

Package ‘marindicators’

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Title Marine Ecosystem and Fishing Pressure Indicators

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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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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**.

ATTRIBUTE	INDICATOR	FUNCTION
Biodiversity	All Biodiversity indicators	allBiodiversity()
Biodiversity	Margalef’s Species Richness	margalef()
Biodiversity	Species Richness	speciesRichness()
Biodiversity	Shannon’s Diversity Index	shannon()
Biodiversity	Hill’s Diversity Index	hillN1()
Biodiversity	Kempton’s Q	kemptonQ()
Biodiversity	Hill’s Dominance	hillN2()
Biodiversity	Pielou’s Species Evenness	pielouEvenness()
Biodiversity	Heips Evenness Index	heips()
Structure & Functioning	All Structure & Functioning indicators	allStructure()
Structure & Functioning	Large Fish Indicator	largeFishIndicator()
Structure & Functioning	Large Species Indicator	largeSpeciesIndicator()

Structure & Functioning	Proportion of Predatory Fish	biomassRatio()
Structure & Functioning	Biomass of Trophic Guilds¹	resourcePotential
Structure & Functioning	Biomass Ratio(s)	biomassRatio()
Structure & Functioning	Mean Length (weighted by abundance)	meanLengthCommunity()
Structure & Functioning	Mean Length (weighted by biomass)	meanLengthCommunity()
Structure & Functioning	Mean Trophic Level of Community	meanTLCommunity()
Structure & Functioning	Community Condition	communityCondition()
Structure & Functioning	Trophic Guild Condition²	communityCondition()
Stability & Resistance	All Stability & Resistance indicators	allStability()
Stability & Resistance	Mean Lifespan	meanMaxAge()
Stability & Resistance	Mean Max Length (weighted by abundance)	meanMaxLength()
Stability & Resistance	Mean Max Length (weighted by biomass)	meanMaxLength()
Stability & Resistance	Intrinsic Vulnerability Index of Landings	IVILandings()
Stability & Resistance	Biomass per Trophic Level³	biomassPerTL()
Stability & Resistance	Coefficient of Variation of Biomass	CVBiomass()
Resource Potential	All Resource Potential indicators	allPotential()
Resource Potential	Biomass	resourcePotential()
Resource Potential	Biomass of Key Groups⁴	resourcePotential()
Resource Potential	Fishing in Balance	fishingInBalance()
Fishing Pressure	All Fishing Pressure indicators	allPressure()
Fishing Pressure	Fishing Pressure	fishingPressure()
Fishing Pressure	Fishing Pressure on Groups⁵	fishingPressure()
Fishing Pressure	Marine Trophic Index	meanTLLandings()
Fishing Pressure	Mean Trophic Level of Landings	meanTLLandings()
Fishing Pressure	Diversity of Target Species	speciesRichness()
Fishing Pressure	Landings	landings()
Fishing Pressure	Landings of Fished Groups⁶	landings()

¹Biomass of piscivores and zoopiscivores

²Condition of large benthivores, medium benthivores, piscivores, and zoopiscivores

³Biomass at trophic level 2

⁴Biomass of invertebrates, gadoids, flatfish, and skates

⁵Fishing Pressure on clupeids

⁶Landings 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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

<code>allBiodiversity</code>	<i>Calculates all Biodiversity indicators</i>
------------------------------	---

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

```
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

<code>X</code>	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).
<code>metric</code>	A character string indicating which column in <code>X</code> to use to calculate the indicators. Default is <code>metric = "ABUNDANCE"</code> .
<code>groups</code>	A vector indicating the species group(s) for which to calculate the indicators. If <code>groups = "ALL"</code> , all species will be included; otherwise, each entry must be a character string matching the name of a column in <code>species.table</code> . Default is <code>groups = "ALL"</code> .

<code>species.table</code>	A table where the column names match the entries in <code>groups</code> . Column entries are species codes indicating the species from <code>X</code> included in each group. <code>species.table</code> may also include columns for other species groups; these will be ignored. If <code>groups = "ALL"</code> , this table is not required. Default is <code>species.table = NULL</code> .
<code>TL.table</code>	A dataframe with columns <code>SPECIES</code> and the corresponding <code>TL</code> (trophic level). Entries in the <code>SPECIES</code> column should be the unique values of species codes in <code>X</code> (or a subset thereof). Other columns in <code>TL.table</code> are ignored. If <code>TL.table = NULL</code> , Kempton's <code>Q</code> will not be calculated.
<code>percentiles</code>	The percentiles used to determine <code>R1</code> and <code>R2</code> for calculating Kempton's <code>Q</code> . Default is <code>percentiles = c(0.25, 0.75)</code> .
<code>minTL</code>	Minimum trophic level for species included to calculate Kempton's <code>Q</code> . Default is <code>minTL = 0</code> .
<code>years</code>	A vector of years for which to calculate indicators.
<code>raw</code>	A logical value. If <code>raw = TRUE</code> , the raw indicator values are returned by the function. If <code>raw = FALSE</code> , the raw indicator values are not returned. Default is <code>raw = TRUE</code> . Either <code>raw</code> or <code>std</code> must be <code>TRUE</code> .
<code>std</code>	A logical value. If <code>std = TRUE</code> , 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 <code>std = FALSE</code> , the standardized indicator values are not returned. Default is <code>std = TRUE</code> . Either <code>raw</code> or <code>std</code> must be <code>TRUE</code> .
<code>glob.env</code>	Logical value indicating whether to return output to global environment. Default is <code>glob.env = TRUE</code> .
<code>export.path</code>	File path indicating where to save a <code>.csv</code> file of calculated indicators (named <code>biodiversity_export.id.csv</code> ; see below). If <code>export.file = NULL</code> , the indicator dataframe will not be exported as a <code>.csv</code> file. Default is <code>export.path = NULL</code> .
<code>export.id</code>	Character string to modify the name of the <code>.csv</code> file (if <code>export.path</code> is specified), for example an area name or date of analysis. The exported <code>.csv</code> file is named <code>biodiversity_export.id.csv</code> . Default is <code>export.id = NULL</code> .

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 "GROUND FISH") 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.

Author(s)

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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, 0.75), 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

```
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.

<code>species.table</code>	A table where the column names match the entries in <code>resource.groups</code> . Column entries are the species codes indicating the species from X included in each group. <code>species.table</code> may also include columns for other species groups; these will be ignored.
<code>speciesinfo.table</code>	A table with columns <code>SPECIES</code> and the corresponding <code>TL_LAND</code> (trohic level of landed species). Entries in the <code>SPECIES</code> column should be the unique values of species codes in <code>land</code> (or a subset thereof). Other columns will be ignored.
<code>resource.groups</code>	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 <code>species.table</code> . If <code>resource.groups = NULL</code> , these indicators will not be calculated.
<code>minTL</code>	The minimum trohic level of species to include to calculate FiB. If <code>minTL = NULL</code> , FiB will not be calculated. Default is <code>minTL = 0</code> .
<code>TE</code>	Trophic efficiency, used to calculate FiB. Default is <code>TE = 0.1</code> , i.e., a trohic efficiency of 10%. If <code>TE = NULL</code> , FiB will not be calculated.
<code>base.start</code>	Year indicating the beginning of the baseline period for calculating FiB. The average landings and average mean trohic level of the landings over the baseline period are used as baseline values to calculate FiB. <code>land</code> must include data for the baseline period. If <code>base.start = NULL</code> , FiB will not be calculated.
<code>base.end</code>	Year indicating the end of the baseline period for calculating FiB. The average landings and average mean trohic level of the landings over the baseline period are used as baseline values to calculate FiB. <code>land</code> must include data for the baseline period. If <code>base.end = NULL</code> , FiB will not be calculated.
<code>years</code>	A vector of years for which to calculate indicators.
<code>raw</code>	A logical value. If <code>raw = TRUE</code> , the raw indicator values are returned by the function. If <code>raw = FALSE</code> , the raw indicator values are not returned. Default is <code>raw = TRUE</code> . Either <code>raw</code> or <code>std</code> must be <code>TRUE</code> .
<code>std</code>	A logical value. If <code>std = TRUE</code> , 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 <code>std = FALSE</code> , the standardized indicator values are not returned. Default is <code>std = TRUE</code> . Either <code>raw</code> or <code>std</code> must be <code>TRUE</code> .
<code>glob.env</code>	Logical value indicating whether to return output to global environment. Default is <code>glob.env = TRUE</code> .
<code>export.path</code>	File path indicating where to save a .csv file of calculated indicators (named <code>potential_export.id.csv</code> ; see below). If <code>export.file = NULL</code> , the indicator dataframe will not be exported as a .csv file. Default is <code>export.path = NULL</code> .
<code>export.id</code>	Character string to modify the name of the .csv file (if <code>export.path</code> is specified), for example an area name or date of analysis. The exported .csv file is named <code>potential_export.id.csv</code> . Default is <code>export.id = NULL</code> .

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

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

<code>X</code>	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).
<code>land</code>	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).
<code>species.table</code>	A table where the column names match the entries in <code>landings.groups</code> . Column entries are the species codes indicating the species from <code>land</code> included in each group. <code>species.table</code> may also include columns for other species groups; these will be ignored.
<code>speciesinfo.table</code>	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 <code>land</code> (or a subset thereof). Other columns will be ignored.
<code>landings.groups</code>	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 <code>species.table</code> . If <code>landings.groups = NULL</code> , no Landings indicators will be calculated.
<code>FP.groups</code>	A dataframe with two columns, which must be named <code>group.land</code> and <code>group.X</code> . Each row holds the group names to calculate the fishing pressure on a target group, with the numerator in column <code>group.land</code> and the denominator in column <code>group.X</code> . Each entry must be a character string matching the name of a column in <code>species.table</code> . If <code>FP.groups = NULL</code> , no fishing pressure indicators will be calculated.
<code>minTL</code>	A vector containing minimum trophic level to include when calculating the mean trophic level of the landings. Default is <code>minTL = c(0, 3.25)</code> , which will return the mean trophic level of the landings and the marine trophic index.
<code>years</code>	A vector of years for which to calculate indicators.
<code>raw</code>	A logical value. If <code>raw = TRUE</code> , the raw indicator values are returned by the function. If <code>raw = FALSE</code> , the raw indicator values are not returned. Default is <code>raw = TRUE</code> . Either <code>raw</code> or <code>std</code> must be TRUE.
<code>std</code>	A logical value. If <code>std = TRUE</code> , 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 <code>std = FALSE</code> , the standardized indicator values are not returned. Default is <code>std = TRUE</code> . Either <code>raw</code> or <code>std</code> must be <code>TRUE</code> .
<code>glob.env</code>	Logical value indicating whether to return output to global environment. Default is <code>glob.env = TRUE</code> .
<code>export.path</code>	File path indicating where to save a <code>.csv</code> file of calculated indicators (named <code>pressure_export.id.csv</code> ; see below). If <code>export.file = NULL</code> , the indicator dataframe will not be exported as a <code>.csv</code> file. Default is <code>export.path = NULL</code> .
<code>export.id</code>	Character string to modify the name of the <code>.csv</code> file (if <code>export.path</code> is specified), for example an area name or date of analysis. The exported <code>.csv</code> file is named <code>pressure_export.id.csv</code> . Default is <code>export.id = NULL</code> .

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@dfw-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

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"),
```

```

c("CLUPEIDS", "CLUPEIDS.L"),
c("FLATFISH", "FLATFISH.L"),
c("GROUNDFISH", "GROUNDFISH.L"))))
names(FP.groups) <- c("group.X", "group.land")

# Calculate standardized indicators
allPressure(X = X, land = land, species.table = species.table,
  speciesinfo.table = species.info, landings.groups = landings.groups,
  FP.groups = FP.groups, minTL = c(0, 3.25), years = c(2014:2019), raw = FALSE, std = TRUE)

```

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

```

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

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@dfp-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

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

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

See Also

Other ecosystem structure and function indicators: [biomassRatio](#), [communityCondition](#), [largeFishIndicator](#), [largeSpeciesIndicator](#), [meanTLCommunity](#)

Examples

```
# 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", "GROUND FISH"), c("PREDATORS", "ALL")))
names(ratio.groups) <- c("group1", "group2")
trophicguild.groups <- c("LBENTHIVORE", "MBENTHIVORE", "PISCIVORE", "PLANKTIVORE",
  "ZOO PISCIVORE")
condition.groups <- c("FINFISH", "LBENTHIVORE", "MBENTHIVORE", "PISCIVORE",
  "PLANKTIVORE", "ZOO PISCIVORE")

# 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)
```

biomassPerTL *Calculates the biomass per discrete trophic level*

Description

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

Usage

```
biomassPerTL(X, 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 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).
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 will be ignored.
metric	A character string indicating which column in X to use to calculate indicator. Default is metric = "BIOMASS".
TL.grouping	Size of the trophic level bin for which to aggregate biomass. 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.
years	A vector of years for which to calculate indicator.

Value

Returns a dataframe with columns ID, YEAR, and the corresponding biomass for each trophic level grouping. For example: for TL.grouping = 1, function will return columns BIOMASS_TL2, BIOMASS_TL3, BIOMASS_TL4. For TL.grouping = 0.5, function will return columns 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

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Bundy, A. 2005. Structure and functioning of the eastern Scotian Shelf ecosystem before and after the collapse of groundfish stocks in the early 1990s. Canadian Journal of Fisheries and Aquatic Sciences, 62(7), pp.1453-1473.

Coll M, Shannon LJ, Moloney CL, Palomera I, Tudela S, 2006. Comparing trophic flows and fishing impacts of a NW Mediterranean ecosystem with coastal upwellings by means of standardized ecological models and indicators. Ecol. Model. 198, 53-70.

See Also

Other stability and resistance indicators: [CVBiomass](#), [IVILandings](#), [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 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).

<code>ratio.groups</code>	A dataframe with two columns, which must be named <code>group1</code> and <code>group2</code> . Each row holds the group names for one biomass ratio, with the numerator in column <code>group1</code> and the denominator in column <code>group2</code> . Each entry must be a character string matching the name of a column in <code>species.table</code> or "ALL".
<code>species.table</code>	A table with column names that match the entries of <code>ratio.groups</code> . The entries in each column are the species codes from <code>X</code> indicating which species are included that group. <code>species.table</code> may also include columns for other species groups; these will be ignored. Note that an entry in <code>ratio.groups</code> could be "ALL". In this case, a column in <code>species.table</code> named "ALL" is not required; the function will automatically include all species in <code>X</code> .
<code>metric</code>	A character string indicating which column in <code>X</code> to use to calculate indicator. Default is <code>metric = "BIOMASS"</code> .
<code>years</code>	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:

$$\text{PropPred} = \text{Biomass of Predatory Fish Surveyed} / \text{Total Biomass Surveyed}$$

Predatory fish species are defined as all surveyed fish species that are not largely planktivorous, i.e., 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:

$$B_{\text{invertebrates}} / B_{\text{demersal}}$$

and

$$B_{\text{pelagic}} / B_{\text{demersal}}$$

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Bundy A, Heymans JJ, Morissette L, Savenkoff C (2009) Seals, cod and forage fish: A comparative exploration of variations in the theme of stock collapse and ecosystem change in four Northwest Atlantic ecosystems. Prog Oceanogr 81:188-206

Shin YJ, Shannon LJ, Bundy A, Coll M, Aydin K, Bez N, Blanchard JL, Borges MF, Diallo I, Diaz E, Heymans JJ, Hill L, Johannesen E, Jouffre D, Kifani S, Labrosse P, Link JS, Mackinson S, Masski H, Möllmann C, Neira S, Ojaveer H, Abdallahi KM, Perry I, Thiao D, Yemane D, and Cury PM. 2010. Using indicators for evaluating, comparing and communicating the ecological status of exploited marine ecosystems. Part 2: Setting the scene. ICES Journal of Marine Science, 67: 692-716

See Also

Other ecosystem structure and function indicators: [allStructure](#), [communityCondition](#), [largeFishIndicator](#), [largeSpeciesIndicator](#), [meanTLCommunity](#)

Examples

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

# Species groups of interest
ratio.groups <- data.frame(rbind(c("PELAGIC", "GROUND FISH"), 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

```
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):

$$K = \Sigma(K_j * A_j) / \Sigma A_j$$

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

$$K_j = 100 * W_j / L_j^3$$

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

- Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.
- DFO. 2003. State of the Eastern Scotian Shelf ecosystem. Dartmouth, Nova Scotia
- Choi JS, Frank KT, Petrie BD, Leggett WC. 2005. Integrated Assessment of a Large Marine Ecosystem: a case study of the devolution of the Eastern Scotian Shelf, Canada. Oceanogr Mar Biol Annu Rev 43:47-67
- Ricker, W. E. 1975. Computation and interpretation of biological statistics of fish populations. Bulletin of the Fisheries Research Board of Canada 191:1-382.

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))
```

 CVBiomass

Calculates the Coefficient of Variation of the Biomass

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 $\text{floor}(\text{wind}/2)$ 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.

Details

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

$$\text{CVBiomass} = \text{sd}(\text{total biomass for the past } n \text{ years}) / \text{mean}(\text{total biomass for the past } n \text{ years})$$

Value

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

The first and last $\text{floor}(\text{wind}/2)$ 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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Blanchard F, Boucher J (2001) Temporal variability of total biomass in harvested communities of demersal fishes. Fisheries Research. 49. 283–293. 10.1016/S0165-7836(00)00203-4.

Shin, YJ, Shannon LJ, Bundy A, Coll M, Aydin K, Bez N, Blanchard JL, Borges, MF, Diallo I, Diaz E, Heymans JJ, Hill L, Johannesen E, Jouffre D, Kifani S, Labrosse P, Link JS, Mackinson S, Masski H, Möllmann C, Neira S, Ojaveer H, Ould Mohammed Abdallahi ., Perry I, Thiao D, Yemane D, and Cury PM. 2010. Using indicators for evaluating, comparing and communicating the ecological status of exploited marine ecosystems. Part 2: Setting the scene. ICES Journal of Marine Science, 67: 692-716

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))
```

example_inds	<i>Indicators calculated from the example data included in the package</i>
--------------	--

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	<i>Calculates indicators from all attributes</i>
------------	--

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 <code>TL.grouping = 1</code> so that biomass is aggregated over discrete trophic levels.
<code>wind</code>	Window for the moving average used to calculate the Coefficient of Variation of the Biomass. The first and last <code>floor(wind/2)</code> values of the indicator are assigned NA to account for the moving average. Default is <code>wind = 5</code> years.
<code>negative</code>	If <code>negative = TRUE</code> , 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 <code>negative = FALSE</code> .
<code>resource.groups</code>	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 <code>species.table</code> . If <code>resource.groups = NULL</code> , these indicators will not be calculated.
<code>minTL.FiB</code>	The minimum trophic level of species to include to calculate Fishing-in-Balance.
<code>TE</code>	Trophic efficiency, used to calculate FiB. Default is <code>TE = 0.1</code> , i.e., a trophic efficiency of 10%. If <code>TE = NULL</code> , FiB will not be calculated.
<code>base.start</code>	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. <code>land</code> must include data for the baseline period. If <code>base.start = NULL</code> , FiB will not be calculated.
<code>base.end</code>	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. <code>land</code> must include data for the baseline period. If <code>base.end = NULL</code> , FiB will not be calculated.
<code>landings.groups</code>	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 <code>species.table</code> . If <code>landings.groups = NULL</code> , no Landings indicators will be calculated.
<code>FP.groups</code>	A dataframe with two columns, which must be named <code>group.land</code> and <code>group.X</code> . Each row holds the group names to calculate the fishing pressure on a target group, with the numerator in column <code>group.land</code> and the denominator in column <code>group.X</code> . Each entry must be a character string matching the name of a column in <code>species.table</code> . If <code>FP.groups = NULL</code> , no fishing pressure indicators will be calculated.
<code>minTL.FP</code>	A vector containing minimum trophic level to include when calculating the mean trophic level of the landings. Default is <code>minTL = c(0, 3.25)</code> , which will return the mean trophic level of the landings and the marine trophic index.
<code>raw</code>	A logical value. If <code>raw = TRUE</code> , the raw indicator values are returned by the function. If <code>raw = FALSE</code> , the raw indicator values are not returned. Default is <code>raw = TRUE</code> . Either <code>raw</code> or <code>std</code> must be TRUE.
<code>std</code>	A logical value. If <code>std = TRUE</code> , 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 <code>std = FALSE</code> , the standardized indicator values are not returned. Default is <code>std = TRUE</code> . Either <code>raw</code> or <code>std</code> must be TRUE.

<code>glob.env</code>	Logical value indicating whether to return output to global environment. Default is <code>glob.env = TRUE</code> .
<code>export.path</code>	File path indicating where to save a .csv file of calculated indicators (named <code>allIndicators_export.id.csv</code> ; see below). If <code>export.file = NULL</code> , the indicator dataframe will not be exported as a .csv file. Default is <code>export.path = NULL</code> .
<code>export.id</code>	Character string to modify the name of the .csv file (if <code>export.path</code> is specified), for example an area name or date of analysis. The exported .csv file is named <code>allIndicators_export.id.csv</code> . Default is <code>export.id = NULL</code> .

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 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

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
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)
```

<code>fishingInBalance</code>	<i>Calculates the Fishing-in-Balance Index</i>
-------------------------------	--

Description

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

Usage

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

Arguments

<code>land</code>	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.
<code>TL.table</code>	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.
<code>minTL</code>	The minimum trophic level of species to include. Default is <code>minTL = 0</code> .
<code>TE</code>	Trophic efficiency. Default is <code>TE = 0.1</code> , i.e., a trophic efficiency of 10%.
<code>base.start</code>	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.
<code>base.end</code>	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.
<code>years</code>	A vector of years for which to calculate indicator.

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Pauly D, Christensen V, Walters C. 2000. Ecopath, Ecosim, and Ecospace as tools for evaluating ecosystem impact of fisheries. ICES J Mar Sci 57:697 706

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	<i>Calculates Fishing Pressure</i>
-----------------	------------------------------------

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

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).
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.
species.table	A table with column names that match the entries of 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 SPECIES column of land (for groups in group.land) or X (for groups in group.X). species.table may also include columns for other species groups; these will be ignored. Note that an entry in FP.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 land and/or X.
years	A vector of years for which to calculate indicator.

Details

Fishing pressure (FP):

$$FP = Landings_{FG} / Biomass_{FG}$$

where $Landings_{FG}$ is the landed catch of the fished group and $Biomass_{FG}$ is the biomass of the fished group.

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 $Landings_{FG}$, $Biomass_{FG}$ or both. If $Landings_{FG}$ and $Biomass_{FG}$ 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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Shin, YJ, Shannon LJ, Bundy A, Coll M, Aydin K, Bez N, Blanchard JL, Borges, MF, Diallo I, Diaz E, Heymans JJ, Hill L, Johannesen E, Jouffre D, Kifani S, Labrosse P, Link JS, Mackinson S, Masski H, Möllmann C, Neira S, Ojaveer H, Abdallahi KM, Perry I, Thiao D, Yemane D, and Cury PM. 2010. Using indicators for evaluating, comparing and communicating the ecological status of exploited marine ecosystems. Part 2: Setting the scene. ICES Journal of Marine Science, 67: 692-716

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))
```

heips	<i>Calculates Heip's Evenness Index</i>
-------	---

Description

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

Usage

```
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):

$$HE = (exp^{H'} - 1) / (S - 1)$$

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Heip C. 1974. A new index measuring evenness. J. Mar. Biol. Asso. UK 54: 555-557.

Kenchington T, Kenchington E (2013) Biodiversity Metrics for Use in the Ecosystem Approach to Oceans Management. Can. Tech. Rep. Fish. Aquat. Sci. 3059: vi+188p.

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	<i>Calculates Hill's Index of Diversity (N1)</i>
--------	--

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.

<code>species.table</code>	A table where the column names match the entries in <code>groups</code> . Column entries are species codes indicating the species from <code>X</code> included in each group. <code>species.table</code> may also include columns for other species groups; these will be ignored. If <code>groups = "ALL"</code> , this table is not required. Default is <code>species.table = NULL</code> .
<code>metric</code>	A character string indicating which column in <code>X</code> to use to calculate the indicator. Default is <code>metric = "ABUNDANCE"</code> .
<code>years</code>	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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Greenstreet SP, Rogers SI. 2006. Indicators of the health of the North Sea fish community: identifying reference levels for an ecosystem approach to management. ICES J Mar Sci J du Cons 63:573-593

Hill MO. 1973. Diversity and evenness: a unifying notation and its consequences. Ecology 54: 427-431.

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))
```

hillN2 *Calculates Hill's Species Dominance (N2)*

Description

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

Usage

```
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):

$$HillN2 = 1/\sum p_i^2$$

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.

Author(s)

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

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Greenstreet SP, Rogers SI. 2006. Indicators of the health of the North Sea fish community: identifying reference levels for an ecosystem approach to management. ICES J Mar Sci J du Cons 63:573-593

Hill MO. 1973. Diversity and evenness: a unifying notation and its consequences. Ecology 54: 427-431.

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:

$$IVI = \Sigma(IVI_j * C_j) / \Sigma C_j$$

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

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@dfw-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Cheung WWL, Pitcher TJ, Pauly D. 2005. A fuzzy logic expert system to estimate intrinsic extinction vulnerability of marine fishes to fishing. Biol Conserv 124:97–111

Cheung WWL, Watson R, Morato T, Pitcher, TJ, Pauly, D. 2007. Intrinsic vulnerability in the global fish catch. Mar Ecol Prog Ser 333: 1 - 12

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

```
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.

$$Q = S * (p_2 - p_1) * \log(R_2/R_1)$$

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@dfw-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

Ainsworth, C, Pitcher, T. 2006. Modifying Kempton's species diversity index for use with ecosystem simulation models. Ecological Indicators. 6. 623-630. 10.1016/j.ecolind.2005.08.024.

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Kempton R, Taylor L. 1976. Models and statistics for species diversity. Nature 262:818-820

See Also

Other biodiversity indicators: [allBiodiversity](#), [heips](#), [hillN1](#), [hillN2](#), [margalef](#), [pielouEvenness](#), [shannon](#), [speciesRichness](#)

Examples

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

# Calculate indicator
kemptonQ(X, TL.table = species.info, percentiles = c(.25, 0.75), minTL = 0,
  groups = "ALL", metric = "ABUNDANCE", years = c(2014:2019))
```

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

<code>land</code>	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.
<code>groups</code>	A vector indicating the species group(s) for which to calculate the indicator. If <code>groups = "ALL"</code> , all species will be included; otherwise, each entry must be a character string matching the name of a column in <code>species.table</code> .
<code>species.table</code>	A table with at least one column, where the column names match the entries in <code>groups</code> , and the column entries are species codes from <code>land</code> indicating which species are included that group. <code>species.table</code> may also include columns for other species groups; these will be ignored. If <code>group = "ALL"</code> , this table is not required. Default is <code>species.table = NULL</code> .
<code>years</code>	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@dfw-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

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
```

```
landings(land, groups = landings.groups, species.table = species.table,
         years = c(2014:2019))
```

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_length\$LENGTH >= 35 cm).
years	A vector of years for which to calculate indicator.

Details

Large Fish Indicator (LFI):

$$LFI = \Sigma B_m(L > 35cm) / \Sigma B_m$$

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).

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Greenstreet SPR and Rogers SI. 2006. Indicators of the health of the fish community of the North Sea: identifying reference levels for an Ecosystem Approach to Management. ICES J. Mar. Sci., 63: 573–593.

ICES. 2006. Report of the Working Group on Ecosystem Effects of Fishing Activities. ICES Document CM 2006/ACE: 05. 174 pp.

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

<code>X</code>	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).
<code>group</code>	character string indicating which species to include in the indicator calculation. If <code>group = "ALL"</code> , all species will be included; otherwise, <code>group</code> should match a column name in <code>species.table</code> .
<code>species.table</code>	A table where the column names match the entries in <code>groups</code> . Column entries are species codes indicating the species from <code>X</code> included in each group. <code>species.table</code> may also include columns for other species groups; these will be ignored. If <code>groups = "ALL"</code> , this table is not required. Default is <code>species.table = NULL</code> .
<code>maxlength.table</code>	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 <code>X</code> (or a subset thereof). Other columns in <code>maxlength.table</code> are ignored.
<code>max.length</code>	The threshold for large species (cm). Default is <code>max.length = 85</code> (i.e., large species are those with <code>MAXLENGTH >= 85</code> cm).
<code>metric</code>	A character string indicating which column in <code>X</code> to use to calculate indicator. Default is <code>metric = "BIOMASS"</code> .
<code>years</code>	A vector of years for which to calculate indicator.

Details

Large Species Indicator (LSI):

$$LSI = \sum B_i(L_{max} > 85cm) / \sum B_i$$

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. ID, YEAR, and LargeSpeciesIndicator.

If there are no observations of large species 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

- Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.
- Shephard S, Fung T, Houle JE, Farnsworth KD, Reid DG, Rossberg AG. 2012. Size-selective fishing drives species composition in the Celtic Sea. ICES J Mar Sci 69:223-234
- Shin, YJ, Shannon LJ, Bundy A, Coll M, Aydin K, Bez N, Blanchard JL, Borges, MF, Diallo I, Diaz E, Heymans JJ, Hill L, Johannesen E, Jouffre D, Kifani S, Labrosse P, Link JS, Mackinson S, Masski H, Möllmann C, Neira S, Ojaveer H, Abdallahi KM, Perry I, Thiao D, Yemane D, and Cury PM. 2010. Using indicators for evaluating, comparing and communicating the ecological status of exploited marine ecosystems. Part 2: Setting the scene. ICES Journal of Marine Science, 67: 692-716

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	<i>Calculates Margalef's Species Richness</i>
----------	---

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:

$$S_{Marg} = (S_y - 1) / \log(F_y)$$

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 is assigned NA.

Author(s)

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

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Margalef R. 1958. Information theory in ecology. General Systems 3, 36–71.

See Also

Other biodiversity indicators: [allBiodiversity](#), [heips](#), [hillN1](#), [hillN2](#), [kempstonQ](#), [pielouEvenness](#), [shannon](#), [speciesRichness](#)

Examples

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

meanLengthCommunity	<i>Calculates the Mean Length of the Community weighted by biomass or abundance</i>
---------------------	---

Description

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

Usage

```
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.
----------	--

`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

$$\text{MeanLength} = \frac{\sum(\text{Length}_m * \text{metric}_i)}{\sum \text{metric}_j}$$

where Length_m is the length (cm) of an individual in size class m , metric_i is the biomass or abundance of species i and 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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Shin, YJ, Shannon LJ, Bundy A, Coll M, Aydin K, Bez N, Blanchard JL, Borges, MF, Diallo I, Diaz E, Heymans JJ, Hill L, Johannesen E, Jouffre D, Kifani S, Labrosse P, Link JS, Mackinson S, Masski H, Möllmann C, Neira S, Ojaveer H, Abdallahi KM, Perry I, Thiao D, Yemane D, and Cury PM. 2010. Using indicators for evaluating, comparing and communicating the ecological status of exploited marine ecosystems. Part 2: Setting the scene. ICES Journal of Marine Science, 67: 692-716

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	<i>Calculates the Mean Maximum Age of fish in the community</i>
------------	---

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Shin, YJ, Shannon LJ, Bundy A, Coll M, Aydin K, Bez N, Blanchard JL, Borges, MF, Diallo I, Diaz E, Heymans JJ, Hill L, Johannesen E, Jouffre D, Kifani S, Labrosse P, Link JS, Mackinson S, Masski H, Möllmann C, Neira S, Ojaveer H, Abdallahi KM, Perry I, Thiao D, Yemane D, and Cury PM. 2010. Using indicators for evaluating, comparing and communicating the ecological status of exploited marine ecosystems. Part 2: Setting the scene. ICES Journal of Marine Science, 67: 692-716

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

```
meanMaxLength(X, group, species.table = NULL, maxlength.table, metric,
years)
```

Arguments

<code>X</code>	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).
<code>group</code>	character string indicating which species to include in the indicator calculation. If <code>group = "ALL"</code> , all species will be included; otherwise, <code>group</code> should match a column name in <code>species.table</code> .
<code>species.table</code>	A table where the column names match the entries in <code>groups</code> . Column entries are species codes indicating the species from <code>X</code> included in each group. <code>species.table</code> may also include columns for other species groups; these will be ignored. If <code>groups = "ALL"</code> , this table is not required. Default is <code>species.table = NULL</code> .
<code>maxlength.table</code>	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 <code>X</code> (or a subset thereof). Other columns in <code>maxlength.table</code> are ignored.
<code>metric</code>	A character string indicating which column in <code>X</code> to use to calculate indicator. Default is <code>metric = "BIOMASS"</code> .
<code>years</code>	A vector of years for which to calculate indicator.

Details

Mean Maximum Length:

$$\text{MeanMaximumLength} = \Sigma(L_{max,i} * M_i) / \Sigma M_i$$

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

- Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.
- Shin YJ, Rochet MJ, Jennings S, Field JG, Gislason H. 2005. Using size-based indicators to evaluate the ecosystem effects of fishing. In: ICES Journal of Marine Science. p 384-396

See Also

Other stability and resistance indicators: [CVBiomass](#), [IVILandings](#), [allStability](#), [biomassPerTL](#), [meanMaxAge](#)

Examples

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

# Calculate indicators
# Weighted by abundance
meanMaxLength(X, group = "FINFISH", species.table = species.table,
  maxlength.table = species.info, metric = "ABUNDANCE", years = c(2014:2019))
#Weighted by biomass
meanMaxLength(X, group = "FINFISH", species.table = species.table,
  maxlength.table = species.info, metric = "BIOMASS", years = c(2014:2019))
```

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

<code>X</code>	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).
<code>TL.table</code>	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.
<code>metric</code>	A character string indicating which column in X to use to calculate indicator. Default is <code>metric = "BIOMASS"</code> .
<code>years</code>	A vector of years for which to calculate indicator.

Details

Mean trophic level (TL):

$$TL = \Sigma(TL_i * B_i) / \Sigma B_i$$

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@dfw-mpo.gc.ca>, Adam Cook, Catalina Gomez, Alida Bundy

References

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Christensen V. 1998. Fishery-induced changes in a marine ecosystem: insight from models of the Gulf of Thailand. J. Fish Bio. 53:128-142. Article No. jb980809

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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	<i>Calculates the Mean Trophic Level or Marine Trophic Index of fisheries landings</i>
----------------	--

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 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. Set minTL = 0 to calculate the mean trophic level of the landings; Set minTL = 3.25 to calculate the marine trophic index. Default is minTL = 0.
years	A vector of years for which to calculate indicator.

Details

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

$$TL_{Land} = \Sigma(TL_i * Y_i) / Y$$

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_{Land} , but only includes species with trophic level greater than or equal to an explicitly stated trophic level minTL. For instance, Pauly and Watson 2005 adopted a trophic level minTL of 3.25 to emphasize changes in the relative abundance of higher trophic level fishes, and Shannon et al. 2014 used a 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

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Shannon L, Coll M, Bundy A, Gascuel D, Heymans, JJ, Kleisner K, Lynam CP, Piroddi C, Tam J, Travers-Trolet M and Shin Y. 2014. Trophic level-based indicators to track fishing impacts across marine ecosystems. Marine Ecology Progress Series, 512, pp.115-140.

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

References

- Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.
- Greenstreet SP, Rogers SI. 2006. Indicators of the health of the North Sea fish community: identifying reference levels for an ecosystem approach to management. ICES J Mar Sci J du Cons 63:573-593
- Pielou EC. 1975. Ecological Diversity. Wiley, New York. ISBN 0-471-68925-4

See Also

Other biodiversity indicators: [allBiodiversity](#), [heips](#), [hillN1](#), [hillN2](#), [kemptonQ](#), [margalef](#), [shannon](#), [speciesRichness](#)

Examples

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

resourcePotential	<i>Calculates the Resource Potential of species groups</i>
-------------------	--

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. |

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

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

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

Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.

Greenstreet SP, Rogers SI. 2006. Indicators of the health of the North Sea fish community: identifying reference levels for an ecosystem approach to management. ICES J Mar Sci J du Cons 63:573-593

Magurran, AE. 1988. Ecological Diversity and its Measurement. Chapman and Hall, London. 179 pp.

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))
```

species.info

Species information

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	<i>Example input for argument species.table</i>
---------------	---

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	<i>Calculates Species Richness of the community or the Diversity of Target Species</i>
-----------------	--

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 (TS_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

- Bundy A, Gomez C, Cook AM. 2017. Guidance framework for the selection and evaluation of ecological indicators. Can. Tech. Rep. Fish. Aquat. Sci. 3232: xii + 212 p.
- Hurlbert SH. 1971. The non-concept of species diversity: a critique and alternative parameters. Ecology, 52, 577-86.

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))
```

X

Example fishery independent survey data

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.

X_length

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

X_length

Format

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

YEAR Year the observation was recorded

ID Area where the observation was recorded

SPECIES Numeric code indicating the species sampled

LENGTH Length class of sample species, in cm

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 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.

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