Package ‘marindicators’

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Description Provides functions to calculate indicators for four marine ecosystem attributes (Biodiversity, Ecosystem Structure and Functioning, Ecosystem Stability and Resistance to Perturbations, Resource Potential) and one marine ecosystem pressure (Fishing Pressure) from fishery independent trawl survey data and commercial landings data. All indicators were selected and evaluated using the “Indicator Selection Guidance Framework” developed by Bundy, Gomez, and Cook (2017, ISBN: 978-0-660-23573-8).

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  marindicators-package ................................................... 2
  allBiodiversity .......................................................... 5
<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>allPotential</td>
<td>7</td>
</tr>
<tr>
<td>allPressure</td>
<td>9</td>
</tr>
<tr>
<td>allStability</td>
<td>12</td>
</tr>
<tr>
<td>allStructure</td>
<td>14</td>
</tr>
<tr>
<td>biomassPerTL</td>
<td>18</td>
</tr>
<tr>
<td>biomassRatio</td>
<td>19</td>
</tr>
<tr>
<td>communityCondition</td>
<td>21</td>
</tr>
<tr>
<td>CVBiomass</td>
<td>23</td>
</tr>
<tr>
<td>exampleInds</td>
<td>25</td>
</tr>
<tr>
<td>extractAll</td>
<td>25</td>
</tr>
<tr>
<td>fishingInBalance</td>
<td>30</td>
</tr>
<tr>
<td>fishingPressure</td>
<td>32</td>
</tr>
<tr>
<td>heips</td>
<td>34</td>
</tr>
<tr>
<td>hillN1</td>
<td>35</td>
</tr>
<tr>
<td>hillN2</td>
<td>37</td>
</tr>
<tr>
<td>IVILandings</td>
<td>38</td>
</tr>
<tr>
<td>kemptonQ</td>
<td>40</td>
</tr>
<tr>
<td>land</td>
<td>42</td>
</tr>
<tr>
<td>landings</td>
<td>42</td>
</tr>
<tr>
<td>largeFishIndicator</td>
<td>44</td>
</tr>
<tr>
<td>largeSpeciesIndicator</td>
<td>45</td>
</tr>
<tr>
<td>Length_Weight</td>
<td>47</td>
</tr>
<tr>
<td>margalef</td>
<td>48</td>
</tr>
<tr>
<td>meanLengthCommunity</td>
<td>49</td>
</tr>
<tr>
<td>meanMaxAge</td>
<td>51</td>
</tr>
<tr>
<td>meanMaxLength</td>
<td>52</td>
</tr>
<tr>
<td>meanTLCRociety</td>
<td>54</td>
</tr>
<tr>
<td>meanTLLandings</td>
<td>56</td>
</tr>
<tr>
<td>pielouEvenness</td>
<td>57</td>
</tr>
<tr>
<td>resourcePotential</td>
<td>59</td>
</tr>
<tr>
<td>shannon</td>
<td>61</td>
</tr>
<tr>
<td>species.info</td>
<td>62</td>
</tr>
<tr>
<td>species.table</td>
<td>63</td>
</tr>
<tr>
<td>speciesRichness</td>
<td>63</td>
</tr>
<tr>
<td>X</td>
<td>65</td>
</tr>
<tr>
<td>X_length</td>
<td>66</td>
</tr>
</tbody>
</table>

**Index**

marindicators-package  
*Calculates Marine Ecosystem and Fishing Pressure Indicators*
Description

The marindicators package provides functions to calculate indicators for four marine ecosystem attributes (Biodiversity, Ecosystem Structure and Functioning, Ecosystem Stability and Resistance to Perturbations, Resource Potential) and one marine ecosystem pressure (Fishing Pressure) from fishery independent trawl survey data and commercial landings data. All indicators were selected and evaluated using the “Indicator Selection Guidance Framework” developed by Bundy, Gomez, and Cook (2017).

Details

A comprehensive evaluation and selection of robust ecological indicators is one of the key steps in the process of implementing an Ecosystem Approach to fisheries management and to track progress towards meeting ecosystem goals. The indicators included in this package were selected using the “Indicator Selection Guidance Framework” developed by Bundy, Gomez, and Cook (2017) to select and evaluate potential indicators for ecosystem monitoring and assessment at different spatial scales using established selection criteria.

The framework was successfully tested for the Scotian Shelf Bioregion, Canada. In Step 1, four ecosystem attributes and one pressure were defined: Biodiversity, Ecosystem Structure and Functioning, Ecosystem Stability and Resistance to Perturbations, Resource Potential, and Fishing Pressure. In Step 2, 186 indicators were selected to represent these attributes and pressure. The qualitative screening in Step 3 reduced this set to 68 indicators (Table 1), which were calculated in Step 4. The quantitative screening in Step 5 resulted in a final suite of 30 non-redundant ecological and fishing pressure indicators derived from fishery independent and dependent data (Step 6). For more information, including attribute definitions and the methods used to select the final suite of indicators, please refer to the guidance framework document (Bundy, Gomez, and Cook, 2017).

The marindicators package provides functions to calculate the suite of marine ecosystem indicators calculated in Step 4 of the guidance framework (Table 1; Bundy, Gomez, and Cook, 2017). Some functions may be used to calculate additional indicators, for example by specifying different species groups or using alternative values for arguments with default values.

Table 1: Indicators for each ecosystem attribute and pressure and the marindicators function used to calculate each indicator. Indicators included in the final suite for the Scotian Shelf Bioregion are highlighted in bold.

<table>
<thead>
<tr>
<th>ATTRIBUTE</th>
<th>INDICATOR</th>
<th>FUNCTION</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biodiversity</td>
<td>All Biodiversity indicators</td>
<td>allBiodiversity()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Margalef’s Species Richness</td>
<td>margalef()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Species Richness</td>
<td>speciesRichness()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Shannon’s Diversity Index</td>
<td>shannon()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Hill’s Diversity Index</td>
<td>hillN1()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Kempton’s Q</td>
<td>kemptonQ()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Hill’s Dominance</td>
<td>hillN2()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Pielou’s Species Evenness</td>
<td>pielouEvenness()</td>
</tr>
<tr>
<td>Biodiversity</td>
<td>Heips Evenness Index</td>
<td>heips()</td>
</tr>
<tr>
<td>Structure &amp; Functioning</td>
<td>All Structure &amp; Functioning indicators</td>
<td>allStructure()</td>
</tr>
<tr>
<td>Structure &amp; Functioning</td>
<td>Large Fish Indicator</td>
<td>largeFishIndicator()</td>
</tr>
<tr>
<td>Structure &amp; Functioning</td>
<td>Large Species Indicator</td>
<td>largeSpeciesIndicator()</td>
</tr>
<tr>
<td>Category</td>
<td>Indicator</td>
<td>Function</td>
</tr>
<tr>
<td>----------------------------------</td>
<td>---------------------------------------------------------------------------</td>
<td>------------------------</td>
</tr>
<tr>
<td><strong>Structure &amp; Functioning</strong></td>
<td>Proportion of Predatory Fish</td>
<td>biomassRatio()</td>
</tr>
<tr>
<td><strong>Structure &amp; Functioning</strong></td>
<td>Biomass of Trophic Guilds(^1)</td>
<td>resourcePotential()</td>
</tr>
<tr>
<td><strong>Structure &amp; Functioning</strong></td>
<td>Biomass Ratio(s)</td>
<td>biomassRatio()</td>
</tr>
<tr>
<td><strong>Structure &amp; Functioning</strong></td>
<td>Mean Length (weighted by abundance)</td>
<td>meanLengthCommunity()</td>
</tr>
<tr>
<td><strong>Structure &amp; Functioning</strong></td>
<td>Mean Length (weighted by biomass)</td>
<td>meanLengthCommunity()</td>
</tr>
<tr>
<td><strong>Structure &amp; Functioning</strong></td>
<td>Mean Trophic Level of Community</td>
<td>meanTLCommunity()</td>
</tr>
<tr>
<td><strong>Structure &amp; Functioning</strong></td>
<td>Community Condition</td>
<td>communityCondition()</td>
</tr>
<tr>
<td><strong>Trophic Guild Condition(^2)</strong></td>
<td></td>
<td>communityCondition()</td>
</tr>
<tr>
<td><strong>Stability &amp; Resistance</strong></td>
<td>All Stability &amp; Resistance indicators</td>
<td>allStability()</td>
</tr>
<tr>
<td><strong>Stability &amp; Resistance</strong></td>
<td>Mean Lifespan</td>
<td>meanMaxAge()</td>
</tr>
<tr>
<td><strong>Stability &amp; Resistance</strong></td>
<td>Mean Max Length (weighted by abundance)</td>
<td>meanMaxLength()</td>
</tr>
<tr>
<td><strong>Stability &amp; Resistance</strong></td>
<td>Mean Max Length (weighted by biomass)</td>
<td>meanMaxLength()</td>
</tr>
<tr>
<td><strong>Stability &amp; Resistance</strong></td>
<td>Intrinsic Vulnerability Index of Landings</td>
<td>IVILandings()</td>
</tr>
<tr>
<td><strong>Stability &amp; Resistance</strong></td>
<td>Biomass per Trophic Level(^3)</td>
<td>biomassPerTL()</td>
</tr>
<tr>
<td><strong>Stability &amp; Resistance</strong></td>
<td>Coefficient of Variation of Biomass</td>
<td>CVBiomass()</td>
</tr>
<tr>
<td><strong>Resource Potential</strong></td>
<td>All Resource Potential indicators</td>
<td>allPotential()</td>
</tr>
<tr>
<td><strong>Resource Potential</strong></td>
<td>Biomass</td>
<td>resourcePotential()</td>
</tr>
<tr>
<td><strong>Resource Potential</strong></td>
<td>Biomass of Key Groups(^4)</td>
<td>resourcePotential()</td>
</tr>
<tr>
<td><strong>Resource Potential</strong></td>
<td>Fishing in Balance</td>
<td>fishingInBalance()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>All Fishing Pressure indicators</td>
<td>allPressure()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>Fishing Pressure</td>
<td>fishingPressure()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>Fishing Pressure on Groups(^5)</td>
<td>fishingPressure()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>Marine Trophic Index</td>
<td>meanTLandings()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>Mean Trophic Level of Landings</td>
<td>meanTLandings()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>Diversity of Target Species</td>
<td>speciesRichness()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>Landings</td>
<td>landings()</td>
</tr>
<tr>
<td><strong>Fishing Pressure</strong></td>
<td>Landings of Fished Groups(^6)</td>
<td>landings()</td>
</tr>
</tbody>
</table>

\(^1\) Biomass of piscivores and zoopiscivores  
\(^2\) Condition of large benthivores, medium benthivores, piscivores, and zoopiscivores  
\(^3\) Biomass at trophic level 2  
\(^4\) Biomass of invertebrates, gadoids, flatfish, and skates  
\(^5\) Fishing Pressure on clupeids  
\(^6\) Landings of skates, flatfish, and large pelagics

The data required to apply the **marindicators** package depends on the indicator(s) to be calculated. In general, indicators related to ecosystem attributes require annual fishery independent survey data, while indicators related to the ecosystem pressure require annual commercial landings data. Additional species information is required to calculate some indicators, including: trophic level, intrinsic vulnerability index, maximum recorded age, maximum recorded length, and annual length-at-weight data. See the vignette or the help page for a specific function for more information on data requirements.

The functions in this package provide the user with three options for calculating indicators:

1. Individual functions, which calculate a single indicator for one or more user-defined species groups.
2. “allAttribute” functions, which call the individual functions to calculate and return all (or a subset) of the indicators for an attribute or pressure.
3. extractAll() function, which calls the “allAttribute” functions to calculate and return all of the indicators.

See the vignette "Introduction to marindicators" or the help files below for more details on these functions.

References

allBiodiversity  
Calculates all Biodiversity indicators

Description
This function calculates all (or a subset) of the Biodiversity indicators for \( j \) areas and \( i \) years. The user can choose whether the function returns the indicator dataframe to the global environment, exports the dataframe to a csv file, or both. The user can also choose whether the function returns the raw indicator values, the standardized (z-score) values, or both.

Usage

```r
allBiodiversity(X, metric = "ABUNDANCE", groups = "ALL", species.table = NULL, TL.table, percentiles = c(0.25, 0.75), minTL = 0, years, raw = TRUE, std = TRUE, glob.env = TRUE, export.path = NULL, export.id = NULL)
```

Arguments

\( X \)
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns \( \text{YEAR}, \text{ID}, \text{SPECIES}, \) and \( \text{ABUNDANCE} \). \( \text{YEAR} \) indicates the year the observation was recorded, \( \text{ID} \) is an area code indicating where the observation was recorded, \( \text{SPECIES} \) is a numeric code indicating the species sampled, and \( \text{ABUNDANCE} \) is the corresponding abundance (stratified and corrected for catchability as required).

\( \text{metric} \)
A character string indicating which column in \( X \) to use to calculate the indicators. Default is \text{metric} = "ABUNDANCE".

\( \text{groups} \)
A vector indicating the species group(s) for which to calculate the indicators. If \text{groups} = "ALL", all species will be included; otherwise, each entry must be a character string matching the name of a column in \text{species.table}. Default is \text{groups} = "ALL".
species.table  A table where the column names match the entries in groups. Column entries are species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored. If groups = "ALL", this table is not required. Default is species.table = NULL.

TL.table  A dataframe with columns SPECIES and the corresponding TL (trophic level). Entries in the SPECIES column should be the unique values of species codes in X (or a subset thereof). Other columns in TL.table are ignored. If TL.table = NULL, Kempton’s Q will not be calculated.

percentiles  The percentiles used to determine R1 and R2 for calculating Kempton’s Q. Default is percentiles = c(0.25,0.75).

minTL  Minimum trophic level for species included to calculate Kempton’s Q. Default is minTL = 0.

years  A vector of years for which to calculate indicators.

raw  A logical value. If raw = TRUE, the raw indicator values are returned by the function. If raw = FALSE, the raw indicator values are not returned. Default is raw = TRUE. Either raw or std must be TRUE.

std  A logical value. If std = TRUE, the standardized indicator values for each area ID are returned by the function. Indicators are standardized using z-scores, i.e., by subtracting the mean and dividing by the standard deviation (ignoring NA values). If std = FALSE, the standardized indicator values are not returned. Default is std = TRUE. Either raw or std must be TRUE.

glob.env  Logical value indicating whether to return output to global environment. Default is glob.env = TRUE.

export.path  File path indicating where to save a .csv file of calculated indicators (named biodiversity_export.id.csv; see below). If export.file = NULL, the indicator dataframe will not be exported as a .csv file. Default is export.path = NULL.

export.id  Character string to modify the name of the .csv file (if export.path is specified), for example an area name or date of analysis. The exported .csv file is named biodiversity_export.id.csv. Default is export.id = NULL.

Details

This function calculates the Biodiversity indicators: Species Richness, Shannon’s Index of Diversity, Margalef’s Species Richness, Pielou’s Species Evenness, Hill’s N1, Hill’s N2, Heip’s Evenness Index, and Kempton’s Q. If trophic level data are not available to calculate Kempton’s Q, the remaining Biodiversity indicators will be returned. See the help file for the individual functions for information on how each indicator is calculated.

Notes on indicator calculations: In the individual functions, the user generally has control over which metric (e.g., "BIOMASS" or "ABUNDANCE") and group (e.g., "ALL" or "GROUNDFISH") are used to calculate the indicator. Here, the same metric and group are used to calculate each indicator. Defaults are metric = "ABUNDANCE" and group = "ALL".

Value

Returns a dataframe with columns ID, YEAR, and indicators corresponding to the arguments supplied to the function. Standardized indicators are noted with _s in the name.
**allPotential**

**Author(s)**
Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

**See Also**
Other biodiversity indicators: heips, hillN1, hillN2, kemptonQ, margalef, pielouEvenness, shannon, speciesRichness

**Examples**

data(X)

# Calculate raw and standardized indicators
allBiodiversity(X = X, metric = "ABUNDANCE", groups = "ALL", TL.table = species.info, percentiles = c(.25, .75), minTL = 0, years = c(2014:2019), raw = TRUE, std = TRUE)

---

**allPotential**  
*Calculates all Resource Potential indicators*

**Description**
This function calculates all (or a subset) of the Resource Potential indicators for \( j \) areas and \( i \) years. The user can choose whether the function returns the indicator dataframe to the global environment, exports the dataframe to a .csv file, or both. The user can also choose whether the function returns the raw indicator values, the standardized (z-score) values, or both.

**Usage**

```r
allPotential(X, land, species.table, speciesinfo.table, resource.groups, minTL = 0, TE = 0.1, base.start, base.end, years, raw = TRUE, std = TRUE, glob.env = TRUE, export.path = NULL, export.id = NULL)
```

**Arguments**

- **X**: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, BIOMASS, and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and BIOMASS/ABUNDANCE is the corresponding biomass/abundance (stratified and corrected for catchability as required).

- **land**: A dataframe of commercial landings data with columns YEAR, ID, SPECIES and CATCH. YEAR indicates the year the landing was recorded, ID is an area code indicating where the landing was recorded, SPECIES is a numeric code indicating the species landed, and CATCH is the corresponding landed weight.
species.table  A table where the column names match the entries in resource.groups. Column entries are the species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored.

speciesinfo.table  A table with columns SPECIES and the corresponding TL_LAND (trophic level of landed species). Entries in the SPECIES column should be the unique values of species codes in land (or a subset thereof). Other columns will be ignored.

resource.groups  A vector indicating the species groups for which to calculate the resource potential. Each entry must be a character string matching the name of a column in species.table. If resource.groups = NULL, these indicators will not be calculated.

minTL  The minimum trophic level of species to include to calculate FiB. If minTL = NULL, FiB will not be calculated. Default is minTL = 0.

TE  Trophic efficiency, used to calculate FiB. Default is TE = 0.1, i.e., a trophic efficiency of 10%. If TE = NULL, FiB will not be calculated.

base.start  Year indicating the beginning of the baseline period for calculating FiB. The average landings and average mean trophic level of the landings over the baseline period are used as baseline values to calculate FiB. land must include data for the baseline period. If base.start = NULL, FiB will not be calculated.

base.end  Year indicating the end of the baseline period for calculating FiB. The average landings and average mean trophic level of the landings over the baseline period are used as baseline values to calculate FiB. land must include data for the baseline period. If base.end = NULL, FiB will not be calculated.

years  A vector of years for which to calculate indicators.

raw  A logical value. If raw = TRUE, the raw indicator values are returned by the function. If raw = FALSE, the raw indicator values are not returned. Default is raw = TRUE. Either raw or std must be TRUE.

std  A logical value. If std = TRUE, the standardized indicator values for each area ID are returned by the function. Indicators are standardized using z-scores, i.e., by subtracting the mean and dividing by the standard deviation (ignoring NA values). If std = FALSE, the standardized indicator values are not returned. Default is std = TRUE. Either raw or std must be TRUE.

glob.env  Logical value indicating whether to return output to global environment. Default is glob.env = TRUE.

export.path  File path indicating where to save a .csv file of calculated indicators (named potential_export.id.csv; see below). If export.file = NULL, the indicator dataframe will not be exported as a .csv file. Default is export.path = NULL.

export.id  Character string to modify the name of the .csv file (if export.path is specified), for example an area name or date of analysis. The exported .csv file is named potential_export.id.csv. Default is export.id = NULL.

Details

This function calculates the Resource Potential indicators: Abundance and Biomass of the community, Resource Potential of predefined species groups, and Fishing-in-Balance (FiB). If data are not
available to calculate one or more of these indicators, a subset will be returned. See the help file for the individual functions for information on how each indicator is calculated.

Value

Returns a dataframe with columns ID, YEAR, and indicators corresponding to the arguments supplied to the function. Standardized indicators are noted with _s in the name.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other resource potential indicators: fishingInBalance, resourcePotential

Examples

# Compile data
data(X)
data(land)
data(species.table)
data(species.info)

# Species groups of interest
resource.groups <- c("ALL", "CLUPEIDS", "FINFISH", "FLATFISH", "FORAGE", "GADOIDS", "GROUNDFISH")

# Calculate standardized indicators
allPotential(X = X, land = land, species.table = species.table, speciesinfo.table = species.info, resource.groups = resource.groups, TE = 0.1, base.start = 2014, base.end = 2015, years = c(2014:2019), raw = FALSE, std = TRUE)

allPressure

Calculates all Pressure indicators

Description

This function calculates all (or a subset) of the Pressure indicators for j areas and i years. The user can choose whether the function returns the indicator dataframe to the global environment, exports the dataframe to a .csv file, or both. The user can also choose whether the function returns the raw indicator values, the standardized (z-score) values, or both.
Usage

allPressure(X, land, species.table, speciesinfo.table, landings.groups, FP.groups, minTL = c(0, 3.25), years, raw = TRUE, std = TRUE, glob.env = TRUE, export.path = NULL, export.id = NULL)

Arguments

X
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, and BIOMASS. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and BIOMASS is the corresponding biomass (stratified and corrected for catchability as required).

land
A dataframe of commercial landings data with columns YEAR, ID, SPECIES and CATCH. YEAR indicates the year the landing was recorded, ID is an area code indicating where the landing was recorded, SPECIES is a numeric code indicating the species landed, and CATCH is the corresponding landed weight (in the same units as BIOMASS in X).

species.table
A table where the column names match the entries in landings.groups. Column entries are the species codes indicating the species from land included in each group. species.table may also include columns for other species groups; these will be ignored.

speciesinfo.table
A table with columns SPECIES and the corresponding TL_LAND (trophic level of landed species). Entries in the SPECIES column should be the unique values of species codes in land (or a subset thereof). Other columns will be ignored.

landings.groups
A vector indicating the species groups for which to calculate the landings. Each entry must be a character string matching the name of a column in species.table. If landings.groups = NULL, no Landings indicators will be calculated.

FP.groups
A dataframe with two columns, which must be named group.land and group.X. Each row holds the group names to calculate the fishing pressure on a target group, with the numerator in column group.land and the denominator in column group.X. Each entry must be a character string matching the name of a column in species.table. If FP.groups = NULL, no fishing pressure indicators will be calculated.

minTL
A vector containing minimum trophic level to include when calculating the mean trophic level of the landings. Default is minTL = c(0, 3.25), which will return the mean trophic level of the landings and the marine trophic index.

years
A vector of years for which to calculate indicators.

raw
A logical value. If raw = TRUE, the raw indicator values are returned by the function. If raw = FALSE, the raw indicator values are not returned. Default is raw = TRUE. Either raw or std must be TRUE.

std
A logical value. If std = TRUE, the standardized indicator values for each area ID are returned by the function. Indicators are standardized using z-scores, i.e.,
allPressure

by subtracting the mean and dividing by the standard deviation (ignoring NA values). If std = FALSE, the standardized indicator values are not returned. Default is std = TRUE. Either raw or std must be TRUE.

glob.env Logical value indicating whether to return output to global environment. Default is glob.env = TRUE.

export.path File path indicating where to save a .csv file of calculated indicators (named pressure_export.id.csv; see below). If export.file = NULL, the indicator dataframe will not be exported as a .csv file. Default is export.path = NULL.

export.id Character string to modify the name of the .csv file (if export.path is specified), for example an area name or date of analysis. The exported .csv file is named pressure_export.id.csv. Default is export.id = NULL.

Details

This function calculates the Pressure indicators: Diversity of the Target Species, Total Landings, Landings of Target Groups, Fishing Pressure on the Community, Fishing Pressure on Target Groups, Mean Trophic Level of the Landings, and the Marine Trophic Index. If data are not available to calculate one or more of these indicators, a subset will be returned. See the help file for the individual functions for information on how each indicator is calculated.

Value

Returns a dataframe with columns ID, YEAR, and indicators corresponding to the arguments supplied to the function. Standardized indicators are noted with _s in the name.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other fishing pressure indicators: fishingPressure, landings, meanTLLandings, speciesRichness

Examples

# Compile data
data(X)
data(land)
data(species.table)
data(species.info)

# Species groups of interest
landings.groups <- c("ALL", "CLUPEIDS.L", "FLATFISH.L", "GROUNDFISH.L")
FP.groups <- data.frame(rbind(c("ALL", "ALL"),
allStability

Calculates all Stability and Resistance indicators

Description

This function calculates all (or a subset) of the Stability and Resistance indicators for \( j \) areas and \( i \) years. The user can choose whether the function returns the indicator dataframe to the global environment, exports the dataframe to a .csv file, or both. The user can also choose whether the function returns the raw indicator values, the standardized (z-score) values, or both.

Usage

```r
allStability(X, land, maxlength.group, species.table, speciesinfo.table,
TL.grouping = 1, wind = 5, negative = FALSE, years, raw = TRUE,
std = TRUE, glob.env = TRUE, export.path = NULL,
export.id = NULL)
```

Arguments

- **X**: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns `YEAR`, `ID`, `SPECIES`, `BIOMASS`, and `ABUNDANCE`. `YEAR` indicates the year the observation was recorded, `ID` is an area code indicating where the observation was recorded, `SPECIES` is a numeric code indicating the species sampled, and `BIOMASS/ABUNDANCE` is the corresponding biomass/abundance (stratified and corrected for catchability as required).
- **land**: A dataframe of commercial landings data with columns `YEAR`, `ID`, `SPECIES` and `CATCH`. `YEAR` indicates the year the landing was recorded, `ID` is an area code indicating where the landing was recorded, `SPECIES` is a numeric code indicating the species landed, and `CATCH` is the corresponding landed weight.
- **maxlength.group**: A character string indicating the species group for which to calculate the mean maximum length of fish in the community. Must be set to "ALL" or match a column name in `species.table`. If `maxlength.group = NULL`, the mean maximum length will not be calculated.
- **species.table**: A table where the column names match the entries in `resource.groups`, `ratio.groups`, and/or `condition.groups`. Column entries are the species codes indicating the species from \( X \) (or `X_length`) included in each group. `species.table` may also include columns for other species groups; these will be ignored.
speciesinfo.table

A table with columns SPECIES and the corresponding TL, MAXLENGTH, MAXAGE, and IVI (trophic level, maximum recorded age, maximum recorded length, and intrinsic vulnerability index). Entries in the SPECIES column should be the unique values of species codes in \( X \) (or a subset thereof). If there are different species codes in \( X \) and Land, the Intrinsic Vulnerability Index of the Landings indicator should be calculated separately using the function IVILandings().

TL.grouping

Size of the trophic level bin for which to aggregate biomass when calculating Biomass per Trophic Level. For example, if TL.grouping = 1, trophic levels are binned from 1.00 - 1.99, 2.00 - 2.99, etc. If TL.grouping = 0.5, trophic levels are binned from 1.00 - 1.49, 1.50 - 1.99, 2.00 - 2.49, 2.50 - 2.99, etc. Default is TL.grouping = 1 so that biomass is aggregated over discrete trophic levels.

wind

Window for the moving average used to calculate the Coefficient of Variation of the Biomass. The first and last floor(wind/2) values of the indicator are assigned NA to account for the moving average. Default is wind = 5 years.

negative

If negative = TRUE, the Coefficient of Variation of the Biomass will be multiplied by -1 so that the expected response is to decrease with increasing fishing pressure. Default is negative = FALSE.

years

A vector of years for which to calculate indicators.

raw

A logical value. If raw = TRUE, the raw indicator values are returned by the function. If raw = FALSE, the raw indicator values are not returned. Default is raw = TRUE. Either raw or std must be TRUE.

std

A logical value. If std = TRUE, the standardized indicator values for each area ID are returned by the function. Indicators are standardized using z-scores, i.e., by subtracting the mean and dividing by the standard deviation (ignoring NA values). If std = FALSE, the standardized indicator values are not returned. Default is std = TRUE. Either raw or std must be TRUE.

glob.env

Logical value indicating whether to return output to global environment. Default is glob.env = TRUE.

export.path

File path indicating where to save a .csv file of calculated indicators (named stability_export.id.csv; see below). If export.file = NULL, the indicator dataframe will not be exported as a .csv file. Default is export.path = NULL.

export.id

Character string to modify the name of the .csv file (if export.path is specified), for example an area name or date of analysis. The exported .csv file is named stability_export.id.csv. Default is export.id = NULL.

Details

This function calculates the Stability and Resistance indicators: Biomass per Trophic Level, Intrinsic Vulnerability Index, Coefficient of Variation of the Biomass, Mean Lifespan, and Mean Maximum Length (weighted by biomass and abundance). If data are not available to calculate one or more of these indicators, a subset will be returned. See the help file for the individual functions for information on how each indicator is calculated.

Notes on indicator calculations: In the individual functions, the user generally has control over which metric (e.g., BIOMASS or ABUNDANCE) is used to calculate the indicator. Here, BIOMASS is...
allStructure

used to calculate Coefficient of Variation of the Biomass, Mean Lifespan, Biomass per Trophic Level, and Mean Maximum Length weighted by biomass. ABUNDANCE is used to calculate Mean Maximum Length weighted by abundance. See individual functions for more flexibility.

Value

Returns a dataframe with columns ID, YEAR, and indicators corresponding to the arguments supplied to the function. Standardized indicators are noted with _s in the name.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other stability and resistance indicators: CVBiomass, IVILandings, biomassPerTL, meanMaxAge, meanMaxLength

Examples

# Compile data
data(X)
data(land)
data(species.info)
data(species.table)

# Calculate raw and standardized indicators
allStability(X = X, land = land, maxlength.group = "FINFISH", species.table = species.table, speciesinfo.table = species.info, TL.grouping = 1, wind = 5, negative = FALSE, years = c(2014:2019), raw = TRUE, std = TRUE)

allStructure

Calculates all Structure and Functioning indicators

Description

This function calculates all (or a subset) of the Structure and Functioning indicators for \( j \) areas and \( i \) years. The user can choose whether the function returns the indicator dataframe to the global environment, exports the dataframe to a .csv file, or both. The user can also choose whether the function returns the raw indicator values, the standardized (z-score) values, or both.
Usage

allStructure(X, X_length, LSI.group, LFI.group, max.length = 85,
            large.fish = 35, guild.groups, condition.groups, ratio.groups,
            species.table, speciesinfo.table, LenWt.table, years, raw = TRUE,
            std = TRUE, glob.env = TRUE, export.path = NULL,
            export.id = NULL)

Arguments

 X A dataframe of fishery independent data derived from research vessel survey
data or model output, with columns YEAR, ID, SPECIES, and BIOMASS. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and BIOMASS is the corresponding biomass (stratified and corrected for catchability as required).

 X_length A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, LENGTH, BIOMASS and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, and SPECIES is a numeric code indicating the species sampled. LENGTH is the length class (cm) and BIOMASS/ABUNDANCE is the corresponding biomass/abundance at length (stratified and corrected for catchability as required). Species for which there are no length data should be assigned LENGTH = -99. These observations are removed by the function.

 LSI.group A character string indicating the species group for which to calculate the Large Species Indicator. Must be set to "ALL" or match a column name in species.table. If LSI.group = NULL, the Large Species Indicator will not be calculated.

 LFI.group A character string indicating the species group for which to calculate the Large Fish Indicator. Must be set to "ALL" or match a column name in species.table. If LFI.group = NULL, the Large Fish Indicator will not be calculated.

 max.length The threshold for large species (cm). Default is max.length = 85 (i.e., large species are those with MAXLENGTH >= 85 cm).

 large.fish Threshold for large fish (cm). Default is large.fish = 35 (i.e., large fish are those with X_length$LENGTH >= 35 cm).

 guild.groups A vector indicating the species groups for which to calculate the resource potential. Each entry must be a character string matching the name of a column in species.table. If guild.groups = NULL, these indicators will not be calculated.

 condition.groups A vector indicating the species groups for which to calculate Fulton’s community condition factor. Each entry must be a character string matching the name of a column in species.table. If condition.groups = NULL, the community condition indicators will not be calculated.

 ratio.groups A dataframe with two columns, which must be named group1 and group2. Each row holds the group names for one biomass ratio, with the numerator in column...
allStructure

group1 and the denominator in column group2. Each entry must be a character string matching the name of a column in species.table or "ALL". If ratio.groups = NULL, biomass ratio indicators will not be calculated.

species.table A table where the column names match the entries in guild.groups, ratio.groups, and/or condition.groups. Column entries are the species codes indicating the species from X (or X_length) included in each group. species.table may also include columns for other species groups; these will be ignored.

speciesinfo.table A table with columns SPECIES and the corresponding TL and MAXLENGTH (trophic level and maximum recorded length). Entries in the SPECIES column should be the unique values of species codes in X/X_length (or a subset thereof). Other columns will be ignored.

LenWt.table A table of annual length at weight data with 5 columns. YEAR, ID, and SPECIES are as described in X_length. LENGTH is fish length at the corresponding WEIGHT (fish weight).

years A vector of years for which to calculate indicators.

raw A logical value. If raw = TRUE, the raw indicator values are returned by the function. If raw = FALSE, the raw indicator values are not returned. Default is raw = TRUE. Either raw or std must be TRUE.

std A logical value. If std = TRUE, the standardized indicator values for each area ID are returned by the function. Indicators are standardized using z-scores, i.e., by subtracting the mean and dividing by the standard deviation (ignoring NA values). If std = FALSE, the standardized indicator values are not returned. Default is std = TRUE. Either raw or std must be TRUE.

glob.env Logical value indicating whether to return output to global environment. Default is glob.env = TRUE.

export.path File path indicating where to save a .csv file of calculated indicators (named structure_export.id.csv; see below). If export.file = NULL, the indicator dataframe will not be exported as a .csv file. Default is export.path = NULL.

export.id Character string to modify the name of the .csv file (if export.path is specified), for example an area name or date of analysis. The exported .csv file is named structure_export.id.csv. Default is export.id = NULL.

Details

This function calculates the Structure and Functioning indicators: Biomass, Biomass Ratio(s), Large Species Indicator, Trophic Level of the Community, Large Fish Indicator, Mean Length (weighted by biomass and abundance), and Community Condition. If data are not available to calculate one or more of these indicators, a subset will be returned. See the help file for the individual functions for information on how each indicator is calculated.

Notes on indicator calculations: In the individual functions, the user generally has control over which metric is used to calculate the indicator (e.g., BIOMASS or ABUNDANCE). Here, BIOMASS is used to calculate Biomass, Biomass Ratio(s), Large Species Indicator, Large Fish Indicator, Trophic Level of the Community, and Mean Length weighted by biomass. ABUNDANCE is used to calculate Mean Length weighted by abundance and Community Condition. See individual functions for more flexibility.
Value

Returns a dataframe with columns ID, YEAR, and indicators corresponding to the arguments supplied to the function. Standardized indicators are noted with _s in the name.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other ecosystem structure and function indicators: `biomassRatio, communityCondition, largeFishIndicator, largeSpeciesIndicator, meanTLCommunity`

Examples

```r
# Compile data
data(X)
data(X_length)
data(species.table)
data(species.info)
data(Length_Weight)

# Species groups of interest
ratio.groups <- data.frame(rbind(c("PELAGIC", "GROUNDFISH"), c("PREDATORS", "ALL")))
names(ratio.groups) <- c("group1", "group2")
trophicguild.groups <- c("LBENTHIVORE", "MBENTHIVORE", "PISCIVORE", "PLANKTIVORE", "ZOOPISCIVORE")
condition.groups <- c("FINFISH", "LBENTHIVORE", "MBENTHIVORE", "PISCIVORE", "PLANKTIVORE", "ZOOPISCIVORE")

# Calculate raw indicators
allStructure(X = X, X_length = X_length,
             LSI.group = "ALL", LFI.group = "ALL",
             max.length = 85, large.fish = 35,
             guild.groups = trophicguild.groups, condition.groups = condition.groups,
             ratio.groups = ratio.groups,
             species.table = species.table, speciesinfo.table = species.info,
             LenWt.table = Length_Weight,
             years = c(2014:2019), raw = TRUE, std = FALSE)
```
Calculates the biomass per discrete trophic level

**Description**

This function calculates the biomass per discrete trophic level for \( j \) areas and \( i \) years.

**Usage**

\[
\text{biomassPerTL}(X, \text{TL.table, metric = "BIOMASS", TL.grouping = 1, years})
\]

**Arguments**

- **X**: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns \text{YEAR}, ID, SPECIES, and BIOMASS. \text{YEAR} indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and BIOMASS is the corresponding biomass (stratified and corrected for catchability as required).

- **TL.table**: A dataframe with columns SPECIES and the corresponding TL (trophic level). Entries in the SPECIES column should be the unique values of species codes in \( X \) (or a subset thereof). Other columns in \text{TL.table} will be ignored.

- **metric**: A character string indicating which column in \( X \) to use to calculate indicator. Default is \text{metric = "BIOMASS"}.

- **TL.grouping**: Size of the trophic level bin for which to aggregate biomass. For example, if \text{TL.grouping = 1}, trophic levels are binned from 1.00 - 1.99, 2.00 - 2.99, etc. If \text{TL.grouping = 0.5}, trophic levels are binned from 1.00 - 1.49, 1.50 - 1.99, 2.00 - 2.49, 2.50 - 2.99, etc. Default is \text{TL.grouping = 1}.

- **years**: A vector of years for which to calculate indicator.

**Value**

Returns a dataframe with columns ID, \text{YEAR}, and the corresponding biomass for each trophic level grouping. For example: for \text{TL.grouping = 1}, function will return columns BIOMASS\_TL2, BIOMASS\_TL3, BIOMASS\_TL4. For \text{TL.grouping = 0.5}, function will return columns BIOMASS\_TL2, BIOMASS\_TL2.5, BIOMASS\_TL3, BIOMASS\_TL3.5, BIOMASS\_TL4, BIOMASS\_TL4.5.

If there is no data for spatial scale \( j \) in year \( i \), indicator value is assigned NA.

**Author(s)**

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy
biomassRatio

References


See Also

Other stability and resistance indicators: CVBiomass, IVI_landings, allStability, meanMaxAge, meanMaxLength

Examples

# Compile data
data(X)
data(species.info)

# Calculate indicators
biomassPerTL(X = X, TL.table = species.info, metric = "BIOMASS", TL.grouping = 1, years = c(2014:2019))

biomassRatio

Calculates the biomass ratio between two species groups

Description

This function calculates the biomass ratio between two pre-defined species groups for \( j \) areas and \( i \) years.

Usage

biomassRatio(X, ratio.groups, species.table, metric = "BIOMASS", years)

Arguments

\( X \quad \) A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, and BIOMASS. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and BIOMASS is the corresponding biomass (stratified and corrected for catchability as required).
ratio.groups  A dataframe with two columns, which must be named group1 and group2. Each row holds the group names for one biomass ratio, with the numerator in column group1 and the denominator in column group2. Each entry must be a character string matching the name of a column in species.table or "ALL".

species.table  A table with column names that match the entries of ratio.groups. The entries in each column are the species codes from X indicating which species are included that group. species.table may also include columns for other species groups; these will be ignored. Note that an entry in ratio.groups could be "ALL". In this case, a column in species.table named "ALL" is not required; the function will automatically include all species in X.

metric  A character string indicating which column in X to use to calculate indicator. Default is metric = "BIOMASS".

years  A vector of years for which to calculate indicator.

Details

One useful biomass ratio is the proportion of predatory fish in the community, which is estimated by:

PropPred = Biomass of Predatory Fish Surveyed/Total Biomass Surveyed

Predatory fish species are defined as all surveyed fish species that are not largely planktivorous, ie., fish that are piscivorous, or that feed on invertebrates larger than the macrozooplankton category (0.2 cm; Shin et al. 2010). Phytoplankton, zooplankton and detritus feeders should be excluded. This indicator captures changes in the trophic structure and changes in the functional diversity of fish in the ecosystem.

Other useful biomass (B) ratios indicators include:

\[ \frac{B_{\text{invertebrates}}}{B_{\text{demersal}}} \]

and

\[ \frac{B_{\text{pelagic}}}{B_{\text{demersal}}} \]

Value

Returns a dataframe with columns ID and YEAR, and a column for each biomass ratio, named after the entries in ratio.groups, e.g. group1_group2.

If there is no data for spatial scale \( j \) in year \( i \), indicator values is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

communityCondition


See Also

Other ecosystem structure and function indicators: allStructure, communityCondition, largeFishIndicator, largeSpeciesIndicator, meanTLCommunity

Examples

```r
# Compile data
data(X)
data(species.table)

# Species groups of interest
ratio.groups <- data.frame(rbind(c("PELAGIC", "GROUNDFISH"), c("PREDATORS", "ALL")))
names(ratio.groups) <- c("group1", "group2")

# Calculate indicators
biomassRatio(X, ratio.groups = ratio.groups, species.table = species.table, 
metric = "BIOMASS", years = c(2014:2019))
```

---

communityCondition **Calculates Fulton’s Condition Index for the community**

Description

This function calculates Fulton’s Condition Index for \( j \) areas and \( i \) years.

Usage

```r
communityCondition(X_length, groups, species.table = NULL, LenWt.table, 
years)
```

Arguments

- **X_length**: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, LENGTH, and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, and SPECIES is a numeric code indicating the species sampled. LENGTH is the length class (cm) and ABUNDANCE is the
corresponding abundance at length (stratified and corrected for catchability as required). Species for which there are no length data should be assigned LENGTH = -99. These observations are removed by the function.

groups A vector indicating the species group(s) for which to calculate the indicator. If groups = "ALL", all species will be included; otherwise, each entry must be a character string matching the name of a column in species.table.

species.table A table where the column names match the entries in groups. Column entries are species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored. If groups = "ALL", this table is not required. Default is species.table = NULL.

LenWt.table A table of annual length at weight data with 5 columns. YEAR, ID, and SPECIES are as described in X_length. LENGTH is fish length at the corresponding WEIGHT (fish weight).

years A vector of years for which to calculate indicator.

Details

Fulton’s Condition Index \((K)\):

\[
K = \frac{\Sigma(K_j \ast A_j)}{\Sigma A_j}
\]

where the sum is over all species, \(j\), \(A_j\) is the abundance of species \(j\), and

\[
K_j = 100 \ast \frac{W_j}{L_j^3}
\]

where \(W_j\) is the mean weight at length \(L\) for species \(j\) (Ricker, 1975).

Value

Returns a dataframe with columns ID and YEAR, and a column CCondition_group for each entry in groups.

If there is no data for spatial scale \(j\) in year \(i\), indicator value is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


CVBiomass

Description

This function calculates the Coefficient of Variation of the Biomass for \( j \) areas and \( i \) years.

Usage

CVBiomass(X, wind = 5, negative = FALSE, years)

Arguments

\( X \)
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, and BIOMASS. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, and BIOMASS is the total recorded biomass (stratified and corrected for catchability as required). (Note: if \( X \) has an additional SPECIES column, the function will automatically calculate the total biomass).

\( wind \)
Window for the moving average. The first and last floor(wind/2) values of the indicator are assigned NA to account for the moving average. Default is wind = 5 years.

\( negative \)
If negative = TRUE, the indicator will be multiplied by -1 so that the expected response is to decrease with increasing fishing pressure. Default is negative = FALSE.

\( years \)
A vector of years for which to calculate indicator.

See Also

Other ecosystem structure and function indicators: allStructure, biomassRatio, largeFishIndicator, largeSpeciesIndicator, meanTLCommunity

Examples

# Compile data
data(X_length)
data(species.table)
data(Length_Weight)

# Species groups of interest
condition.groups <- c("FINFISH", "LBENTHIVORE", "PISCIVORE", "PLANKTIVORE")

# Calculate indicators
communityCondition(X_length, LenWt.table = Length_Weight, groups = condition.groups, species.table = species.table, years = c(2014:2019))
Details

The Coefficient of Variation of the Biomass (CVBiomass) was estimated as an n-year moving average (Blanchard and Boucher, 2001):

\[
CVBiomass = \frac{sd(\text{total biomass for the past n years})}{\text{mean(\text{total biomass for the past n years})}}
\]

Value

Returns a dataframe with three columns: ID, YEAR, and CVBiomass.

The first and last floor(wind/2) values of the indicator are assigned NA to account for the moving average. If there is no data for spatial scale j in year i, indicator value is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other stability and resistance indicators: IVILandings, allStability, biomassPerTL, meanMaxAge, meanMaxLength

Examples

data(X)
CVBiomass(X, wind = 5, negative = TRUE, years = c(2014:2019))
**Description**

A dataframe of indicators for AREA1 and AREA2 from 2014 - 2019, calculated from the example data described in this package. Type `?X, ?X_length, ?land, ?species.info, ?species.table, or ?Length_Weight` for information on the example data.

**Usage**

`example_inds`

**Format**

This example data is a dataframe with 12 rows and 114 variables:

- **YEAR** Year for which indicator was calculated
- **ID** Area for which the indicator was calculated

**56 Raw Indicators** Raw values of Biodiversity, Structure and Functioning, Stability and Resistance, Potential and Fishing Pressure indicators.

**56 Standardized Indicators** The same indicators noted above, but standardized using z-score (subtract mean and divide by standard deviation).

**Source**

These are example indicators calculated from made-up example data.

**extractAll**

Calculates indicators from all attributes

**Description**

This function calculates all of the indicators described in this package. The user can choose whether the function returns the indicator dataframe to the global environment, exports the dataframe to a .csv file, or both. The user can also choose whether the function returns the raw indicator values, the standardized (z-score) values, or both.
Usage

extractAll(X, X_length, land, speciesinfo.table, species.table, years, metric.bio = "ABUNDANCE", group.bio = "ALL", percentiles = c(0.25, 0.75), minTL.bio = 0, LSI.group, max.length = 85, LFI.group, large.fish = 35, LenWt.table, guild.groups, condition.groups, ratio.groups, maxlength.group, TL.grouping = 1, wind = 5, negative = FALSE, resource.groups, minTL.FiB = 0, TE = 0.1, base.start, base.end, landings.groups, FP.groups, minTL.FP = c(0, 3.25), raw = TRUE, std = TRUE, glob.env = TRUE, export.path = NULL, export.id = NULL)

Arguments

X
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, BIOMASS and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and ABUNDANCE is the corresponding abundance (stratified and corrected for catchability as required).

X_length
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, LENGTH, BIOMASS and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, and SPECIES is a numeric code indicating the species sampled. LENGTH is the length class (cm) and ABUNDANCE is the corresponding abundance at length (stratified and corrected for catchability as required). Species for which there are no length data should be assigned LENGTH = -99. These observations are removed by the function.

land
A dataframe of commercial landings data with columns YEAR, ID, SPECIES and CATCH. YEAR indicates the year the landing was recorded, ID is an area code indicating where the landing was recorded, SPECIES is a numeric code indicating the species landed, and CATCH is the corresponding landed weight. If land = NULL, the landings-based indicators will not be calculated.

speciesinfo.table
A table with columns SPECIES and the corresponding TL, MAXLENGTH, MAXAGE, IVI, and TL_LAND (trophic level, maximum recorded age, maximum recorded length, intrinsic vulnerability index, and trophic level of the landings). Entries in the SPECIES column should be the unique values of species codes in X/X_length (or a subset thereof). If there are different species codes in X and land, the Fishing-in-Balance, Intrinsic Vulnerability Index of Landings, Mean Trophic Level of the Landings, and Marine Trophic Index should be calculated using their respective single functions (see manual or vignette).

species.table
A table where the column names match the entries in condition.groups, FP.groups, group.bio, guild.groups, landings.group, LFI.group, LSI.group, maxlength.group, ratio.groups, and resource.groups. Column entries are the species codes indicating the species from X (or X_length) included in each group. species.table may also include columns for other species groups; these will be ignored.

years
A vector of years for which to calculate indicators.
**metric.bio**
A character string indicating which column in X to use to calculate the biodiversity indicators. Default is **metric = "ABUNDANCE"**.

**group.bio**
A character string indicating which species to include in the calculation of the Biodiversity indicators. If **group = "ALL"**, all species will be included; otherwise, **group.bio** should match a column name in species.table. Default is **group.bio = "ALL"**.

**percentiles**
The percentiles used to determine R1 and R2 for calculating Kempton’s Q. Default is **percentiles = c(0.25, 0.75)**.

**minTL.bio**
Minimum trophic level for species included to calculate Kempton’s Q. Default is **minTL.bio = 0**.

**LSI.group**
A character string indicating the species group for which to calculate the Large Species Indicator. Must be set to "ALL" or match a column name in species.table. If **LSI.group = NULL**, the Large Species Indicator will not be calculated.

**max.length**
The threshold for large species (cm). Default is **max.length = 85** (i.e., large species are those with MAXLENGTH >= 85 cm).

**LFI.group**
A character string indicating the species group for which to calculate the Large Fish Indicator. Must be set to "ALL" or match a column name in species.table. If **LFI.group = NULL**, the Large Fish Indicator will not be calculated.

**large.fish**
Threshold for large fish (cm). Default is **large.fish = 35** (i.e., large fish are those with X_length$LENGTH >= 35 cm).

**LenWt.table**
A table of annual length at weight data with 5 columns. YEAR, ID, and SPECIES are as described in X_length. **LENGTH** is fish length at the corresponding **WEIGHT** (fish weight).

**guild.groups**
A vector indicating the species groups for which to calculate the resource potential. Each entry must be a character string matching the name of a column in species.table. If **guild.groups = NULL**, these indicators will not be calculated.

**condition.groups**
A vector indicating the species groups for which to calculate Fulton’s community condition factor. Each entry must be a character string matching the name of a column in species.table. If **condition.groups = NULL**, the community condition indicators will not be calculated.

**ratio.groups**
A dataframe with two columns, which must be named group1 and group2. Each row holds the group names for one biomass ratio, with the numerator in column group1 and the denominator in column group2. Each entry must be a character string matching the name of a column in species.table or "ALL". If **ratio.groups = NULL**, biomass ratio indicators will not be calculated.

**maxlength.group**
A character string indicating the species group for which to calculate the mean maximum length of fish in the community. Must be set to "ALL" or match a column name in species.table. If **maxlength.group = NULL**, the mean maximum length will not be calculated.

**TL.grouping**
Size of the trophic level bin for which to aggregate biomass when calculating Biomass per Trophic Level. For example, if **TL.grouping = 1**, trophic levels are binned from 1.00 - 1.99, 2.00 - 2.99, etc. If **TL.grouping = 0.5**, trophic
levels are binned from 1.00 - 1.49, 1.50 - 1.99, 2.00 - 2.49, 2.50 - 2.99, etc. Default is TL.grouping = 1 so that biomass is aggregated over discrete trophic levels.

**wind**
Window for the moving average used to calculate the Coefficient of Variation of the Biomass. The first and last floor(wind/2) values of the indicator are assigned NA to account for the moving average. Default is wind = 5 years.

**negative**
If negative = TRUE, the Coefficient of Variation of the Biomass and the Intrinsic Vulnerability Index of the Landings will be multiplied by -1 so that their expected response is to decrease with increasing fishing pressure. Default is negative = FALSE.

**resource.groups**
A vector indicating the species groups for which to calculate the resource potential. Each entry must be a character string matching the name of a column in species.table. If resource.groups = NULL, these indicators will not be calculated.

**minTL.FiB**
The minimum trophic level of species to include to calculate Fishing-in-Balance.

**TE**
Trophic efficiency, used to calculate FiB. Default is TE = 0.1, i.e., a trophic efficiency of 10%. If TE = NULL, FiB will not be calculated.

**base.start**
Year indicating the beginning of the baseline period for calculating FiB. The average landings and average mean trophic level of the landings over the baseline period are used as baseline values to calculate FiB. land must include data for the baseline period. If base.start = NULL, FiB will not be calculated.

**base.end**
Year indicating the end of the baseline period for calculating FiB. The average landings and average mean trophic level of the landings over the baseline period are used as baseline values to calculate FiB. land must include data for the baseline period. If base.end = NULL, FiB will not be calculated.

**landings.groups**
A vector indicating the species groups for which to calculate the landings. Each entry must be a character string matching the name of a column in species.table. If landings.groups = NULL, no Landings indicators will be calculated.

**FP.groups**
A dataframe with two columns, which must be named group.land and group.X. Each row holds the group names to calculate the fishing pressure on a target group, with the numerator in column group.land and the denominator in column group.X. Each entry must be a character string matching the name of a column in species.table. If FP.groups = NULL, no fishing pressure indicators will be calculated.

**minTL.FP**
A vector containing minimum trophic level to include when calculating the mean trophic level of the landings. Default is minTL = c(0, 3.25), which will return the mean trophic level of the landings and the marine trophic index.

**raw**
A logical value. If raw = TRUE, the raw indicator values are returned by the function. If raw = FALSE, the raw indicator values are not returned. Default is raw = TRUE. Either raw or std must be TRUE.

**std**
A logical value. If std = TRUE, the standardized indicator values for each area ID are returned by the function. Indicators are standardized using z-scores, i.e., by subtracting the mean and dividing by the standard deviation (ignoring NA values). If std = FALSE, the standardized indicator values are not returned. Default is std = TRUE. Either raw or std must be TRUE.
extractAll

glob.env Logical value indicating whether to return output to global environment. Default is \texttt{glob.env = TRUE}.

export.path File path indicating where to save a .csv file of calculated indicators (named allIndicators_export.id.csv; see below). If \texttt{export.file = NULL}, the indicator dataframe will not be exported as a .csv file. Default is \texttt{export.path = NULL}.

export.id Character string to modify the name of the .csv file (if export.path is specified), for example an area name or date of analysis. The exported .csv file is named allIndicators_export.id.csv. Default is \texttt{export.id = NULL}.

Details

This function calculates the indicators for each attribute and pressure: Biodiversity, Structure and Functioning, Stability and Resistance, Resource Potential, and Fishing Pressure.

See the help file for the individual functions for information on how each indicator is calculated.

Value

Returns a dataframe with columns \texttt{ID}, \texttt{YEAR}, and indicators corresponding to the arguments supplied to the function. Standardized indicators are noted with \_s in the name.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

Examples

# Compile data
data(X)
data(X_length)
data(land)
data(species.table)
data(species.info)
data(Length_Weight)

# Species groups of interest
trophicguild.groups <- c("LBENTHIVORE", "MBENTHIVORE", "PISCIVORE", "PLANKTIVORE",
                           "ZOOPISCIVORE")
condition.groups <- c("FINFISH", "PISCIVORE", "PLANKTIVORE", "ZOOPISCIVORE")
resource.groups <- c("ALL", "CLUPEIDS", "FINFISH", "FLATFISH", "FORAGE",
                     "GADOIDS", "GROUNDFISH", "PELAGIC", "SKATES")
ratio.groups <- data.frame(rbind(c("PELAGIC", "GROUNDFISH"), c("PREDATORS", "ALL")))
names(ratio.groups) <- c("group1", "group2")

landings.groups <- c("ALL", "CLUPEIDS.L", "FLATFISH.L", "GROUNDFISH.L")
FP.groups <- data.frame(rbind(c("ALL", "ALL"),
                              c("CLUPEIDS", "CLUPEIDS.L"),
                              c("FLATFISH", "FLATFISH.L"),
                              c("GROUNDFISH", "GROUNDFISH.L")))
names(FP.groups) <- c("group.X", "group.land")
# Calculate raw and standardized indicators

```r
extractAll(X = X, X_length = X_length, land = land,
          speciesinfo.table = species.info, species.table = species.table, years = c(2014:2019),
          LSI.group = "ALL", LFI.group = "ALL", LenWt.table = Length_Weight,
          guild.groups = trophicguild.groups, condition.groups = condition.groups,
          ratio.groups = ratio.groups,
          maxlength.group = "FINFISH",
          resource.groups = resource.groups,
          minTL.FiB = 0, base.start = 2014, base.end = 2015,
          landings.groups = landings.groups, FP.groups = FP.groups,
          raw = TRUE, std = TRUE, export.path = NULL)
```

---

**fishingInBalance**: Calculates the Fishing-in-Balance Index

**Description**

This function calculates the Fishing-in-Balance (FiB) Index of fisheries landings for \( j \) areas and \( i \) years.

**Usage**

```r
fishingInBalance(land, TL.table, minTL = 0, TE = 0.1, base.start, base.end, years)
```

**Arguments**

- **land**: A dataframe of commercial landings data with columns `YEAR`, `ID`, `SPECIES` and `CATCH`. `YEAR` indicates the year the landing was recorded, `ID` is an area code indicating where the landing was recorded, `SPECIES` is a numeric code indicating the species landed, and `CATCH` is the corresponding landed weight.

- **TL.table**: A dataframe with columns `SPECIES` and the corresponding `TL_LAND` (trophic level). Entries in the `SPECIES` column should be the unique values of species codes in `land` (or a subset thereof). Other columns in `TL.table` are ignored.

- **minTL**: The minimum trophic level of species to include. Default is `minTL = 0`.

- **TE**: Trophic efficiency. Default is `TE = 0.1`, i.e., a trophic efficiency of 10%.

- **base.start**: Year indicating the beginning of the baseline period. The average landings and average mean trophic level of the landings over the baseline period are used as baseline values to calculate FiB (see Details). `land` must include data for the baseline period.

- **base.end**: Year indicating the end of the baseline period. The average landings and average mean trophic level of the landings over the baseline period are used as baseline values to calculate FiB (see Details). `land` must include data for the baseline period.

- **years**: A vector of years for which to calculate indicator.
**fishingInBalance**

**Details**

Fishing-in-Balance (FiB) Index:

\[ FiB = \log(Y_k (1/TE)^{TL_k}) - \log(Y_0 (1/TE)^{TL_0}) \]

where \( Y \) is the catch, \( TL \) is the mean trophic level in the catch, \( TE \) is the transfer efficiency, \( k \) is any year, and 0 refers to any year used as a baseline. By default, \( TE \) is set to 0.10 (Pauly and Christensen 1995).

This indicator captures changes in fishing strategies and their impact on system productivity: a positive FiB index indicates that the fishery has expanded and/or bottom-up effects are occurring, and there is more catch than expected, while a negative FiB index indicates it is likely that the fishing impact is so high that the ecosystem function is impaired and the ecosystem is less productive owing to excessive fishery removals (Pauly et al., 2000).

**Value**

Returns a dataframe with three columns: ID, YEAR, and FishingInBalance.

If there are no observations in land for spatial scale \( j \) and year \( i \), indicator value is set to NA.

**Author(s)**

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

**References**


**See Also**

Other resource potential indicators: allPotential, resourcePotential

**Examples**

data(land)
data(species.info)
fishingInBalance(land, TL.table = species.info, minTL = 0, TE = 0.1, base.start = 2014, base.end = 2015, years = c(2014:2019))
fishingPressure \hspace{1em} Calculates Fishing Pressure

Description
This function calculates Fishing Pressure on a fished group for \( j \) areas and \( i \) years.

Usage
fishingPressure(X, land, FP.groups, species.table, years)

Arguments
\begin{itemize}
\item **X** \hspace{1em} A dataframe of fishery independent data derived from research vessel survey data or model output, with columns \texttt{YEAR}, \texttt{ID}, \texttt{SPECIES}, and \texttt{BIOMASS}. \texttt{YEAR} indicates the year the observation was recorded, \texttt{ID} is an area code indicating where the observation was recorded, \texttt{SPECIES} is a numeric code indicating the species sampled, and \texttt{BIOMASS} is the corresponding biomass (stratified and corrected for catchability as required).
\item **land** \hspace{1em} A dataframe of commercial landings data with columns \texttt{YEAR}, \texttt{ID}, \texttt{SPECIES} and \texttt{CATCH}. \texttt{YEAR} indicates the year the landing was recorded, \texttt{ID} is an area code indicating where the landing was recorded, \texttt{SPECIES} is a numeric code indicating the species landed, and \texttt{CATCH} is the corresponding landed weight (in the same units as \texttt{BIOMASS} in \texttt{X}).
\item **FP.groups** \hspace{1em} A dataframe with two columns, which must be named \texttt{group.land} and \texttt{group.X}. Each row holds the group names to calculate the fishing pressure on a target group, with the numerator in column \texttt{group.land} and the denominator in column \texttt{group.X}. Each entry must be a character string matching the name of a column in \texttt{species.table}.
\item **species.table** \hspace{1em} A table with column names that match the entries of \texttt{FP.groups}. The entries in each column are the species codes for the species included in that group. Species codes should be a subset of those in the \texttt{SPECIES} column of \texttt{land} (for groups in \texttt{group.land}) or \texttt{X} (for groups in \texttt{group.X}). \texttt{species.table} may also include columns for other species groups; these will be ignored. Note that an entry in \texttt{FP.groups} could be "ALL". In this case, a column in \texttt{species.table} named "ALL" is not required; the function will automatically include all species in \texttt{land} and/or \texttt{X}.
\item **years** \hspace{1em} A vector of years for which to calculate indicator.
\end{itemize}

Details
Fishing pressure (FP):
\[ FP = \frac{\text{Landings}_{FG}}{\text{Biomass}_{FG}} \]
where \( \text{Landings}_{FG} \) is the landed catch of the fished group and \( \text{Biomass}_{FG} \) is the biomass of the fished group.
fishingPressure

This indicator measures the level of exploitation or total fishing pressure at the ecosystem or species group level. Change in this indicator can result from change in LandingsFG, BiomassFG or both. If LandingsFG and BiomassFG change in the same direction, exploitation rate may not change.

Value

Returns a dataframe with columns: ID and YEAR, and a column for each target group, named FP_group.X.

If biomass of group.X is NA and landings of group.land are zero, fishing pressure is set to zero. Otherwise, if biomass of group.X is NA, fishing pressure is set to NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other fishing pressure indicators: allPressure, landings, meanTLLandings, speciesRichness

Examples

# Compile data
data(X)
data(land)
data(species.table)

# Species groups of interest
FP.groups <- data.frame(rbind(c("ALL", "ALL"),
c("CLUPEIDS", "CLUPEIDS.L"),
c("FLATFISH", "FLATFISH.L"),
c("GROUNDFISH", "GROUNDFISH.L")))
names(FP.groups) <- c("group.X", "group.land")

# Calculate indicators
fishingPressure(X = X, land = land, FP.groups = FP.groups,
species.table = species.table, years = c(2014:2019))
Calculates Heip’s Evenness Index

Description

This function calculates Heip’s Evenness Index (HE) of the community for \( j \) areas and \( i \) years.

Usage

```r
heips(X, groups, species.table = NULL, metric = "ABUNDANCE", years)
```

Arguments

- **X**: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and ABUNDANCE is the corresponding abundance (stratified and corrected for catchability as required).

- **groups**: A vector indicating the species group(s) for which to calculate the indicator. If `groups = "ALL"`, all species will be included; otherwise, each entry must be a character string matching the name of a column in `species.table`.

- **species.table**: A table where the column names match the entries in `groups`. Column entries are species codes indicating the species from `X` included in each group. `species.table` may also include columns for other species groups; these will be ignored. If `groups = "ALL"`, this table is not required. Default is `species.table = NULL`.

- **metric**: A character string indicating which column in `X` to use to calculate the indicator. Default is `metric = "ABUNDANCE"`.

- **years**: A vector of years for which to calculate indicator.

Details

Heip’s Evenness Index (HE):

\[
HE = \frac{exp^{H'} - 1}{(S - 1)}
\]

where \( H' \) is Shannon’s index of diversity and \( S \) is species richness. This index ranges from 0 to 1 and measures how equally the species richness contributes to the total abundance or biomass of the community (Heip, 1974).

Value

Returns a dataframe with columns ID and YEAR, and a column Heips_group for each entry in groups.

If there is no data for spatial scale \( j \) in year \( i \), indicator value is assigned NA.
Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other biodiversity indicators: allBiodiversity, hillN1, hillN2, kemptonQ, margalef, pielouEvenness, shannon, speciesRichness

Examples

data(X)
heips(X, groups = "ALL", species.table = NULL, metric = "ABUNDANCE", years = c(2014:2019))

---

hillN1

Calculates Hill’s Index of Diversity (N1)

Description

This function calculates Hill’s Index of Diversity (N1) for j areas and i years.

Usage

hillN1(X, groups, species.table = NULL, metric = "ABUNDANCE", years)

Arguments

X

A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and ABUNDANCE is the corresponding abundance (stratified and corrected for catchability as required).

groups

A vector indicating the species group(s) for which to calculate the indicator. If groups = "ALL", all species will be included; otherwise, each entry must be a character string matching the name of a column in species.table.
species.table  A table where the column names match the entries in groups. Column entries are species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored. If groups = "ALL", this table is not required. Default is species.table = NULL.

metric  A character string indicating which column in X to use to calculate the indicator. Default is metric = "ABUNDANCE".

years  A vector of years for which to calculate indicator.

Details

Hill's N1 Diversity Index is the exponential of the Shannon-Weiner index.

\[ HillN1 = e^{-\sum p_i \ln(p_i)} \]

\( p_i \) is the proportion of the total sample contributed by the \( i \)(th) species and \( S \) is the number of species recorded in the sample. This index is sensitive to the number of species recorded in the sample (Hill, 1973).

Value

Returns a dataframe with columns ID and YEAR, and a column HillDiversity_group for each entry in groups.

If there is no data for spatial scale \( j \) in year \( i \), indicator values is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other biodiversity indicators: allBiodiversity, heips, hillN2, kemptonQ, margalef, pielouEvenness, shannon, speciesRichness

Examples

data(X)
hillN1(X, groups = "ALL", metric = "ABUNDANCE", years = c(2014:2019))
Calculates Hill’s Species Dominance (N2)

**Description**

This function calculates Hill’s Species Dominance (N2) for j areas and i years.

**Usage**

```r
hillN2(X, groups, species.table = NULL, metric = "ABUNDANCE", years)
```

**Arguments**

- **X** A dataframe of fishery independent data derived from research vessel survey data or model output, with columns `YEAR`, `ID`, `SPECIES`, and `ABUNDANCE`. `YEAR` indicates the year the observation was recorded, `ID` is an area code indicating where the observation was recorded, `SPECIES` is a numeric code indicating the species sampled, and `ABUNDANCE` is the corresponding abundance (stratified and corrected for catchability as required).
- **groups** A vector indicating the species group(s) for which to calculate the indicator. If `groups = "ALL"`, all species will be included; otherwise, each entry must be a character string matching the name of a column in `species.table`.
- **species.table** A table where the column names match the entries in `groups`. Column entries are species codes indicating the species from `X` included in each group. `species.table` may also include columns for other species groups; these will be ignored. If `groups = "ALL"`, this table is not required. Default is `species.table = NULL`.
- **metric** A character string indicating which column in `X` to use to calculate the indicator. Default is `metric = "ABUNDANCE"`.
- **years** A vector of years for which to calculate indicator.

**Details**

Hill’s Species Dominance (HillN2):

\[
HillN2 = \frac{1}{\Sigma p_i^2}
\]

\(p_i\) is the proportion of the total sample contributed by the i(th) species. HillN2 is the inverse of the Simpson’s index. This index is sensitive to the evenness of the distribution of individuals between species (Hill, 1973).

**Value**

Returns a dataframe with columns `ID` and `YEAR`, and a column `HillDominance_group` for each entry in `groups`.

If there is no data for spatial scale \(j\) in year \(i\), indicator values is assigned NA.
IVILandings

Author(s)
Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

See Also
Other biodiversity indicators: allBiodiversity, heips, hillN1, kemptonQ, margalef, pielouEvenness, shannon, speciesRichness

Examples
data(X)
hillN2(X, groups = "ALL", metric = "ABUNDANCE", years = c(2014:2019))

---

IVILandings Calculates the Intrinsic Vulnerability Index of commercial landings

Description
This function calculates the Intrinsic Vulnerability Index (IVI) of the commercial landings for \( j \) areas and \( i \) years.

Usage
IVILandings(land, IVI.table, negative = FALSE, years)

Arguments
land A dataframe of commercial landings data with columns YEAR, ID, SPECIES and CATCH. YEAR indicates the year the landing was recorded, ID is an area code indicating where the landing was recorded, SPECIES is a numeric code indicating the species landed, and CATCH is the corresponding landed weight.
IVI.table A dataframe with columns SPECIES and the corresponding IVI (intrinsic vulnerability index). Entries in the SPECIES column should be the unique values of species codes in land (or a subset thereof). Other columns in IVI.table are ignored.
negative: If negative = TRUE, the indicator will be multiplied by -1 so that the expected response is to decrease with increasing fishing pressure. Default is negative = FALSE.

years: A vector of years for which to calculate indicator.

Details

The weighted Intrinsic Vulnerability Index (IVI) of species in the commercial landings was estimated as:

\[ IVI = \frac{\sum (IVI_j \times C_j)}{\sum C_j} \]

where the sum is over all species, \( j \). The vulnerability for each species was determined by considering several traits including maximum length, age at first maturity, longevity, von Bertalanffy growth parameter, natural mortality, fecundity, spatial behaviour and geographic range (e.g. species with larger body size, higher longevity, higher age at maturity, and lower growth rates have higher vulnerability indexes and should be less able to sustain high fishing mortality; Cheung et al. 2005). The index values ranges from 1 to 100, with 100 being the most vulnerable. See Appendix 1 from Cheung et al., 2007: [http://www.int-res.com/articles/suppl/m333p001_app.pdf](http://www.int-res.com/articles/suppl/m333p001_app.pdf)

Value

Returns a dataframe with three columns: ID, YEAR, and IVILandings.

If there are no observations in land for spatial scale \( j \) in year \( i \), indicator value is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other stability and resistance indicators: CVBiomass, allStability, biomassPerTL, meanMaxAge, meanMaxLength

Examples

# Compile data
data(land)
data(species.info)
# Calculate indicator
IVILandings(land, IVI.table = species.info, negative = TRUE, years = c(2014:2019))

---

## kemptonQ

*Calculates Kempton’s Biodiversity Index*

### Description

This function calculates Kempton’s Biodiversity index (Q) for \( j \) areas and \( i \) years.

### Usage

```r
kemptonQ(X, TL.table, percentiles = c(0.25, 0.75), minTL = 0, groups,
species.table = NULL, metric = "ABUNDANCE", years)
```

### Arguments

- **X**
  - A dataframe of fishery independent data derived from research vessel survey data or model output, with columns `YEAR`, `ID`, `SPECIES`, and `ABUNDANCE`. `YEAR` indicates the year the observation was recorded, `ID` is an area code indicating where the observation was recorded, `SPECIES` is a numeric code indicating the species sampled, and `ABUNDANCE` is the corresponding abundance (stratified and corrected for catchability as required).

- **TL.table**
  - A dataframe with columns `SPECIES` and the corresponding `TL` (trophic level). Entries in the `SPECIES` column should be the unique values of species codes in `X` (or a subset thereof). Other columns in `TL.table` are ignored.

- **percentiles**
  - The percentiles used to determine R1 and R2. Default is `percentiles = c(0.25, 0.75)`.

- **minTL**
  - Minimum trophic level for species included in the calculation. Default is `minTL = 0`.

- **groups**
  - A vector indicating the species group(s) for which to calculate the indicator. If `groups = "ALL"`, all species will be included; otherwise, each entry must be a character string matching the name of a column in `species.table`.

- **species.table**
  - A table where the column names match the entries in `groups`. Column entries are species codes indicating the species from `X` included in each group. `species.table` may also include columns for other species groups; these will be ignored. If `groups = "ALL"`, this table is not required. Default is `species.table = NULL`.

- **metric**
  - A character string indicating which column in `X` to use to calculate the indicator. Default is `metric = "ABUNDANCE"`.

- **years**
  - A vector of years for which to calculate indicator.
Details

Kempton’s Biodiversity Index \((Q)\) is a relative index of diversity calculated from the Kempton’s Q75 index developed for expressing species diversity.

\[
Q = S \cdot (p_2 - p_1) \cdot \log(R_2/R_1)
\]

\(S\) is the total number of species or functional groups, \(p_1\) and \(p_2\) are the lower and upper percentiles of interest and \(R_1\) and \(R_2\) are the corresponding lower and upper quartiles of the species abundance distribution. \(p_1\) and \(p_2\) are defaulted to 0.25 and 0.75, respectively (Kempton and Taylor, 1976).

Value

Returns a dataframe with columns ID and YEAR, and a column KemptonQ_minTL_group for each entry in groups.

If there is no data for spatial scale \(j\) in year \(i\), indicator values is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other biodiversity indicators: allBiodiversity, heips, hillN1, hillN2, margalef, pielouEvenness, shannon, speciesRichness

Examples

```r
# Compile data
data(X)
data(species.info)

# Calculate indicator
kemptonQ(X, TL.table = species.info, percentiles = c(.25, .75), minTL = 0,
groups = "ALL", metric = "ABUNDANCE", years = c(2014:2019))
```
**landings**

---

**land**

*Example commercial landings data*

---

**Description**

A dataframe of example commercial landings data for two areas (AREA1 and AREA2) from 2014 - 2019.

**Usage**

`land`

**Format**

This example data is a dataframe with 612 rows and 4 variables:

- **YEAR**: Year the observation was recorded
- **ID**: Area where the observation was recorded
- **SPECIES**: Numeric code indicating the species sampled (can be consistent with X or not; see vignette)
- **CATCH**: Corresponding landed weight (in the same units as BIOMASS in X)

**Details**

Indicators calculated using fishery dependent data (among other arguments): Intrinsic Vulnerability Index, Fishing-in-Balance, Diversity of the Target Species, Fishing Pressure, Landings, Marine Trophic Index, and Mean Trophic Index of Landings.

**Source**

This is made-up example data.

---

**landings**

*Calculates the Landings per fished group*

---

**Description**

This function calculates the commercial landings of predefined species groups for $j$ areas and $i$ years.

**Usage**

`landings(land, groups, species.table = NULL, years)`
Arguments

land A dataframe of commercial landings data with columns YEAR, ID, SPECIES and CATCH. YEAR indicates the year the landing was recorded, ID is an area code indicating where the landing was recorded, SPECIES is a numeric code indicating the species landed, and CATCH is the corresponding landed weight.

groups A vector indicating the species group(s) for which to calculate the indicator. If groups = "ALL", all species will be included; otherwise, each entry must be a character string matching the name of a column in species.table.

species.table A table with at least one column, where the column names match the entries in groups, and the column entries are species codes from land indicating which species are included that group. species.table may also include columns for other species groups; these will be ignored. If group = "ALL", this table is not required. Default is species.table = NULL.

years A vector of years for which to calculate indicator.

Details

Calculates the Landings of predefined species groups.

Value

Returns a dataframe with columns ID and YEAR, and a column landings_group for each entry in groups.

If there is no data for a given year, the indicator value is set to 0.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other fishing pressure indicators: allPressure, fishingPressure, meanTLLandings, speciesRichness

Examples

# Compile data
data(land)
data(species.table)

# Species of interest
landings.groups <- c("ALL", "CLUPEIDS.L", "FLATFISH.L", "GROUNDFISH.L")

# Calculate indicators
largeFishIndicator

Calculates the Large Fish Indicator

Description

This function calculates the Large Fish Indicator (LFI) for \( j \) areas and \( i \) years.

Usage

largeFishIndicator(X_length, group, species.table = NULL, metric = "BIOMASS", large.fish = 35, years)

Arguments

X_length A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, LENGTH, and BIOMASS. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, and SPECIES is a numeric code indicating the species sampled. LENGTH is the length class (cm) and BIOMASS is the corresponding abundance at length (stratified and corrected for catchability as required). Species for which there are no length data should be assigned LENGTH = -99. These observations are removed by the function.

group character string indicating which species to include in the indicator calculation. If group = "ALL", all species will be included; otherwise, group should match a column name in species.table.

species.table A table where the column names match the entries in groups. Column entries are species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored. If groups = "ALL", this table is not required. Default is species.table = NULL.

metric A character string indicating which column in X to use to calculate indicator. Default is metric = "BIOMASS".

large.fish Threshold for large fish (cm). Default is large.fish = 35 (i.e., large fish are those with \( X_{\text{length}} \cdot \text{LENGTH} \geq 35 \) cm).

years A vector of years for which to calculate indicator.

Details

Large Fish Indicator (LFI):

\[
LFI = \frac{\sum B_m (L > 35 \text{ cm})}{\sum B_m}
\]

\( B_m \) is biomass of individuals in a body size class centered at mass \( m \), and \( L \) is the length (cm) of an individual. This indicator describes the proportion (by weight) of the fish community that is larger than some length threshold (default here is 35 cm, i.e., the proportion of biomass occupying the top predator trophic level; Greenstreet and Rogers, 2006).
largeSpeciesIndicator

Value
Returns a dataframe with 3 columns, ID, YEAR, and LargeFishIndicator.
If there are no observations of large fish or no observations in X for spatial scale j in year i, indicator value is assigned NA.

Author(s)
Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

See Also
Other ecosystem structure and function indicators: allStructure, biomassRatio, communityCondition, largeSpeciesIndicator, meanTLCommunity

Examples
# Compile data
data(X_length)
data(species.table)

# Calculate indicator
largeFishIndicator(X_length, group = "FINFISH", species.table = species.table,
                   metric = "BIOMASS", years = c(2014:2019))

largeSpeciesIndicator  Calculates the Large Species Indicator

Description
This function calculates the Large Species Indicator (LSI) for j areas and i years.

Usage
largeSpeciesIndicator(X, group, species.table = NULL, maxlength.table,
                   max.length = 85, metric = "BIOMASS", years)
Arguments

\( \textbf{X} \)  
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns \texttt{YEAR}, \texttt{ID}, \texttt{SPECIES}, and \texttt{BIOMASS}. \texttt{YEAR} indicates the year the observation was recorded, \texttt{ID} is an area code indicating where the observation was recorded, \texttt{SPECIES} is a numeric code indicating the species sampled, and \texttt{BIOMASS} is the corresponding biomass (stratified and corrected for catchability as required).

\texttt{group}  
character string indicating which species to include in the indicator calculation. If \texttt{group = "ALL"}, all species will be included; otherwise, \texttt{group} should match a column name in \texttt{species.table}.

\texttt{species.table}  
A table where the column names match the entries in \texttt{groups}. Column entries are species codes indicating the species from \texttt{X} included in each group. \texttt{species.table} may also include columns for other species groups; these will be ignored. If \texttt{groups = "ALL"}, this table is not required. Default is \texttt{species.table = NULL}.

\texttt{maxlength.table}  
A dataframe with columns \texttt{SPECIES} and \texttt{MAXLENGTH}, the maximum recorded length of the corresponding species. Entries in the \texttt{SPECIES} column should be the unique values of species codes in \texttt{X} (or a subset thereof). Other columns in \texttt{maxlength.table} are ignored.

\texttt{max.length}  
The threshold for large species (cm). Default is \texttt{max.length = 85} (i.e., large species are those with \texttt{MAXLENGTH} \( \geq 85 \) cm).

\texttt{metric}  
A character string indicating which column in \texttt{X} to use to calculate indicator. Default is \texttt{metric = "BIOMASS"}.

\texttt{years}  
A vector of years for which to calculate indicator.

Details

Large Species Indicator (LSI):

\[
LSI = \frac{\Sigma B_i (L_{max} > 85cm)}{\Sigma B_i}
\]

where \( B_i \) is biomass of individual species, \( i \), and \( L_{max} \) is the maximum asymptotic length in cm (threshold default here is 85 cm; Shin et al., 2010).

Value

Returns a dataframe with 3 columns. \texttt{ID}, \texttt{YEAR}, and \texttt{LargeSpeciesIndicator}.

If there are no observations of large species or no observations in \texttt{X} for spatial scale \( j \) in year \( i \), indicator value is assigned \texttt{NA}.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy
References


See Also

Other ecosystem structure and function indicators: allStructure, biomassRatio, communityCondition, largeFishIndicator, meanTLCommunity

Examples

data(X)
data(species.table)
largeSpeciesIndicator(X, group = "ALL", species.table = species.table, maxlength.table = species.info, max.length=85, metric = "BIOMASS", years = c(2014:2019))

---

**Length.Weight**

*Example length-weight data*

**Description**

A dataframe of example length-weight data for two areas (AREA1 and AREA2) from 2014 - 2019.

**Usage**

Length.Weight

**Format**

This example data is a dataframe with 98 436 rows and 5 variables:

YEAR Year the observation was recorded
ID Area where the observation was recorded
SPECIES Numeric code indicating the species sampled
LENGTH Length (class) 1 cm intervals
WEIGHT Corresponding weight of sampled fish
Details
Indicator calculated using length-weight data (among other arguments): Community Condition

Source
This is example data was modified from Fisheries and Oceans Canada summer research vessel trawl survey for the Scotian Shelf.

margalef  Calculates Margalef’s Species Richness

Description
This function calculates Margalef’s Species Richness for j areas and i years.

Usage
margalef(X, groups, species.table = NULL, metric = "ABUNDANCE", years)

Arguments
X A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, and ABUNDANCE. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and ABUNDANCE is the corresponding abundance (stratified and corrected for catchability as required).
groups A vector indicating the species group(s) for which to calculate the indicator. If groups = "ALL", all species will be included; otherwise, each entry must be a character string matching the name of a column in species.table.
species.table A table where the column names match the entries in groups. Column entries are species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored. If groups = "ALL", this table is not required. Default is species.table = NULL.
metric A character string indicating which column in X to use to calculate the indicator. Default is metric = "ABUNDANCE".
years A vector of years for which to calculate indicator.

Details
Margalef’s Species Richness:
\[ S_{Marg} = \frac{(S_y - 1)}{\log(F_y)} \]

\( S_y \) is the count of the number of species recorded in all trawl catches collected in year \( y \). \( F \) is the total count of all individuals caught in year \( y \) (Margalef, 1958).
**Value**

Returns a dataframe with columns ID and YEAR, and a column MargalefRichness_group for each entry in groups.

If there is no data for spatial scale \( j \) in year \( i \), indicator values are assigned NA.

**Author(s)**

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

**References**


**See Also**

Other biodiversity indicators: `allBiodiversity`, `heips`, `hillN1`, `hillN2`, `kemptonQ`, `pielouEvenness`, `shannon`, `speciesRichness`

**Examples**

```r
data(X)
margalef(X, groups = c("ALL", "GROUNDFISH"), metric = "ABUNDANCE", years = c(2014:2019))
```

**Description**

This function calculates the Mean Length of the Community weighted by biomass or abundance for \( j \) areas and \( i \) years.

**Usage**

```r
meanLengthCommunity(X_length, metric, years)
```

**Arguments**

- `X_length`: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns YEAR, ID, SPECIES, LENGTH, and BIOMASS. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, and SPECIES is a numeric code indicating the species sampled. LENGTH is the length class (cm) and BIOMASS is the corresponding abundance at length (stratified and corrected for catchability as required). Species for which there are no length data should be assigned LENGTH = -99. These observations are removed by the function.
meanLengthCommunity

metric A character string indicating which column in \( X \) to use to calculate indicator.
years A vector of years for which to calculate indicator.

Details

\[
\text{MeanLength} = \frac{\sum (\text{Length}_m \times \text{metric}_i)}{\sum \text{metric}_j}
\]

where \( \text{Length}_m \) is the length (cm) of an individual in size class \( m \), \( \text{metric}_i \) is the biomass or abundance of species \( i \) and \( \text{metric}_j \) is the total biomass or abundance of the community (Shin et al., 2010).

Value

Returns a dataframe with 3 columns. ID, YEAR, and MeanLength_metric.

If there is no data for spatial scale \( j \) in year \( i \), indicator value is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


Examples

data(X_length)
# Weighted by abundance
meanLengthCommunity(X_length, metric = "ABUNDANCE", years = c(2014:2019))
# Weighted by biomass
meanLengthCommunity(X_length, metric = "BIOMASS", years = c(2014:2019))
**meanMaxAge**

*Calculates the Mean Maximum Age of fish in the community*

**Description**

This function calculates the Mean Maximum Age (MMA) of fish in the community for *j* areas and *i* years.

**Usage**

`meanMaxAge(X, age.table, metric = "BIOMASS", years)`

**Arguments**

- **X**
  A dataframe of fishery independent data derived from research vessel survey data or model output, with columns `YEAR`, `ID`, `SPECIES`, and `BIOMASS`. `YEAR` indicates the year the observation was recorded, `ID` is an area code indicating where the observation was recorded, `SPECIES` is a numeric code indicating the species sampled, and `BIOMASS` is the corresponding biomass (stratified and corrected for catchability as required).

- **age.table**
  A dataframe with columns `SPECIES` and `MAXAGE`, the maximum recorded age of the corresponding species. Entries in the `SPECIES` column should be the unique values of species codes in `X` (or a subset thereof). Other columns in `age.table` are ignored.

- **metric**
  A character string indicating which column in `X` to use to calculate indicator. Default is `metric = "BIOMASS"`.

- **years**
  A vector of years for which to calculate indicator.

**Details**

Mean Maximum Age:

\[
MeanMaximumAge = \frac{\sum (age_{max,i} * B_i)}{\sum B_i}
\]

where the sum is over all species *i*, and *B_i* is biomass of species *i*. The mean lifespan or longevity is considered to be a fixed parameter per species. Lifespan may vary under fishing pressure, so Shin et al. (2010) adopted the maximum longevity observed for each species \(age_{max,i}\). The variation of this indicator captures changes in species composition, and therefore changes in average lifespan (Shin et al., 2010).

**Value**

Returns a dataframe with 3 columns: `ID`, `YEAR`, and `MeanLifespan`.

If there is no data for spatial scale *j* in year *i*, indicator value is assigned NA.
Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other stability and resistance indicators: CVBiomass, IVILandings, allStability, biomassPerTL, meanMaxLength

Examples

# Compile data
data(X)
data(species.info)

# Calculate indicator
meanMaxAge(X, age.table = species.info, metric = "BIOMASS", years = c(2014:2019))

meanMaxLength

*Calculates the Mean Maximum Length of fish in the community*

Description

This function calculates the Mean Maximum Length of fish in the community weighted by biomass or abundance for \( j \) areas and \( i \) years.

Usage

\[
\text{meanMaxLength}(X, \text{group, species.table = NULL, maxlen.length.table, metric, years})
\]
**Arguments**

- **X**
  A dataframe of fishery independent data derived from research vessel survey data or model output, with columns `YEAR`, `ID`, `SPECIES`, and `BIOMASS`. `YEAR` indicates the year the observation was recorded, `ID` is an area code indicating where the observation was recorded, `SPECIES` is a numeric code indicating the species sampled, and `BIOMASS` is the corresponding biomass (stratified and corrected for catchability as required).

- **group**
  Character string indicating which species to include in the indicator calculation. If `group = "ALL"`, all species will be included; otherwise, group should match a column name in `species.table`.

- **species.table**
  A table where the column names match the entries in `groups`. Column entries are species codes indicating the species from `X` included in each group. `species.table` may also include columns for other species groups; these will be ignored. If `groups = "ALL"`, this table is not required. Default is `species.table = NULL`.

- **maxlength.table**
  A dataframe with columns `SPECIES` and `MAXLENGTH`, the maximum recorded length of the corresponding species. Entries in the `SPECIES` column should be the unique values of species codes in `X` (or a subset thereof). Other columns in `maxlength.table` are ignored.

- **metric**
  A character string indicating which column in `X` to use to calculate indicator. Default is `metric = "BIOMASS"`.

- **years**
  A vector of years for which to calculate indicator.

**Details**

Mean Maximum Length:

\[ MeanMaximumLength = \frac{\sum(L_{max,i} \times M_i)}{\sum M_i} \]

where \( L_{max,i} \) is the maximum asymptotic length (cm) of species \( i \), and \( M_i \) is biomass or abundance of species \( i \) (excluding invertebrates; Shin et al., 2005).

**Value**

Returns a dataframe with 3 columns. `ID`, `YEAR`, and `MMLength_metric`.

If there is no data for spatial scale \( j \) in year \( i \), indicator value is assigned `NA`.

**Author(s)**

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

**References**


meanTLCommunity

Calculates the Mean Trophic Level of the community

Description

This function calculates the Mean Trophic Level of the community weighted by biomass for \( j \) areas and \( i \) years.

Usage

```
meanTLCommunity(X, TL.table, metric = "BIOMASS", years)
```

Arguments

- **X**: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns \( \text{YEAR}, \text{ID}, \text{SPECIES}, \) and \( \text{BIOMASS} \). \( \text{YEAR} \) indicates the year the observation was recorded, \( \text{ID} \) is an area code indicating where the observation was recorded, \( \text{SPECIES} \) is a numeric code indicating the species sampled, and \( \text{BIOMASS} \) is the corresponding biomass (stratified and corrected for catchability as required).
- **TL.table**: A dataframe with columns \( \text{SPECIES} \) and the corresponding \( \text{TL} \) (trophic level). Entries in the \( \text{SPECIES} \) column should be the unique values of species codes in \( X \) (or a subset thereof). Other columns in \( \text{TL.table} \) are ignored.
- **metric**: A character string indicating which column in \( X \) to use to calculate indicator. Default is \( \text{metric = "BIOMASS"} \).
- **years**: A vector of years for which to calculate indicator.
Details

Mean trophic level (TL):

\[ TL = \frac{\sum(TL_i \times B_i)}{\sum B_i} \]

\( TL_i \) is trophic level of species \( i \), and \( B_i \) is the biomass of species \( i \).

This indicator is based on trophic levels of all species with available biomass time series, weighted by annual species-specific biomass, to reflect the structure of the community (Christensen, 1998).

Value

Returns a dataframe with 3 columns: ID, YEAR, and MeanTLCommunity.

If there is no data for spatial scale \( j \) in year \( i \), indicator value is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other ecosystem structure and function indicators: allStructure, biomassRatio, communityCondition, largeFishIndicator, largeSpeciesIndicator

Examples

# Compile data
data(X)
data(species.info)

# Calculate indicator
meanTLCommunity(X, TL.table = species.info, metric = "BIOMASS", years = c(2014:2019))
meanTLLandings  

Calculates the Mean Trophic Level or Marine Trophic Index of fisheries landings

Description

This function calculates the Mean Trophic Level or Marine Trophic Index of fisheries landings for \( j \) areas and \( i \) years.

Usage

meanTLLandings(land, TL.table, minTL = 0, years)

Arguments

- **land**: A dataframe of commercial landings data with columns \( \text{YEAR} \), \( \text{ID} \), \( \text{SPECIES} \) and \( \text{CATCH} \). \( \text{YEAR} \) indicates the year the landing was recorded, \( \text{ID} \) is an area code indicating where the landing was recorded, \( \text{SPECIES} \) is a numeric code indicating the species landed, and \( \text{CATCH} \) is the corresponding landed weight.
- **TL.table**: A dataframe with columns \( \text{SPECIES} \) and the corresponding \( TL_{\text{LAND}} \) (trophic level). Entries in the \( \text{SPECIES} \) column should be the unique values of species codes in \( \text{land} \) (or a subset thereof). Other columns in \( \text{TL.table} \) are ignored.
- **minTL**: The minimum trophic level of species to include. Set \( \text{minTL} = 0 \) to calculate the mean trophic level of the landings; Set \( \text{minTL} = 3.25 \) to calculate the marine trophic index. Default is \( \text{minTL} = 0 \).
- **years**: A vector of years for which to calculate indicator.

Details

Mean trophic level of fisheries landings \( (TL_{\text{Land}}) \):

\[
TL_{\text{Land}} = \frac{\sum(TL_i * Y_i)}{Y}
\]

where \( TL_i \) is the trophic level of species \( i \), \( Y_i \) is the landings of species \( i \), and \( Y \) is the total landings of all species. Trophic Level of individual species can be estimated either through an Ecopath model or dietary analysis, or taken from a global database such as Fishbase.

This indicator captures the average trophic level of the species exploited in the fishery. In general, it reflects a transition from long-lived, high trophic level, demersal fish toward short-lived, low trophic level pelagic fish and invertebrates (Pauly et al., 1998).

The marine trophic index is calculated similarly to \( TL_{\text{Land}} \), but only includes species with trophic level greater than or equal to an explicitly stated trophic level \( \text{minTL} \). For instance, Pauly and Watson 2005 adopted a trophic level \( \text{minTL} \) of 3.25 to emphasize changes in the relative abundance of higher trophic level fishes, and Shannon et al. 2014 used a \( \text{minTL} \) of 4.0 to examine changes within the apex predator community. If used in this way, this indicator highlights changes in the relative abundance of the more threatened high-trophic level fishes (Pauly et al., 1998).
Value

Returns a dataframe with three columns: ID, YEAR, and if minTL = 0: MeanTL.Landings, if minTL = 3.25: MTI.Landings, or if minTL is a different value: MeanTL.Landings_minTL.

If there are no observations in land for spatial scale $j$ in year $i$, indicator value is set to NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other fishing pressure indicators: allPressure, fishingPressure, landings, speciesRichness

Examples

# Compile data
data(land)
data(species.info)

# Calculate indicators
# Mean trophic level of landings
meanTLLandings(land, TL.table = species.info, minTL = 0, years = c(2014:2019))
# Marine trophic index
meanTLLandings(land, TL.table = species.info, minTL = 3.25, years = c(2014:2019))

---

pielouEvenness  Calculates Pielou’s Species Evenness

Description

This function calculates Pielou’s Species Evenness for $j$ areas and $i$ years.
Usage

`pielouEvenness(X, groups, species.table = NULL, metric = "ABUNDANCE", years)`

Arguments

**X**
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns `YEAR`, `ID`, `SPECIES`, and `ABUNDANCE`. `YEAR` indicates the year the observation was recorded, `ID` is an area code indicating where the observation was recorded, `SPECIES` is a numeric code indicating the species sampled, and `ABUNDANCE` is the corresponding abundance (stratified and corrected for catchability as required).

**groups**
A vector indicating the species group(s) for which to calculate the indicator. If `groups = "ALL"`, all species will be included; otherwise, each entry must be a character string matching the name of a column in `species.table`.

**species.table**
A table where the column names match the entries in `groups`. Column entries are species codes indicating the species from `X` included in each group. `species.table` may also include columns for other species groups; these will be ignored. If `groups = "ALL"`, this table is not required. Default is `species.table = NULL`.

**metric**
A character string indicating which column in `X` to use to calculate the indicator. Default is `metric = "ABUNDANCE"`.

**years**
A vector of years for which to calculate indicator.

Details

Pielou’s Species Evenness:

\[ J' = -\sum p_i \ln(p_i)/\ln(S) \]

\( p_i \) is the proportion of the total sample contributed by the i(th) species and \( S \) is the number of species recorded in the sample. Pielou’s Index is the Shannon-Weiner Index computed for the sample \( S \) and represents a measure of evenness of the community (Pielou, 1966).

Value

Returns a dataframe with columns `ID` and `YEAR`, and a column `PielouEvenness_group` for each entry in `groups`.

If there is no data for spatial scale \( j \) in year \( i \), indicator values is assigned \( NA \).

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy
resourcePotential

References

See Also
Other biodiversity indicators: allBiodiversity, heips, hillN1, hillN2, kemptonQ, margalef, shannon, speciesRichness

Examples

```
data(X)
pieluEvenness(X, groups = "ALL", species.table = NULL, metric = "ABUNDANCE",
years = c(2014:2019))
```

resourcePotential

**Calculates the Resource Potential of species groups**

Description
This function calculates the Biomass or Abundance of a pre-defined group of species for \(j\) areas and \(i\) years.

Usage
```
resourcePotential(X, groups, species.table = NULL, metric = "BIOMASS",
years)
```

Arguments
- **X**: A dataframe of fishery independent data derived from research vessel survey data or model output, with columns `YEAR`, `ID`, `SPECIES`, and `BIOMASS` or `ABUNDANCE`. `YEAR` indicates the year the observation was recorded, `ID` is an area code indicating where the observation was recorded, `SPECIES` is a numeric code indicating the species sampled, and `BIOMASS/ABUNDANCE` is the corresponding biomass/abundance (stratified and corrected for catchability as required).
- **groups**: A vector indicating the species group(s) for which to calculate the indicator. If `groups` = "ALL", all species will be included; otherwise, each entry must be a character string matching the name of a column in `species.table`. 
resourcePotential

species.table  A table where the column names match the entries in groups. Column entries are species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored. If groups = "ALL", this table is not required. Default is species.table = NULL.

metric  A character string indicating which column in X to use to calculate indicator. Default is metric = "BIOMASS".

years  A vector of years for which to calculate indicator.

Details

This indicator reflects temporal dynamics of species groups.

Value

Returns a dataframe with columns ID and YEAR, and a column metric_group (e.g., BIOMASS_FINFISH) for each entry in groups.

If there is no data for a given year, the indicator value will be NA for that year.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References


See Also

Other resource potential indicators: allPotential, fishingInBalance

Examples

# Compile data
data(X)
data(species.table)

# Calculate total abundance and biomass
resourcePotential(X, groups = "ALL", metric = "ABUNDANCE", years = c(2014:2019))
resourcePotential(X, groups = "ALL", metric = "BIOMASS", years = c(2014:2019))

# Calculate biomass of trophic guilds
trophicguild.groups <- c("LBENTHIVORE", "MBENTHIVORE", "PISCIVORE", "PLANKTIVORE", "ZOOPISCIVORE")
resourcePotential(X, groups = trophicguild.groups,
                 species.table = species.table, metric = "BIOMASS", years = c(2014:2019))

# Calculate biomass of fished groups
resource.groups <- c("ALL", "CLUPEIDS", "FINFISH", "FLATFISH", "FORAGE", "GADOIDS", "GROUNDFISH")
resourcePotential(X, groups = resource.groups, species.table = species.table,
metric = "BIOMASS", years = c(2014:2019))

shannon

Calculates Shannon’s Index of Diversity

Description
This function calculates Shannon’s Index of Diversity for \( j \) areas and \( i \) years.

Usage
shannon(X, groups, species.table = NULL, metric = "ABUNDANCE", years)

Arguments
X
A dataframe of fishery independent data derived from research vessel survey data or model output, with columns \( \text{YEAR}, \text{ID}, \text{SPECIES}, \text{ABUNDANCE} \). \( \text{YEAR} \) indicates the year the observation was recorded, \( \text{ID} \) is an area code indicating where the observation was recorded, \( \text{SPECIES} \) is a numeric code indicating the species sampled, and \( \text{ABUNDANCE} \) is the corresponding abundance (stratified and corrected for catchability as required).

groups
A vector indicating the species group(s) for which to calculate the indicator. If \( \text{groups} = \text{"ALL"} \), all species will be included; otherwise, each entry must be a character string matching the name of a column in \( \text{species.table} \).

species.table
A table where the column names match the entries in \( \text{groups} \). Column entries are species codes indicating the species from \( \text{X} \) included in each group. \( \text{species.table} \) may also include columns for other species groups; these will be ignored. If \( \text{groups} = \text{"ALL"} \), this table is not required. Default is \( \text{species.table} = \text{NULL} \).

metric
A character string indicating which column in \( \text{X} \) to use to calculate the indicator. Default is \( \text{metric} = \text{"ABUNDANCE"} \).

years
A vector of years for which to calculate indicator.

Details
Shannon’s index of diversity (\( H' \)):
\[
H' = -\sum p_i \ln(p_i)
\]

\( p_i \) is the proportion of the total sample contributed by the \( i \)(th) species and \( S \) is the number of species recorded in the sample. This index is sensitive to the number of species recorded in the sample (Magurran, 1988).

Value
Returns a dataframe with columns \( \text{ID} \) and \( \text{YEAR} \), and a column \( \text{ShannonDiversity_group} \) for each entry in \( \text{groups} \).

If there is no data for spatial scale \( j \) in year \( i \), indicator values is assigned NA.
species.info

Author(s)
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References

See Also
Other biodiversity indicators: allBiodiversity, heips, hillN1, hillN2, kemptonQ, margalef, pielouEvenness, speciesRichness

Examples
data(X)
shannon(X, groups = c("ALL", "FINFISH"), metric = "ABUNDANCE", years = c(2014:2019))

Description
Additional species information required to calculate several indicators (see vignette).

Usage
species.info

Format
This example data is a dataframe with 306 rows and 6 variables:

SPECIES Species codes
TL Trophic level of species caught in fishery independent surveys
MAXLENGTH Maximum recorded length of of species caught in fishery independent surveys
MAXAGE Maximum recorded age of of species caught in fishery independent surveys
IVI Vulnerability of commercial species
TL_LAND Trophic level of commercial species
**Source**

This is example data using species that are of interest in the Scotian Shelf Bioregion.

---

**species.table**

*Example input for argument species.table*

---

**Description**

A dataframe of the species groups of interest and the species included in each.

**Usage**

species.table

**Format**

This example data is a dataframe with 7000 rows and 15 variables:

- **column names** Each column is named after a species group of interest
- **column entries** The column entries are the species codes of species included in the group

**Source**

This is example data using species groups that are of interest for the Scotian Shelf Bioregion.

---

**speciesRichness**

*Calculates Species Richness of the community or the Diversity of Target Species*

---

**Description**

This function counts the number of species recorded in fishery independent survey data or commercial landings data for $i$ years and $j$ areas.

**Usage**

speciesRichness(X, groups, species.table = NULL, metric, years)
Arguments

X
A dataframe of fishery independent data derived from research vessel survey data or model output, OR commercial landings data. Fishery independent survey data has columns YEAR, ID, SPECIES, and ABUNDANCE and/or BIOMASS. YEAR indicates the year the observation was recorded, ID is an area code indicating where the observation was recorded, SPECIES is a numeric code indicating the species sampled, and ABUNDANCE/BIOMASS is the corresponding abundance/biomass (stratified and corrected for catchability as required).

Similarly, commercial landings data should have columns YEAR, ID, SPECIES are as above, and CATCH is the corresponding landed weight.

groups
A vector indicating the species group(s) for which to calculate the indicator. If groups = "ALL", all species will be included; otherwise, each entry must be a character string matching the name of a column in species.table.

species.table
A table where the column names match the entries in groups. Column entries are species codes indicating the species from X included in each group. species.table may also include columns for other species groups; these will be ignored. If groups = "ALL", this table is not required. Default is species.table = NULL.

metric
A character string indicating which column in X to use to calculate the indicator. Default is metric = "ABUNDANCE".

years
A vector of years for which to calculate indicator.

Details

Two useful species richness indicators are: "Species Richness" (S) of the surveyed community in an area and "Diversity of the Target Species" (TS) in the commercial fishery, which is a measure of the distribution of fishing pressure.

Species richness (S_y) is the count of the number of species recorded in all research vessel trawl surveys collected in year y for a given area (Hurlbert, 1971).

The diversity of the target species for year y (T S_y) is the count of the number of target species recorded in all trawl catches collected in that year for a given area.

Value

Returns a dataframe with columns ID and YEAR, and if metric = "ABUNDANCE", a column SpeciesRichness_group for each entry in groups OR if metric = "CATCH", a column DiversityTargetSpp_group for each entry in groups.

If there is no data for spatial scale j in year i, indicator values is assigned NA.

Author(s)

Danielle Dempsey <Danielle.Dempsey@dfo-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy
References


See Also

Other biodiversity indicators: allBiodiversity, heips, hillN1, hillN2, kemptonQ, margalef, pielouEvenness, shannon

Other fishing pressure indicators: allPressure, fishingPressure, landings, meanTLLandings

Examples

# Calculate species richness (community)
data(X)
speciesRichness(X, groups = "ALL", metric = "BIOMASS", years = c(2014:2019))

# Calculate diversity of target species
data(land)
speciesRichness(land, groups = "ALL", metric = "CATCH", years = c(2014:2019))

Description

A dataframe of example fishery independent survey data for two areas (AREA1 and AREA2) from 2014 - 2019.

Usage

X

Format

This example data is a dataframe with 2003 rows and 5 variables:

YEAR  Year the observation was recorded
ID Area where the observation was recorded
SPECIES Numeric code indicating the species sampled
ABUNDANCE Abundance of the species sampled, stratified and corrected for catchability
BIOMASS Biomass of the sampled species, stratified and corrected for catchability
Details

Indicators calculated using fishery independent data (among other arguments): Heip’s Evenness Index, Hill’s N1, Hill’s N2, Kempton’s Q, Margalef’s Species Richness, Pielou’s Species Evenness, Shannon’s Diversity Index, Biomass ratio(s), Abundance/Biomass of Species Groups, Large Species Indicator, Mean Trophic Level of the Community, CV of Biomass, Mean Maximum Lifespan, Mean Maximum Length, and Fishing Pressure.

Source

This is made-up example data modified from Fisheries and Oceans Canada summer research vessel trawl survey for the Scotian Shelf Bioregion.

---

\textit{X\_length}

\textit{Example length-based fishery independent survey data}

Description

A dataframe of example length-based fishery independent survey data for two areas (AREA1 and AREA2) from 2014 - 2019.

Usage

\texttt{X\_length}

Format

This example data is a dataframe with 14378 rows and 6 variables:

- \texttt{YEAR} Year the observation was recorded
- \texttt{ID} Area where the observation was recorded
- \texttt{SPECIES} Numeric code indicating the species sampled
- \texttt{LENGTH} Length class of sample species, in cm
- \texttt{ABUNDANCE} Abundance of the species sampled, stratified and corrected for catchability
- \texttt{BIOMASS} Biomass of the sampled species, stratified and corrected for catchability

Details

Indicators calculated using length-based fishery independent survey data (among other arguments): Community Condition, Large Fish Indicator, Mean Length.

Source

This is made-up example data modified from Fisheries and Oceans Canada summer research vessel trawl survey for the Scotian Shelf Bioregion.
Index

*Topic datasets
  example_inds, 25
  land, 42
  Length_Weight, 47
  species.info, 62
  species.table, 63
  X, 65
  X_length, 66

allBiodiversity, 5, 35, 36, 38, 41, 49, 59, 62, 65
allPotential, 7, 31, 60
allPressure, 9, 33, 43, 57, 65
allStability, 12, 19, 24, 39, 52, 54
allStructure, 14, 21, 23, 45, 47, 55

biomassPerTL, 14, 18, 24, 39, 52, 54
biomassRatio, 17, 19, 23, 45, 47, 55

communityCondition, 17, 21, 23, 45, 47, 55
CVBiomass, 14, 19, 23, 39, 52, 54

element_inds, 25
extractAll, 25

fishingInBalance, 9, 30, 60
fishingPressure, 11, 32, 43, 57, 65

heips, 7, 34, 36, 38, 41, 49, 59, 62, 65
hillN1, 7, 35, 36, 38, 41, 49, 59, 62, 65
hillN2, 7, 35, 36, 37, 41, 49, 59, 62, 65

IVILandings, 14, 19, 24, 38, 52, 54
kemptonQ, 7, 35, 36, 38, 40, 49, 59, 62, 65

land, 42
landings, 11, 33, 42, 57, 65
largeFishIndicator, 17, 21, 23, 44, 47, 55
largeSpeciesIndicator, 17, 21, 23, 45, 49, 55

Length_Weight, 47
margalef, 7, 35, 36, 38, 41, 48, 59, 62, 65
marindicators-package, 2
meanLengthCommunity, 49
meanMaxAge, 14, 19, 24, 39, 51, 54
meanMaxLength, 14, 19, 24, 39, 52, 52
meanTLLandings, 11, 33, 43, 56, 65

pielouEvenness, 7, 35, 36, 38, 41, 49, 57, 62, 65

resourcePotential, 9, 31, 59

shannon, 7, 35, 36, 38, 41, 49, 59, 61, 65
species.info, 62
species.table, 63
speciesRichness, 7, 11, 33, 35, 36, 38, 41, 43, 49, 57, 59, 62, 63

X, 65
X_length, 66