior.

The original constrained prior on final biomass is set by this line within the code:

```
finalbio <- if(ct[nyr]/max(ct) > 0.5) {c(0.3,0.7)} else {c(0.01,0.4)}
```

the model uses a uniform prior if that line is replaced with:

```
finalbio <- c(0.01,0.7)
```

3. Use data at a different spatial resolution than the final assessment

See notes above for 'fis_proparea_saup2rgn'

4. Calculate B, or Bmsy

The CMSY model calculates B/Bmsy as a ratio, it does not estimate the two variables separately.

5. Use catch per unit of effort (CPUE) The CMSY model requires total biomass removed by fisheries, and uses catch as a proxy for that. It cannot use CPUE. Other more sophisticated stock assessment models use CPUE and may be employed. We do not provide documentation for the use of these other models.

6. Use other life-history characteristics, in addition to resilience The CMSY model does not use more detailed information. Other more sophisticated stock assessment models use other life-history traits such as fecundity, larval dispersal, r, K, Lmax, etc., and may be employed. We do not provide documentation for the use of these other models.