Package ‘fishmethods’

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Title Fisheries Methods and Models in R

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Description Fishery methods and models from Quinn and Deriso (1999), Haddon(2001) , and literature.

License GPL (>= 2)

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R topics documented:

`fishmethods-package` *Fisheries Methods and Models in R*

Description

Fisheries methods and models that extract Marine Recreational Fisheries Statistics data, estimate population parameters (e.g., mortality, abundance, age structure, etc.), run dynamic pool models, and compare population characteristics using special statistical techniques required in fisheries sampling.

Details

Package:	fishmethods
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Author(s)

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Maintainer: Gary A. Nelson <Gary.Nelson@state.ma.us>

References

Specified for each function under help pages.

`agesurv` *Age-based Survival Estimators*

Description

Calculates annual survival (S) and instantaneous total mortality rates (Z) from age frequency by using catch curve (ln(numbers) versus age in linear regression), Heincke, and Chapman-Robson methods.

Usage

```
agesurv(age = NULL, full = NULL, last = NULL,
estimate = c("s", "z"), method = c("cc", "he", "cr"))
```

Arguments

`age`	the vector of ages. Each row represents the age of an individual.
`full`	the fully-recruited age
`last`	the maximum age to include in the calculation. If not specified, the oldest age is used.
`estimate`	argument to select estimate type: "s" for annual survival, "z" for instantaneous total mortality. Default is both.
`method`	argument to select the estimation method: "cc" for catch curve, "he" for Heincke, and "cr" for Chapman-Robson. Default is all.

Details

The individual age data are tabulated and subsetted based on the `full` and `last` arguments. Most calculations follow descriptions in Seber(1982), pages 414-418. If only two ages are present, a warning message is generated and the catch curve method is not calculated. Plus groups are not allowed.

Value

`results`	list element containing table of parameters and standard errors.
`data`	list element containing the age frequency data used in the analysis.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Seber, G. A. F. 1982. The Estimation of Animal Abundance and Related Parameters, Second Edition. The Blackburn Press, Caldwell, New Jersey. 654 pages. Quinn, T. J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press, New York, New York. 542 pages.

Examples

```
data(rockbass)
agesurv(age=rockbass$age,full=6)
```

`agesurvcl` *Age-Based Survival and Mortality Estimators for Cluster Sampling*

Description

Calculates the survival and mortality estimators of Jensen (1996) where net hauls are treated as samples

Usage

```
agesurvcl(age = NULL, group = NULL, full = NULL, last = NULL)
```

Arguments

`age`	the vector of ages. Each row represents the age of an individual.
`group`	the vector containing variable used to identify the sampling unit (e.g., haul). Identifier can be numeric or character.
`full`	the fully-recruited age.
`last`	the maximum age to include in the calculation. If not specified, the oldest age is used.

Details

The individual age data are tabulated and subsetted based on `full` and `last`. The calculations follow Jensen(1996). If only two ages are present, a warning message is generated.

Value

Matrix containing estimates of annual mortality (a), annual survival (S), and instantaneous total mortality (Z) and associated standard errors.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Jensen, A. L. 1996. *Ratio estimation of mortality using catch curves*. Fisheries Research 27: 61-67.

See Also

`agesurv`

Examples

```
data(Jensen)
agesurvcl(age=Jensen$age,group=Jensen$group,full=0)
```

`alkD` *Sample Size Determination for Age Subsampling Using the D statistic*

Description

Calculates the D statistic (sqrt of accumulated variance among ages; Lai 1987) for a range of age sample sizes using data from an age-length key. Assumes a two-stage random sampling design with proportional or fixed allocation.

Usage

```
alkD(x, lss = NULL, minss = NULL, maxss = NULL, sampint = NULL,
     allocate = 1)
```

Arguments

`x`	a data frame containing an age-length key (similar to Table 8.3 on page 307 of Quinn and Deriso (1999)). The first column must contain the length intervals as numeric labels (no ranges), the second column must contain the number of samples within each length interval (Ll in Q & D), and the third and remaining columns must contain the number of samples for each age class within each length interval (one column for each age class). Column labels are not necessary but are helpful. Columns l and Al in Table 8.3 should not be included. Empty cells must contain zeros.
`lss`	the sample size for length frequency
`minss`	the minimum age sample size
`maxss`	the maximum age sample size. Value can not be larger than the sample size for the length frequency(`lss`)
`sampint`	the sample size interval
`allocate`	the type of allocation: 1=proportional, 2=fixed.

Details

Following Quinn and Deriso (1999:pages 308-309), the function calculates the D statistic (sqrt of accumulated variance among ages; Lai 1987) for a range of age sample sizes defined by `minss`, `maxss`, and `sampint` at a given length sample size `lss`. The size of an age sample at a desired level of D can be obtained by the comparison. See reference to Table 8.8, p. 314 in Quinn and Deriso.

Value

`label`	list element containing the summary of input criteria
`comp2`	list element containing the D statistic for each age sample size given lss

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Quinn, T. J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press, New York, New York. 542 pages

Lai, H.L. 1987. Optimum allocation for estimating age composition using age-length keys. U.S. Fish. Bull. 85:179-185

See Also

`alkss` `alkprop`

Examples

```
data(alkdata)
alkD(alkdata,lss=1000,minss=25,maxss=1000,sampint=20,allocate=1)
```

`alkdata` *Age-Length Key for Gulf of Hauraki snapper, 1992-1993*

Description

The `alkdata` data frame has 39 rows and 16 columns. The age-length key for Gulf of Hauraki snapper shown in Table 8.3 of Quinn and Deriso (1999)

Usage

```
alkdata
```

Format

This data frame contains the following columns:

len	length interval
nl	number measured in length interval
A3	number of fish aged in each age class 3 within each length interval
A4	number of fish aged in each age class 4 within each length interval
A5	number of fish aged in each age class 5 within each length interval
A6	number of fish aged in each age class 6 within each length interval
A7	number of fish aged in each age class 7 within each length interval
A8	number of fish aged in each age class 8 within each length interval
A9	number of fish aged in each age class 9 within each length interval
A10	number of fish aged in each age class 10 within each length interval
A11	number of fish aged in each age class 11 within each length interval
A12	number of fish aged in each age class 12 within each length interval
A13	number of fish aged in each age class 13 within each length interval
A14	number of fish aged in each age class 14 within each length interval
A15	number of fish aged in each age class 15 within each length interval
A16	number of fish aged in each age class 16 within each length interval

Source

Quinn, T. J. and R. B. Deriso. 1999. *Quantitative Fish Dynamics*. Oxford University Press, New York, NY. 542 p.

`alkprop` *Age-Length Key Proportions-At-Age*

Description

Calculates proportions-at-age and standard errors from an age-length key assuming a two-stage random sampling design.

Usage

```
alkprop(x)
```

Arguments

`x`	a data frame containing an age-length key (similar to Table 8.3 on page 307 of Quinn and Deriso (1999)). The first column must contain the length intervals as single numeric labels (no ranges), the second column must contain the number of samples within each length interval (Ll in Q & D), and the third and remaining columns must contain the number of samples for each age class within each length interval (one column for each age class). Column labels are not necessary but are helpful. Columns l and Al in Table 8.3 should not be included. Empty cells must contain zeros.

Details

If individual fish from catches are sampled randomly for lengths and then are further subsampled for age structures, Quinn and Deriso (1999: pages 304-305) showed that the proportions of fish in each age class and corresponding standard errors can be calculated assuming a two-stage random sampling design. See reference to Table 8.4, page 308 in Quinn and Deriso.

Value

`results`	list element containing a table of proportions, standard errors, and coefficients of variation for each age class.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Quinn, T. J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press, New York, New York. 542 pages

See Also

`alkD` `alkss`

Examples

```
data(alkdata)
alkprop(alkdata)
```

`alkss` *Sample Size Determination for Age Subsampling*

Description

Calculates sample sizes for age subsampling assuming a two-stage random sampling design with proportional or fixed allocation.

Usage

```
alkss(x, lss = NULL, cv = NULL, allocate = 1)
```

Arguments

`x`	a data frame containing an age-length key (similar to Table 8.3 on page 307 of Quinn and Deriso (1999)). The first column must contain the length intervals as numeric labels (no ranges), the second column must contain the number of samples within each length interval (Ll in Q & D), and the third and remaining columns must contain the number of samples for each age class within each length interval (one column for each age class). Column labels are not necessary but are helpful. Columns l and Al in Table 8.3 should not be included. Empty cells must contain zeros.
`lss`	the sample size for length frequency
`cv`	the desired coefficient of variation
`allocate`	the type of allocation: 1=proportional, 2=fixed.

Details

If individual fish from catches are sampled randomly for lengths and then are further subsampled for age structures, Quinn and Deriso (1999: pages 306-309) showed that sample sizes for age structures can be determined for proportional (the number of fish aged is selected proportional to the length frequencies) and fixed (a constant number are aged per length class) allocation assuming a two-stage random sampling design. Sample sizes are determined based on the length frequency sample size, a specified coefficient of variation, and proportional or fixed allocation. The number of age classes is calculated internally. See reference to Table 8.6, p. 312 in Quinn and Deriso.

Value

`label`	list element containing the summary of input criteria
`n`	list element containing the sample size estimates for each age

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Quinn, T. J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press, New York, New York. 542 pages

See Also

`alkD` `alkprop`

Examples

```
data(alkdata)
alkss(alkdata,lss=1000,cv=0.25,allocate=1)
```

`baglimit` *Bag Limit Analysis of Marine Recreational Fisheries Statistics Survey Data*

Description

Analysis of Marine Recreational Fisheries Statistics data to determine the effect a simulated bag limit would have on the overall reduction in harvest.

Usage

```
baglimit(intdir = NULL, estdir = NULL, species = NULL,
  state = NULL, mode = NULL, wave = NULL, styr = NULL,
  endyr = NULL, bag = NULL)
```

Arguments

`intdir`	the path and main directory (in quotes) under which raw intercept sub-directories are stored.
`estdir`	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
`species`	10-digit NODC species code. A complete list of species codes is provided at the MRFSS website
`state`	state(s) code of data to include. A complete list of state codes is provided at the MRFSS website. Atlantic and Gulf States: 23= ME, 33= NH, 25= MA, 44= RI, 9= CT, 36= NY, 34= NJ, 10= DE, 24= MD, 51= VA,37= NC, 45= SC, 13= GA, 12= FL (121=East FL, 122=West FL), 1=AL, 28= MS, and 22= LA. Any combination of states can be included in c(). North Atlantic= c(9, 23, 25, 33, 44), Mid Atlantic= c(10, 24, 34, 36, 51), South Atlantic= c(13, 37, 45, 121), Gulf of Mexico= c(1, 22, 28, 122).

`wave`	bimothly wave(s) of data to include. Bimothly Waves: 1= Jan-Feb, 2= Mar-Apr, 3= May-Jun, 4= Jul-Aug, 5= Sept-Oct, and 6= Nov-Dec. Any combination of waves can be included in c().
`mode`	the fishing mode(s) of data to include. Valid codes will depend on year. Years 1982-2004: 3= Shore, 6= Party & Charter Boats, and 7= Private & Rental Boats. Years 2005-present: 3= Shore, 4= Party Boat, 5= Charter Boat, and 7= Private & Rental Boats. Any combination of modes can be included in c().
`styr`	the starting year of data to include.
`endyr`	the ending year of data to include.
`bag`	the bag limit(s) to simulate. If multiple bag limits, separate values by commas in c().

Details

Raw intercept and catch & effort estimates must be extracted using function `extractMRFSS` before bag limit simulations can be done. Species-specific intercept data and associated effort estimates for each state, year, wave and mode are extracted. Harvest numbers with multiple contributors (CNTRBTRS) are split evenly among the number of contributors (fractional harvest frequencies may result). The analytical steps given in Chapter 7 of `Recreational Fisheries Data Users Manual` are followed. Estimated total harvest from the `No Bag Limit` table should be close to the MRFSS harvest estimate.

Value

`No Bag Limit`	list element containing the table of catch, trip,intercept and harvest information with no bag limit.
`Bag Limit i`	list elements containing the table of catch, trip,intercept and harvest information with each bag limit applied. The number of elements will depend on number of bag limit simulations.
`Results`	the percent reduction in harvest associated with each bag limit.
`Details`	a list element summarizing the selected arguments.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Marine Recreational Fisheries Statistics Survey - Recreational Fisheries Data User's Manual

`http://www.st.nmfs.noaa.gov/st1/recreational/SurveyMaterials.html`

See Also

`extractMRFSS`

Examples

```
## Example of a typical specification. Example is for bluefish from New
## York in 1990 (all waves and modes)- not a working example
## Not run:
baglimit(intdir="C:/Temp",estdir="C:/Temp",species=8835250101,
 state=c(36),mode=c(3,6,7),wave=c(1,2,3,4,5,6),bag=c(5,10,15),
 styr=1990,endyr=1990)
## End(Not run)
```

`bheq1` *Length-based Beverton-Holt Equilibrium Total Instantaneous Mortality Estimator*

Description

The equilibrium Beverton-Holt estimator of instantaneous total mortality (Z) from length data with bootstrapped standard errors

Usage

```
bheq1(len, K = NULL, Linf = NULL, Lc = NULL, nboot = 100)
```

Arguments

`len`	the vector of length data. Each row represents one record per individual fish.
`K`	the growth coefficient from a von Bertalanffy growth model.
`Linf`	the L-infinity coefficient from a von Bertalanffy growth model.
`Lc`	the length at first capture.
`nboot`	the number of bootstrap runs. Default=100.

Details

The standard Beverton-Holt equilibrium estimator of instantaneous total mortality (Z) from length data (page 365 in Quinn and Deriso (1999)) is calculated. The mean length for lengths >=Lc is calculated automatically. Missing data are removed prior to calculation. Estimates of standard error are made by bootstrapping length data >=Lc using package `boot`.

Value

Dataframe of length 1 containing mean length>=Lc, sample size>=Lc, Z estimate and standard error.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Quinn, T. J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press, New York, New York. 542 pages

See Also

`bheq2` `bhnoneq`

Examples

```
data(herring)
bheq1(herring[,1],K=0.54,Linf=339,Lc=240,nboot=200)
```

`bheq2` *Length-based Beverton-Holt Equilibrium Total Instantaneous Mortality Estimator with Bias-Correction*

Description

The equilibrium Beverton-Holt estimator of instantaneous total mortality (Z) from length data using Ehrhardt and Ault (1992) bias-correction

Usage

```
bheq2(len = NULL, Linf = NULL, K = NULL, Lc = NULL, La = NULL,
 nboot = 100)
```

Arguments

`len`	the vector of length data. Each row represents one record per individual fish.
`K`	the growth coefficient from a von Bertalanffy growth model.
`Linf`	the L-infinity coefficient from a von Bertalanffy growth model.
`Lc`	the length at first capture.
`La`	the largest length of the largest size class.
`nboot`	the number of bootstrap runs. Default=100.

Details

The Beverton-Holt equilibrium estimator of instantaneous total mortality (Z) from length data (page 365 in Quinn and Deriso (1999)) using Ehrhardt and Ault (1992) bias-correction is calculated. The mean length for lengths >=Lc is calculated automatically. Missing data are removed prior to calculation. Estimates of standard error are made by bootstrapping length data >=Lc using package `boot`.

Value

Dataframe of length 1 containing mean length>=Lc, sample size>=Lc, Z estimate and standard error.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Quinn, T. J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press, New York, New York. 542 pages

Ehrhardt, N. M. and J. S. Ault. 1992. Analysis of two length-based mortality models applied to bounded catch length frequencies. Trans. Am. Fish. Soc. 121:115-122.

See Also

`bheq1` `bhnoneq`

Examples

```
data(herring)
bheq2(herring[,1],K=0.54,Linf=339,Lc=240,La=314,nboot=200)
```

`bhnoneq` *Length-based Beverton-Holt Nonequilibrium Z Estimator*

Description

A nonequilibrium Beverton-Holt estimator of instantaneous total mortality (Z) from length data.

Usage

```
bhnoneq(year=NULL,mlen=NULL, ss=NULL, K = NULL, Linf = NULL,
Lc = NULL, nbreaks = NULL, styrs = NULL, stZ = NULL,
stsigma = NULL)
```

Arguments

`year`	the vector of year values associated with mean length data. The number of year values must correspond to the number of length records. Include year value even if mean length and numbers (see below) are missing.
`mlen`	the vector of mean lengths for lengths >=Lc. One record for each year.
`ss`	the vector of numbers of observations associated with the mean length.
`K`	the growth coefficient from a von Bertalanffy growth model.
`Linf`	the L-infinity coefficient from a von Bertalanffy growth model.

`Lc`	the length at first capture.
`nbreaks`	the number of times (breaks) mortality is thought to change over the time series. Must be 1 or greater
`styrs`	the starting guess(es) of the year(s) during which mortality is thought to change. The number of starting guesses must match the number of mortality breaks, should be separated by commas within the concatentation function and should be within the range of years present in the data.
`stZ`	the starting guesses of Z values enclosed within the concatentation function. There should be *nbreaks+1* values provided.
`stsigma`	the starting guess of sigma.

Details

The mean lengths for each year for lengths>=Lc. Following Gedamke and Hoening(2006), the model estimates `nbreaks+1` Z values, the year(s) in which the changes in mortality began, the standard deviation of lengths>=Lc, and standard errors of all parameters. An AIC value is produced for model comparison. The estimated parameters for the number of `nbreaks` is equal to `2*nbreaks+2`. Problematic parameter estimates may have extremely large t-values or extremely small standard error. Try different starting values to ensure consistent parameter estimates.

Value

`results`	list element containing table of parameters with estimates, standard errors, and t-values.
`obs`	list element containing year, mean length of lengths >=Lc, and sample size.
`pred`	list element containing year and predicted mean lengths.

Note

Todd Gedamke provided the predicted mean length code in C++.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Gedamke, T. and J. M. Hoenig. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosefish. Trans. Am. Fish. Soc. 135:476-487

See Also

bheq2 bheq2

Examples

```
data(goosefish)
bhnoneq(year=goosefish$year,mlen=goosefish$mlen, ss=goosefish$ss,
K=0.108,Linf=126,Lc=30,nbreaks=1,styrs=c(1982),stZ=c(0.1,0.3),
stsigma=20)
```

`buffalo` *Life Table Data for African Buffalo*

Description

The `buffalo` data frame has 20 rows and 3 columns. Cohort size and deaths for African buffalo from Sinclair (1977) as reported by Krebs (1989) in Table 12.1, page 415.

Usage

```
buffalo
```

Format

This data frame contains the following columns:

age age interval

nx number alive at start of each age interval

dx number dying between age interval X and X+1

Source

Krebs, C. J. 1989. *Ecological Methodologies*. Harper and Row, New York, NY. 654 p.

`catch` *Number of cod captured in 10 standardized bottom trawl hauls from Massachusetts, 1985*

Description

The `catch` data frame has 10 rows and 1 column.

Usage

```
catch
```

Format

This data frame contains the following columns:

value catch data

Source

Massachusetts Division of Marine Fisheries

`catchpertrip` *Catch-Per-Trip Analysis for Marine Recreational Fisheries Statistics Survey Data*

Description

Catch-per-trip analysis for Marine Recreational Fisheries Statistics Survey data following the Chapter 4 of Recreational Fisheries Data User's Manual.

Usage

```
catchpertrip(intdir = NULL, estdir = NULL, species = NULL,
 state = NULL, mode = NULL, wave = NULL, styr = NULL,
 endyr = NULL)
```

Arguments

`intdir`	the path and main directory (in quotes) under which raw intercept sub-directories are stored.
`estdir`	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
`species`	10-digit NODC species code. A complete list of species codes is provided at the MRFSS website.
`state`	state(s) code of data to include. A complete list of state codes is provided at the MRFSS website. Atlantic and Gulf States: 23= ME, 33= NH, 25= MA, 44= RI, 9= CT, 36= NY, 34= NJ, 10= DE, 24= MD, 51= VA, 37= NC, 45= SC, 13= GA, 12= FL (121= East FL, 122= West FL), 1= AL, 28= MS, and 22= LA. Any combination of states can be included in c(). North Atlantic= c(9, 23, 25, 33, 44), Mid Atlantic= c(10, 24, 34, 36, 51), South Atlantic= c(13, 37, 45, 121), Gulf of Mexico= c(1, 22, 28, 122).
`wave`	bimothly wave(s) of data to include. Bimothly Waves: 1= Jan-Feb, 2= Mar-Apr, 3= May-Jun, 4=J ul-Aug, 5= Sept-Oct, and 6= Nov-Dec. Any combination of waves can be included in c().
`mode`	the fishing mode(s) of data to include. Valid codes will depend on year. Years 1982-2004: 3= Shore, 6= Party & Charter Boats, 7= Private & Rental Boats. Years 2005-present: 3= Shore, 4= Party Boat, 5= Charter Boat, and 7= Private & Rental Boats. Any combination of modes can be included in c().
`styr`	the starting year of data to include.
`endyr`	the ending year of data to include.

Details

Raw intercept data and catch/effort estimates must be extracted using function `extractMRFSS` before catch-per-trip analysis can be conducted. When performing catch-per-trip analyses within a state/mode/wave stratum, reweighting of data is not necessary since intercept sampling is random within each stratum and an assumption can be made that the true effort distributions are represented. However, if catch-per-trip analyses are performed among state/mode/wave strata, data must be reweighted prior to pooling among strata. This function properly reweights and combines data for catch-per-trip analyses.

Value

`Results`	Dataframe containing catch level (CATCH), estimated number of trips (TRIPS), intercept frequency (CF) and proportion of successful trips(PROP.TRIP)

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Marine Recreational Fisheries Statistics Survey - Recreational Fisheries Data User's Manual

`http://www.st.nmfs.noaa.gov/st1/recreational/SurveyMaterials.html`

See Also

`extractMRFSS`

Examples

```
## Example of a typical specification - for Mid-Atlantic
## black sea bass wave 4, all modes in 1992. Figure 11 of Chapter 4
## in User Manual
## Not run:
catchpertrip(intdir="C:/Temp",estdir="C:/Temp",species=8835020301,
state=c(10,24,34,36,51),mode=c(3,6,7),wave=c(4), styr=1992,endyr=1993)
## End(Not run)
```

`catchseries` *Summary of Catch Estimates from the Marine Recreational Fisheries Statistics Survey*

Description

Species-specific estimates of harvest weight and numbers of fish, released fish, and total catch are summarized for any combination of year(s), state(s), bimonthly wave(s), fishing mode(s), and fishing area(s) from the Marine Recreational Fisheries Statistics Survey (MRFSS) data.

Usage

```
catchseries(estdir = NULL, species = NULL, state = NULL,
 byst = 1, wave = NULL, bywave = 0, mode = NULL,
 bymode = 0, area = NULL, byarea = 0, styr = NULL,
 endyr = NULL)
```

Arguments

`estdir`	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
`species`	10-digit NODC species code. A complete list of species codes is provided at the MRFSS website
`state`	state(s) code of data to include. A complete list of state codes is provided at the MRFSS website. Atlantic and Gulf States: 23= ME, 33= NH, 25= MA, 44= RI, 9= CT, 36= NY, 34= NJ, 10= DE, 24= MD, 51= VA,37= NC, 45= SC, 13= GA, 12= FL (121= East FL, 122= West FL), 1= AL, 28=M S, and 22= LA. Any combination of states can be included in c(). North Atlantic= c(9, 23, 25, 33, 44), Mid Atlantic= c(10, 24, 34, 36, 51), South Atlantic= c(13, 37, 45, 121), Gulf of Mexico= c(1, 22, 28, 122).
`byst`	numeric value. 0 = combine data from states, 1 = show data on state-by-state basis. Default=1
`wave`	bimothly wave(s) of data to include. Bimothly Waves: 1= Jan-Feb, 2= Mar-Apr, 3= May-Jun, 4= Jul-Aug, 5= Sept-Oct, 6= Nov-Dec. Any combination of waves can be included in c().
`bywave`	numeric value. 0 = combine data across waves, 1 = show data on wave-by-wave basis. Default=0
`mode`	the fishing mode(s) of data to include. Valid codes will depend on year. Years 1982-2004: 3= Shore, 6= Party & Charter Boats, and 7= Private & Rental Boats. Years 2005-present: 3= Shore, 4= Party Boat, 5= Charter Boat, and 7= Private & Rental Boats. Any combination of modes can be included in c().
`bymode`	numeric value. 0 = combine data across modes, 1 = show data on mode-by-mode basis. Default=0
`area`	area code of data to include. Area codes: 1= State Territorial Seas (Ocean<=3 mi excluding Inland), 2= Exclusive Economic Zone (Ocean>3 mi), 3= Ocean <=10 mi West FL and TX, 4= Ocean > 10 mi West FL and TX, 5= Inland, 6= Unknown. Any combination of areas can be included in c().
`byarea`	numeric value. 0 = combine data across areas, 1 = show data on area-by-area basis. Default=0
`styr`	the starting year of data to include.
`endyr`	the ending year of data to include.

Details

Catch/effort estimates must be extracted using function `extractMRFSS` before summarization. Harvest, release and weight estimates are always summed by year regardless of whether other factors (state, mode, wave, and area) are aggregated or not. Additional statistics (standard error and proportional standard error) are provided for each estimate. Definition of estimates can be found at the MRFSS wesbite.

Value

`Details`	a list element summarizing the selected arguments.
`Results`	a list element containing the table of summary statistics (i.e., estimate, standard errors, and proportional standard errors) of harvest and release numbers and harvest weight (kg).

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Marine Recreational Fisheries Statistics Survey

`http://www.st.nmfs.noaa.gov/st1/recreational/index.html`

See Also

`extractMRFSS`

Examples

```
## Not run:
outpt<-catchseries(estdir="C:/Temp",species=8835250101,
  state=c(37,45,13,121),mode=c(4,5,6),bymode=1,wave=c(1:6),
  area=c(1,2,3,4,5,7), styr=2000,endyr=2007)
## End(Not run)
```

`clusmean` *Estimation of Population Attributes and Effective Sample Size for Fishes Collected Via Cluster Sampling*

Description

Calculates mean attribute, variance, and effective sample size for samples collected by simple random cluster sampling.

Usage

```
clusmean(popchar = NULL, cluster = NULL, clustotal = NULL)
```

Arguments

`popchar`	vector of population characteristic measurements (e.g., length, weight, etc.). One row represents the measurement for an individual.
`cluster`	vector of numeric or character codes identifying individual clusters (or hauls).
`clustotal`	vector of total number of fish caught per cluster.

Details

In fisheries, gears (e.g., trawls, haul seines, gillnets, etc.) are used to collect fishes. Often, estimates of mean population attributes (e.g., mean length) are desired. The samples of individual fish are not random samples, but cluster samples because the "haul" is the primary sampling unit. Correct estimation of mean attributes requires the use of cluster sampling formulae. Estimation of the general mean attribute and variance follows Pennington et al. (2002). In addition, the effective sample size (the number of fish that would need to be sampled randomly to obtained the same precision as the mean estimate from cluster sampling) is also calculated. The total number of fish caught in a cluster (`clustotal`) allows correct computation for one- and two-stage sampling of individuals from each cluster (haul).

Value

Matrix table of total number of clusters (n), total number of samples (M), total number of samples measured (m), the mean attribute (R), variance of R (varR), variance of population attribute (s2x), and effective sample size (meff).

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Pennington, M. , L. Burmeister, and V. Hjellvik. 2002. *Assessing the precision of frequency distributions estimated from trawl-survey samples* Fish. Bull. 100:74-80.

Examples

```
data(codlengths)
clusmean(popchar=codlengths$tl,cluster=codlengths$station,
clustotal=codlengths$total)
```

`codcluslen` *Lengths of Atlantic cod caught during Massachusetts Division of Marine Fisheries bottom trawl survey, spring 1985.*

Description

The `codcluslen` data frame has 334 rows and 4 columns.

Usage

```
codcluslen
```

Format

This data frame contains the following columns:

region NorthCape = North of Cape Cod; SouthCape =South of Cape Cod

tow Tow number

length Length class (total length, cm)

number Number in length class

Source

Massachusetts Division of Marine Fisheries

`codlengths` *Individual lengths of Atlantic cod from cooperative trawling in winter of 2000, Massachusetts Bay*

Description

The `codlengths` data frame has 184 rows and 3 columns. Station, total number of fish caught, and total lengths (cm) of Atlantic cod (*Gadus morhua*) collected via trawling from northern Massachusetts during winter of 2000

Usage

```
codlengths
```

Format

This data frame contains the following columns:

station trawl haul ID

total total number of cod caught in trawl haul

tl total length of individual fish measured in each haul

Source

Massachusetts Division of Marine Fisheries, 30 Emerson Avenue, Gloucester, MA 01930.

`codstrcluslen` *Lengths of Atlantic cod caught during Massachusetts Division of Marine Fisheries stratified random bottom trawl survey, spring 1985.*

Description

The `codstrcluslen` data frame has 334 rows and 6 columns.

Usage

```
codstrcluslen
```

Format

This data frame contains the following columns:

region NorthCape = North of Cape Cod; SouthCape = South of Cape Cod

stratum Stratum number

tow Tow number

weights Stratum area (square nautical-miles)

length Length class (total length cm)

number Number in length class

Source

Massachusetts Division of Marine Fisheries, 30 Emerson Avenue, Gloucester, MA 01930

`convmort` *Conversion of Mortality Rates*

Description

Convert instantaneous fishing mortality rate (F) to annual exploitation rate (mu) and vice versa for Type I and II fisheries.

Usage

```
convmort(value = NULL, fromto = 1, type = 2, M = NULL)
```

Arguments

`value`	mortality rate
`fromto`	conversion direction: 1=from F to mu; 2 = from mu to F. Default is 1.
`type`	type of fishery following Ricker (1975): 1=Type I; 2=Type II. Default is 2.
`M`	natural mortality rate (for Type II fishery)

Details

Equations 1.6 and 1.11 of Ricker (1975) are used.

Value

A vector of the same length as `value` containing the converted values.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Ricker, W. E. 1975. Computation and interpretation of biological statistics of fish populations. Bull. Fish. Res. Board. Can. 191: 382 p.

Examples

```
convmort(0.3,fromto=1,type=2,M=0.15)
```

`darter` *Catch Removal Data For Fantail Darter*

Description

The `darter` data frame has 7 rows and 2 columns. Sequence of catch data for the faintail darter from removal experiments by Mahon as reported by White et al.(1982). This dataset is often use to test new depletion estimators because the actual abundance is known (N=1151).

Usage

```
darter
```

Format

This data frame contains the following columns:

catch catch data

effort constant effort data

Source

White, G. C., D. R. Anderson, K. P. Burnham, and D. L. Otis. 1982. *Capture-recapture and Removal Methods for Sampling Closed Populations*. Los Alamos National Laboratory LA-8787-NERP. 235 p.

`deltadist` *Delta Distribution Mean and Variance Estimators*

Description

Calculates the mean and variance of a catch series based on the delta distribution described in Pennington (1983).

Usage

```
deltadist(x = NULL)
```

Arguments

`x`	vector of catch values, one record for each haul. Include zero and nonzero catches. Missing values are deleted prior to estimation.

Details

Data from marine resources surveys usually contain a large proportion of hauls with no catches. Use of the delta-distribution can lead to more efficient estimators of the mean and variance because zeros are treated separately. The methods used here to calculate the delta distribution mean and variance are given in Pennington (1983).

Value

vector containing the delta mean and associated variance.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Pennington, M. 1983. Efficient estimators of abundance for fish and plankton surveys. Biometrics 39: 281-286.

Examples

```
data(catch)
deltadist(catch$value)
```

`deplet` *Catch-Effort Depletion Methods For a Closed Population*

Description

Variable and constant effort models for the estimation of abundance from catch-effort depletion data assuming a closed population.

Usage

```
deplet(catch = NULL, effort = NULL, method = c("l", "d", "ml",
 "hosc", "hesc", "hemqle", "sch"), nboot = 500)
```

Arguments

`catch`	the vector containing catches for each removal period (in sequential order).
`effort`	the vector containing effort associated with catch for each removal period. Rows must match those of catch.
`method`	the depletion method. *Variable Effort Models*: `l`= Leslie estimator, `d`= effort corrected Delury estimator, `ml`= maximum likelihood estimator of Gould and Pollock (1997), `hosc`= sampling coverage estimator for homogeneous model of Chao and Chang (1999), `hesc`= sampling coverage estimator for heterogeneous model of Chao and Chang (1999), and `hemqle`= maximum quasi likelihood estimator for heterogeneous model of Chao and Chang (1999). *Constant Effort Models*: `sch`= maximum likelihood models that test for constant catchability.
`nboot`	the number of bootstrap resamples for estimation of standard errors in the `ml`, `hosc`,`hesc`, and `hemqle` methods

Details

The variable effort models include the Leslie-Davis (`l`) estimator (Leslie and Davis, 1939), the effort-corrected Delury (`d`) estimator (Delury,1947; Braaten, 1969), the maximum likelihood (`ml`) method of Gould and Pollock (1997), sample coverage estimator for the homogeneous model (`hosc`) of Chao and Chang (1999), sample coverage estimator for the heterogeneous model (`hesc`) of Chao and Chang (1999), and the maximum quasi-likelihood estimator for the heterogeneous model (`hemqle`) of Chao and Chang (1999). The variable effort models can be applied to constant effort data by simply filling the `effort` vector with 1s. The constant effort models include only model 1 (constant catchability) and model 2 (different catchability in first period) (`sch`) of Schnute (1983) which are equivalent to the generalized removal models for k=1 and k=2, respectively, of White, Anderson, Burnham, and Otis (1982:p. 111-114). A vector of effort data is not required for the Schnute models. Note: Calculation of the standard error using the `ml` method takes considerable time.

Value

Separate output lists with the method name and extension `.out` are created for each method and contain tables of various statistics associated with the method.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Braaten, D. O. 1969. Robustness of the Delury population estimator. J. Fish. Res. Board Can. 26: 339-355.

Chao, A. and S. Chang. 1999. An estimating function approach to the inference of catch-effort models. Environ. Ecol. Stat. 6: 313-334.

Delury, D. B. 1947. On the estimation of biological populations. Biometrics 3: 145-167.

Gould, W. R. and H. H. Pollock. 1997. Catch-effort maximum likelihood estimation of important population parameters. Can. J. Fish. Aquat. Sci 54: 890-897.

Leslie, P. H. and D. H.S. Davis. 1939. An attempt to determine the absolute number of rats on a given area. J. Anim. Ecol. 9: 94-113.

Schnute, J. 1983. A new approach to estimating populations by the removal method. Can. J. Fish. Aquat. Sci. 40: 2153-2169.

White, G. C., D. R. Anderson, K. P. Burnham, and D. L. Otis. 1982. Capture-recapture and Removal Methods for Sampling Closed Populations. Los Alamos National Laboratory LA-8787-NERP. 235 p.

Examples

```
data(darter)
deplet(catch=darter$catch,effort=darter$effort,method="hosc")
hosc.out
```

`depletM` *Catch-Effort Depletion Methods Incorporating Natural Mortality*

Description

Following Rosenberg et al. (1990), the Leslie-Davis and catch equation depletion methods that incorporate natural mortality are implemented for a single fleet. Initial population size (N0) and catchability coefficients with standard errors are estimated from cpue and catch, respectively, via multiple linear regression (Leslie-Davis) and nonlinear regression (catch equation).

Usage

```
depletM(catch = NULL, effort = NULL, M = NULL,
 method = c("l", "c"),stq = NULL, stN0 = NULL)
```

Arguments

`catch`	the vector containing catches for each removal period (in sequential order).
`effort`	the vector containing effort associated with catch for each removal period. Rows must match those of catch.
`M`	the constant natural mortality rate
`method`	the depletion method: l=Leslie-Davis, c=catch equation. Default is both.
`stq`	initial guess for catchability if the catch equation method is used.
`stN0`	initial guess for N0 if the catch equation method is used.

Details

For the Leslie-Davis method, cpue is calculated internally from catch and effort. The natural mortality rate must be scaled to time period between removal (see Rosenberg et al. (1990) for more details). The `lm` and `nls` functions are the estimation methods for the Leslie-Davis and catch equations, respectively.

Value

`results`	list element containing a table of parameters, estimates, associated standard errors, and confidence intervals for each method
`outpt`	list element containing the calculated regressors, predicted cpue (Leslie) or catch (catch equation) and residuals

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Rosenberg, A.A., G. P. Kirkwood, J. A. Crombie, and J. R. Beddington. 1990. The assessment of stocks of annual squid species. Fish. Res. 335-350.

`extractMRFSS` *Extraction of Marine Recreational Fisheries Statistics Survey Data from SAS Transport Files*

Description

MRFSS intercept and catch/effort data in SAS transport files (.xpt) are extracted using package `foreign` and are saved as .csv files under data and year-specific subdirectories.

Usage

```
extractMRFSS(indir = NULL, outdir = NULL, type = NULL,
 state = NULL, styr = NULL, endyr = NULL)
```

Arguments

`indir`	the path and directory (in quotes) under which the SAS transport files are stored.
`outdir`	the path and main directory (in quotes) under which data- and year-specific subdirectories will be created and .csv files will be stored.
`type`	the type of data to extract. 1 = raw intercept data, 2= catch/effort estimates.
`state`	the state code(s) designating which state(s) data to extract. If multiple states, separate state codes with commas within the concatentation function. If data from all states are desired, do not include the `state=` argument. State codes are found on the MRFSS website.
`styr`	the starting year of data to extract.
`endyr`	the ending year of data to extract.

Details

Download the zipped intercept data and catch/effort estimates from the MRFSS website `http://www.st.nmfs.noaa.gov/st1/recreational/index.html`. Unzip/extract the SAS transport files (.xpt) to the `indir` directory. Using this function, specify the `indir` and `outdir` directories, which data type to extract, the state code(s), and the starting and ending years (from .xpt files) of data to be extracted. If the `outdir` directory is not specified, the files will be stored under the `indir` directory.

Value

Raw intercept data and catch & effort estimates saved as .csv files.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

`http://www.st.nmfs.noaa.gov/st1/recreational/index.html`.

Examples

```
## This is a typical specification, not a working example
## Not run:
extractMRFSS(indir="C:/Temp",outdir="C:/MRFSS",type=1,state=25,
styr=1981,endyr=2007)
## End(Not run)
```

`Gerking` *Mark-Recapture Data for Sunfish in an Indiana Lake*

Description

The `Gerking` data frame has 14 rows and 3 columns. Marked and released sunfish in an Indiana lake for 14 days by Gerking (1953) as reported by Krebs (1989, Table 2.1).

Usage

```
Gerking
```

Format

This data frame contains the following columns:

C column of number of captures (column names is unnecessary).

R column of number of recaptures (column name is unnecessary).

nM column of number of newly marked animal (column name is unnecessary).

Source

Krebs, C. J. 1989. *Ecological Methodologies*. Harper and Row, New York, NY. 654 p.

`goosefish` *Mean Length and Numbers of Lengths for Northern Goosefish, 1963-2002*

Description

The `goosefish` data frame has 40 rows and 3 columns. The mean lengths (mlen) by year and number (ss) of observations for length>=smallest length at first capture (Lc) for northern goosefish used in Gedamke and Hoenig (2006)

Usage

```
goosefish
```

Format

This data frame contains the following columns:

year year code

mlen mean length of goosefish, total length (cm)

ss number of samples used to calculate mean length

Source

Gedamke, T. and J. M. Hoenig. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosefish. Trans. Am. Fish. Soc. 135:476-487

`haddock` *Biological data for haddock (Melanogrammus aeglefinus)*

Description

The `haddock` data frame has 15 rows and 4 columns. Age, weight at spawning, partial recruitment, and fraction mature data for haddock (Melanogrammus aeglefinus) used by Gabriel et al. (1989) to calculate spawning stock biomass-per-recruit.

Usage

```
haddock
```

Format

This data frame contains the following columns:

age vector of ages

ssbwgt vector of weights at spawning for each age

partial partial recruitment vector

pmat vector of fraction of females mature at age

Source

Gabriel, W. L., M. P. Sissenwine, and W. J. Overholtz. 1989. Analysis of spawning stock biomass per recruit: an example for Georges Bank haddock. North American Journal of Fisheries Management 9: 383-391.

`herring` *Total length data for alewive (Alosa pseudoharengus) from Massachusetts waters*

Description

The `herring` data frame has 52 rows and 1 column. Total length (mm)

Usage

```
herring
```

Format

This data frame contains the following columns:

tl total length of individual alewife

Source

Massachusetts Division of Marine Fisheries, 30 Emerson Avenue, Gloucester, MA 01930

`Jensen` *Age Frequency Data for Lake Whitefish By Individual Haul*

Description

The `Jensen` data frame has 312 rows and 2 columns. The age data are from reconstructed catches of lake whitefish reported by Jensen (1996) in Table 1 and were expanded to individual observations from the age frequency table.

Usage

```
Jensen
```

Format

This data frame contains the following columns:

group net haul label

age age of an individual fish

Source

Jensen, A. L. 1996. *Ratio estimation of mortality using catch curves*. Fisheries Research 27: 61-67.

`Kimura` *Length and Age Data For Male and Female Pacific Hake*

Description

The `Kimura` data frame has 24 rows and 3 columns. Mean length-at-age data for male and female Pacific hake as reported by Kimura (1980)

Usage

```
Kimura
```

Format

This data frame contains the following columns:

age fish age

length mean length of fish of age *age*

sex sex code

Source

Kimura, D. K. 1980. *Likelihood methods for the von Bertalanffy growth curve*. U. S. Fishery Bulletin 77:765-776.

`lengthfreq` *Calculate Length Frequencies from Marine Recreational Fisheries Statistics Survey Data*

Description

A combined length frequency table for a species is generated for any combination of year(s), state(s), bimonthly wave(s), fishing mode(s), and fishing area(s) from the Marine Recreational Fisheries Statistics Survey (MRFSS) data. The analytical steps given in Recreational Fisheries Data User's Manual are followed.

Usage

```
lengthfreq(intdir = NULL, estdir = NULL, species = NULL,
 state = NULL, wave = NULL, mode = NULL, area = NULL,
 styr = NULL, endyr = NULL, conveq = FALSE,
 parms = c(0, 1))
```

Arguments

`intdir`	the path and main directory (in quotes) under which raw intercept sub-directories are stored.
`estdir`	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
`species`	10-digit NODC species code. A complete list of species codes is provided at the MRFSS website
`state`	state(s) code of data to include. A complete list of state codes is provided at the MRFSS website. Atlantic and Gulf States: 23= ME, 33= NH, 25= MA, 44= RI, 9= CT, 36= NY, 34= NJ, 10= DE, 24= MD, 51= VA,37= NC, 45= SC, 13= GA, 12= FL (121= East FL, 122= West FL), 1=AL, 28= MS, and 22= LA. Any combination of states can be included in c(). North Atlantic= c(9, 23, 25, 33, 44), Mid Atlantic= c(10, 24, 34, 36, 51), South Atlantic= c(13, 37, 45, 121), Gulf of Mexico= c(1, 22, 28, 122).

`wave`	bimothly wave(s) of data to include. Bimothly Waves: 1= Jan-Feb, 2= Mar-Apr, 3= May-Jun, 4= Jul-Aug, 5= Sept-Oct, and 6= Nov-Dec. Any combination of waves can be included in c().
`mode`	the fishing mode(s) of data to include. Valid codes will depend on year. Years 1982-2004: 3= Shore, 6= Party & Charter Boats, and 7= Private & Rental Boats. Years 2005-present: 3= Shore, 4= Party Boat, 5= Charter Boat, and 7= Private & Rental Boats. Any combination of modes can be included in c().
`area`	area code of data to include. Valid codes are: 1= State Territorial Seas (Ocean<= 3 mi excluding Inland), 2= Federal Exclusive Economic Zone (Ocean > 3 mi), 3= Ocean <=10 mi West FL and TX, 4= Ocean > 10 mi West FL and TX, 5= Inland, and 6= Unknown. Any combination of areas can be included in c().
`conveq`	logical to indicate whether a length conversion equation will be provided. If TRUE, provide the intercept and slope in `parms` argument below. Conversion equation is used to convert MRFSS fork length (mm) to other length measurements.
`parms`	vector containing the intercept (position 1) and slope (position 2) of the conversion equation
`styr`	the starting year of data to include.
`endyr`	the ending year of data to include.

Details

Raw intercept data and catch/effort estimates must be extracted using function `extractMRFSS` before length frequencies can be created. Length frequencies are produced with one-inch length groups identical to the MRFSS website. Before creation of the length frquency table, fork length (in millimeters) is converted to inches. The intercept and slope parameters of a conversion equation can be introduced to convert fork length into other length measurements before creating the length frequencies. Length data and harvest estimates from the catch/effort files are extracted using the argument values. Length frequencies are created for each state/mode/wave/area fished stratum and are weighted with matching harvest estimates before being combined across strata.

Value

`Details`	a list element summarizing the selected arguments.
`Results`	a list element containing the length frequency table with one-inch length group, numbers-at-length, and proportions-at-length

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Marine Recreational Fisheries Statistics Survey - Recreational Fisheries Data User's Manual

`http://www.st.nmfs.noaa.gov/st1/recreational/SurveyMaterials.html`

See Also

`extractMRFSS`

Examples

```
##Example of a typical specification - not a working example
## Not run:
dodo<-lengthfreq(intdir="C:/Temp",estdir="C:/Temp",species=8835250101,
 state=c(25),mode=c(3,4,5,7),wave=c(1,2,3,4,5,6),area=c(1,2,3,4,5,7),
 styr=2007,endyr=2007)
## End(Not run)
```

`lfclus` *Statistical Comparison of Length Frequencies from Simple Random Cluster Sampling*

Description

Statistical comparison of length frequencies is performed using the two-sample Kolmogorov & Smirnov test. Randomization procedures are used to derive the null probability distribution.

Usage

```
lfclus(group = NULL, haul = NULL, len = NULL, number= NULL,
 binsize = NULL, resamples = 100)
```

Arguments

`group`	vector containing the identifier used for group membership of length data. This variable is used to determine the number of groups and comparisons. Identifier can be numeric or character.
`haul`	vector containing the variable used to identify the sampling unit (e.g., haul) of length data. Identifier can be numeric or character.
`len`	vector containing the length class data. There should be one record for each length class by group and haul.
`number`	vector containing the numbers of fish in each length class.
`binsize`	size of the length class (e.g., 5-cm, 10, cm, etc.) used to construct the cumulative length frequency from raw length data. The formula used to create bins is $trunc(len/binsize)*binsize+binsize/2$. If use of the raw length classes is desired, then `binsize=0`.
`resamples`	number of randomizations. Default = 100.

Details

Length frequency distributions of fishes are commonly tested for differences among groups (e.g., regions, sexes, etc.) using a two-sample Kolmogov-Smirnov test (K-S). Like most statistical tests, the K-S test requires that observations are collected at random and are independent of each other to satisfy assumptions. These basic assumptions are violated when gears (e.g., trawls, haul seines, gillnets, etc.) are used to sample fish because individuals are collected in clusters . In this case, the "haul", not the individual fish, is the primary sampling unit and statistical comparisons must take this into account.

To test for difference between length frequency distributions from simple random cluster sampling, a randomization test that uses "hauls" as the primary sampling unit can be used to generate the null probability distribution. In a randomization test, an observed test statistic is compared to an empirical probability density distribution of a test statistic under the null hypothesis of no difference. The observed test statistic used here is the Kolmogorov-Smirnov statistic (Ds) under a two-tailed test:

$$Ds = max|S1(X) - S2(X)|$$

where S1(X) and S2(X) are the observed cumulative length frequency distributions of group 1 and group 2 in the paired comparisons. S1(X) and S2(X) are calculated such that `S(X)=K/n` where K is the number of scores equal to or less than X and n is the total number of length observations (Seigel, 1956).

To generate the empirical probability density function (pdf), haul data are randomly assigned without replacement to the two groups with samples sizes equal to the original number of hauls in each group under comparison. The K-S statistic is calculated from the cumulative length frequency distributions of the two groups of randomized data. The randomization procedure is repeated `resamples` times to obtain the pdf of D. To estimate the significance of Ds, the proportion of all randomized D values that were greater than or equal to Ds, including the occurrence of Ds in the numerator and denominator, is calculated (Manly, 1997).

It is assumed all fish caught are measured. If subsampling occurs, the number at length (measured) must be expanded to the total caught.

Data vectors described in `arguments` should be aggregated so that each record contains the number of fish in each length class by group and haul identifier. For example,

`group`	`tow`	`length`	`number`
North	1	10	2
North	1	12	5
North	2	11	3
North	1	10	17
North	2	14	21
.	.	.	.
.	.	.	.
South	1	12	34
South	1	14	3

Value

`results`	list element containing the Ds statistics from the observed data comparisons and significance probabilities.
`obs_prop`	list element containing the observed cumulative proportions for each group.
`Drandom`	list element containing the D statistics from randomization for each comparison.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Manly, B. F. J. 1997. Randomization, Bootstrap and Monte Carlos Methods in Biology. Chapman and Hall, New York, NY, 399 pp.

Seigel, S. 1956. Nonparametric Statistics for Behavioral Sciences. McGraw-Hill, New York, NY. 312 p.

See Also

`lfstrclus`

Examples

```
data(codcluslen)
lfclus(group=codcluslen$region,haul=codcluslen$tow,len=codcluslen$length,
number=codcluslen$number,binsize=5,resamples=100)
```

`lfstrclus` *Statistical Comparison of Length Frequencies from Stratified Random Cluster Sampling*

Description

Statistical comparison of length frequencies is performed using the two-sample Kolmogorov & Smirnov test. Randomization procedures are used to derive the null probability distribution.

Usage

```
lfstrclus(group = NULL, strata = NULL, weights = NULL,
 haul = NULL, len = NULL, number = NULL, binsize = NULL,
 resamples = 100)
```

Arguments

`group`	vector containing the identifier used for group membership of length data. This variable is used to determine the number of groups and comparisons. Identifier can be numeric or character.
`strata`	vector containing the numeric identifier used for strata membership of length data. There must be a unique identifier for each stratum regardless of group membership.
`weights`	vector containing the strata weights (e.g., area, size, etc.) used to calculate the stratified mean length for a group.
`haul`	vector containing the variable used to identify the sampling unit (e.g., haul) of length data. Identifier can be numeric or character.
`len`	vector containing the length class. Each length class record must have associated group, strata, weights, and haul identifiers.
`number`	vector containing the number of fish in each length class.
`binsize`	size of the length class (e.g., 5-cm, 10, cm, etc.) used to construct the cumulative length frequency from raw length data. The formula used to create bins is $trunc(len/binsize) * binsize + binsize/2$. If use of the raw length classes is desired, then `binsize=0`.
`resamples`	number of randomizations. Default = 100.

Details

Length frequency distributions of fishes are commonly tested for differences among groups (e.g., regions, sexes, etc.) using a two-sample Kolmogov-Smirnov test (K-S). Like most statistical tests, the K-S test requires that observations are collected at random and are independent of each other to satisfy assumptions. These basic assumptions are violated when gears (e.g., trawls, haul seines, gillnets, etc.) are used to sample fish because individuals are collected in clusters . In this case, the "haul", not the individual fish, is the primary sampling unit and statistical comparisons must take this into account.

To test for difference between length frequency distributions from stratified random cluster sampling, a randomization test that uses "hauls" as the primary sampling unit can be used to generate the null probability distribution. In a randomization test, an observed test statistic is compared to an empirical probability density distribution of a test statistic under the null hypothesis of no difference. The observed test statistic used here is the Kolmogorov-Smirnov statistic (Ds) under a two-tailed test:

$$Ds = max|S1(X) - S2(X)|$$

where S1(X) and S2(X) are the observed cumulative proportions at length for group 1 and group 2 in the paired comparisons.

Proportion of fish of length class j in strata-set (group variable) used to derive `Ds` is calculated as

$$p_j = \frac{\sum A_k \bar{X}_{jk}}{\sum A_k \bar{X}_k}$$

where A_k is the weight of stratum k, $\bar{X}_{jk}$ is the mean number per haul of length class `j` in stratum `k`, and $\bar{X}_k$ is the mean number per haul in stratum `k`. The numerator and denominator are summed over all `k`. Before calculation of cumulative proportions, the length class distributions for each group are corrected for missing lengths and are constructed so that the range and intervals of each distribution match.

It is assumed all fish caught are measured. If subsampling occurs, the numbers at length (measured) must be expanded to the total caught.

To generate the empirical probability density function (pdf), length data of hauls from all strata are pooled and then hauls are randomly assigned without replacement to each stratum with haul sizes equal to the original number of stratum hauls. Cumulative proportions are then calculated as described above. The K-S statistic is calculated from the cumulative length frequency distributions of the two groups of randomized data. The randomization procedure is repeated `resamples` times to obtain the pdf of D. To estimate the significance of Ds, the proportion of all randomized D values that were greater than or equal to Ds, including the occurrence of Ds in the numerator and denominator, is calculated (Manly, 1997).

Data vectors described in `arguments` should be aggregated so that each record contains the number of fish in each length class by group, strata, weights, and haul identifier. For example,

`group`	`stratum`	`weights`	`tow`	`length`	`number`
North	10	88	1	10	2
North	10	88	1	12	5
North	10	88	2	11	3
North	11	103	1	10	17
North	11	103	2	14	21
.	.	.	.	.	.
.	.	.	.	.	.
South	31	43	1	12	34
South	31	43	1	14	3

To correctly calculate the stratified mean number per haul, zero tows must be included in the dataset. To designate records for zero tows, fill the length class and number at length with zeros. The first line in the following table shows the appropriate coding for zero tows:

`group`	`stratum`	`weights`	`tow`	`length`	`number`
North	10	88	1	0	0
North	10	88	2	11	3
North	11	103	1	10	17
North	11	103	2	14	21
.	.	.	.	.	.
.	.	.	.	.	.
South	31	43	1	12	34
South	31	43	1	14	3

Value

`results`	list element containing the Ds statistics from the observed data comparisons and significance probabilities.

`obs_prop`	list element containing the cumulative proportions from each group.
`Drandom`	list element containing the D statistics from randomization for each comparison.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Manly, B. F. J. 1997. Randomization, Bootstrap and Monte Carlos Methods in Biology. Chapman and Hall, New York, NY, 399 pp.

Seigel, S. 1956. Nonparametric Statistics for Behavioral Sciences. McGraw-Hill, New York, NY. 312 p.

See Also

`lfclus`

Examples

```
data(codstrcluslen)
lfstrclus(
group=codstrcluslen$region,strata=codstrcluslen$stratum,
 weights=codstrcluslen$weights,haul=codstrcluslen$tow,
 len=codstrcluslen$length,number=codstrcluslen$number,
 binsize=5,resamples=100)
```

`lifetable` *Life Table Construction*

Description

Life tables are constructed from either numbers of individuals of a cohort alive at the start of an age interval (nx) or number of individuals of a cohort dying during the age interval (dx).

Usage

```
lifetable(age = NULL, numbers = NULL, r = NULL, type = 1)
```

Arguments

`age`	vector of age intervals (e.g., 0 to maximum cohort age).
`numbers`	number of individual alive (nx) or dead (dx)
`r`	known rate of increase (r) for methods 3 and 4

`type`	numeric value of method to use to calculate life table. 1 = Age at death recorded directly and no assumption made about population stability or stability of age structure - Method 1 in Krebs (1989). 2 = Cohort size recorded directly and and no assumption made about population stability or stability of age structure - Method 2 in Krebs (1989). 3 = Ages at death recorded for a population with stable age distribution and known rate of increase - Method 5 in Krebs (1989). 4 = Age distribution recorded for a population with a stable age distribution and known rate of increase - Method 6 in Krebs (1989).

Details

Following Krebs (1989:413-420), standard life tables are calculated given age intervals and either cohort size or deaths. X=age interval, nx=number of individuals of a cohort alive at the start of age interval X, lx = proportion of individuals surviving at the start of age interval X, dx = number of individuals of a cohort dying during the age interval X, qx=finite rate of mortality during the age interval X to X+1, px=finite rate of survival during the age interval X to X+1, ex=mean expectation of life for individuals alive at start of age X. For method 5, dx is corrected for population growth by *dx'=dx*exp(r*x)* and in method 6, nx is corrected for the same by *nx*e(r*x)*. See Krebs for formulae.

Value

Dataframe containing life table values.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Krebs, C. J. 1989. *Ecological Methodologies*. Harper and Row, New York, NY. 654 p.

Examples

```
data(buffalo)
lifetable(age=buffalo$age,numbers=buffalo$nx,type=2)
```

`M.empirical` *Estimation of Natural Mortality Rates from Life History Parameters*

Description

The approaches of Pauly (1980), Hoenig (1983), Alverson and Carney (1975), Roff (1984), Gunderson and Dygert (1988), Petersen and Wroblewski (184) and Lorenzen (1996) are encoded for estimation of natural mortality (M).

Usage

```
M.empirical(Linf = NULL, Winf = NULL, Kl = NULL, Kw = NULL,
 T = NULL, tmax = NULL, tm = NULL, GSI = NULL, Wdry = NULL,
 Wwet = NULL, method = c(1, 2, 3, 4, 5, 6, 7, 8))
```

Arguments

`Linf`	Length-infinity value from a von Bertalanffy growth curve (total length-cm).
`Winf`	Weight-infinity value from a von Bertalanffy growth curve (wet weight-grams).
`Kl`	Kl is the growth coefficient (per year) from a von Bertalanffy growth curve for length.
`Kw`	Kw is the growth coefficient (per year) from a von Bertalanffy growth curve for weight.
`T`	the mean water temperature (Celsius) experienced by the stock.
`tmax`	the oldest age observed for the species.
`tm`	the age at maturity.
`GSI`	gonadosomatic index (wet ovary weight over wet body weight).
`Wdry`	total dry weight in grams.
`Wwet`	total wet weight at mean length in grams.
`method`	vector of method code(s). Any combination of methods can employed. `1`= Pauly (1980) length equation - requires Linf, Kl, and T; `2`= Pauly (1980) weight equation - requires Winf, Kw, and T; `3`= Hoenig (1983) joint equation - requires tmax; `4`= Alverson and Carney (1975) - requires Kl and tmax; `5`= Roff (1984) - requires Kl and tm; `6`= Gunderson and Dygert (1988) - requires GSI; `7`= Peterson and Wroblewski (1984) - requires Wdry; `8`= Lorenzen (1996) - requires Wwet

Details

Please read the references below for details about equations. Some estimates of M will not be valid for certain fish groups.

Value

A matrix of M estimates.

Note

Original functions for the Pauly (1980) length equation and the Hoenig (1983) fish equation were provided by Michael H. Prager, National Marine Fisheries Service, Beaufort, North Carolina.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Alverson, D. L. and M. J. Carney. 1975. A graphic review of the growth and decay of population cohorts. J. Cons. Int. Explor. Mer 36: 133-143.

Gunderson, D. R. and P. H. Dygert. 1988. Reproductive effort as a predictor of natural mortality rate. J. Cons. Int. Explor. Mer 44: 200-209.

Hoenig, J. M. 1983. Empirical use of longevity data to estimate mortality rates. Fish. Bull. 82: 898-903.

Lorenzen, K. 1996. The relationship between body weight and natural mortality in juvenile and adult fish: a comparison of natural ecosystems and aquaculture. J. Fish. Biol. 49: 627-647.

Pauly, D. 1980. On the interrelationships between natural mortality, growth parameters, and mean environmental temperature in 175 fish stocks. J. Cons. Int. Explor. Mer: 175-192.

Peterson, I. and J. S. Wroblewski. 1984. Mortality rate of fishes in the pelagic ecosystem. Can. J. Fish. Aquat. Sci. 41: 1117-1120.

Roff, D. A. 1984. The evolution of life history parameters in teleosts. Can. J. Fish. Aquat. Sci. 41: 989-1000.

Examples

```
M.empirical(Linf=30.1,Kl=0.31,T=24,method=c(1))
```

`mrN.single` *Estimate of Population Size from a Single Mark-Recapture Experiment*

Description

Estimates population sizes, standard errors, and confidence intervals for the bias-corrected Petersen and the Bailey binomial estimators.

Usage

```
mrN.single(M = NULL, C = NULL, R = NULL, alpha = 0.05)
```

Arguments

`M`	Number of marked animals released
`C`	Number of animals captured
`R`	Number of animals recaptured
`alpha`	alpha level for confidence intervals

Details

The bias-corrected Petersen estimator and its variance (Seber 2002: p.60), and the Bailey binomial estimator and its variance (Seber 2002: p.61) are calculated. The hypergeometric distribution is used to estimate confidence intervals for the Petersen model and the binomial distribution is used to estimate confidence intervals for the Bailey model.

Value

Dataframe containing the population estimates (N), standard errors of N, the lower confidence limits (LCI), and the upper confidence limits(UCI).

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Seber, G. A. F. 2002. *The Estimation of Animal Abundance and Related Parameters, Second Edition*. The Blackburn Press, Caldwell, New Jersey. 654 p.

Examples

```
mrN.single(M=948,C=421,R=167)
```

`opt_slot` *Optimum Slot and Trophy Size Limits for Recreational Fisheries*

Description

Calculates optimum trophy catch given a slot size over a range of F values. Also, finds Fmax for a cohort given age-at-first recruitment, age-at-first-entry, slot age, and age at which fish are considered trophy size following Jensen (1981).

Usage

```
opt_slot(M = NULL, N = 1000, recage = NULL, entage = NULL,
 trage = NULL, slage = NULL,  stF = 0, endF = 2, intF = 0.05)
```

Arguments

`M`	natural mortality
`N`	cohort size
`recage`	age-at-first recruitment
`entage`	age-at-entry into the fishery
`slage`	upper age of slot for legal fish
`trage`	age of fish considered trophy size
`stF`	starting F of range to explore
`endF`	ending F of range to explore
`intF`	increment of F

Details

Calculations follow equations given in Jensen (1981).

Value

`Catch`	dataframe containing range of Fs and associated total catch, nontrophy, and trophy catch of designated cohort size
`Fmax`	F at which trophy catch is maximum given slot

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Jense, A. L. 1981. Optimum size limits for trout fisheries. Can. J. Fish. Aquat. Sci. 38: 657-661.

See Also

`opt_trophy`

Examples

```
# Example from Jensen (1981) page 661
opt_slot(M=0.70,N=1000,recage=1,entage=1,slage=3,trage=4)
```

`opt_trophy` *Optimum Trophy Size Limits for Recreational Fisheries*

Description

Calculates optimum trophy catch over a range of F values and finds Fmax for a cohort given age-at-first recruitment, age-at-first-entry, and age at which fish are considered trophy size following Jensen (1981).

Usage

```
opt_trophy(M = NULL, N = 1000, recage = NULL, entage = NULL,
 trage = NULL, stF = 0, endF = 2, intF = 0.05)
```

Arguments

`M`	natural mortality
`N`	cohort size
`recage`	age-at-first recruitment
`entage`	age-at-entry into the fishery
`trage`	age of fish considered trophy size
`stF`	starting F of range to explore
`endF`	ending F of range to explore
`intF`	increment of F

Details

Calculations follow equations given in Jensen (1981).

Value

`Catch`	dataframe containing range of Fs and associated total catch and trophy catch of designated cohort size
`Fmax`	F at which trophy catch is maximum

Author(s)

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References

Jense, A. L. 1981. Optimum size limits for trout fisheries. Can. J. Fish. Aquat. Sci. 38: 657-661.

See Also

`opt_slot`

Examples

```
# Example from Jensen (1981) page 659
opt_trophy(M=0.70,N=1000,recage=1,entage=1,trage=4)
```

`powertrend` *Power Analysis For Detecting Trends*

Description

Power analysis for detecting trends in linear regression is implemented following procedures in Gerrodette (1987; 1991).

Usage

```
powertrend(trend = 1, A1 = NULL, PSE = NULL, pserel = 1,
 maxyrs = 3, pR = 100, step = 5, alpha = 0.05, tail = 2)
```

Arguments

`trend`	1 = Linear, 2 = Exponential. Default = 1.
`A1`	the start year abundance. In actuality, it can be population size, productivity, diversity, mortality rate, etc.
`PSE`	the proportional standard error (SE(A)/A) = CV in Gerrodette (1987;1991).
`pserel`	the relationship between abundance and PSE: 1 = 1/sqrt(A1), 2 = constant, 3 = sqrt(A1). Default = 1.

`maxyrs`	the maximum number of samples or years to project start year abundance. Default = 3.
`pR`	the highest positive percent change to investigate. Default = 100.
`step`	the increment of the range of percent change to investigate. Default = 5.
`alpha`	the alpha level (Type I error) to use. Default = 0.05.
`tail`	type of tailed test: 1 = one-tailed, 2= two-tailed. Default = 2.

Details

The probability that an upward or downward trend in abundance (power) will be detected is calculated using linear regression given number of samples (`maxyrs`), estimates of sample variability (`PSE`) and abundance-PSE relationship (`pserel`), and percent rate of change. The program calculates power for each `step` increment beginning at -100 percent for declining changes and ending at `pR` percent for increasing changes. See Gerrodette (1987;1991) for full details. It is assumed that time intervals between samplings is equal.

Value

Dataframe containing columns of number of samples (`years`), trend selected (`trend`), the PSE (`pse`), alpha level (`alpha`), tail of test (`tail`), percent change (`R`) over `maxyrs`, and power (`power`).

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Gerrodette, T. 1987. A power analysis for detecting trends. Ecology. 68(5): 1364-1372.

Gerrodette, T. 1991. Models for power of detecting trends - a reply to Link and Hatfield. Ecology 72(5): 1889-1892.

Examples

```
powertrend(A1=1000,PSE=0.1)
```

`pstrat` *Post-stratification of Marine Recreational Fisheries Statistics Survey Estimates of Catch*

Description

Post-stratified catch and variance estimates are generated from the original intercept data and catch & effort estimates provided by the Marine Recreational Fisheries Statistics Survey (MRFSS).

Usage

```
pstrat(intdir = NULL, estdir = NULL, pstdir = NULL, state = NULL,
 year = NULL, stwave = NULL, endwave = NULL, psfactor = NULL)
```

Arguments

`intdir`	the path and main directory (in quotes) under which raw intercept sub-directories are stored.
`estdir`	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
`pstdir`	the path and main directory (in quotes) under which post-stratified estimates will be stored. The program will store the post-stratification estimates as a .csv file under a subdirectory named *pest*`year`.
`year`	year of data to include.
`state`	state(s) code of data to include. A complete list of state codes is provided at the MRFSS website. Atlantic and Gulf States: 23= ME, 33= NH, 25= MA, 44= RI, 9= CT, 36= NY, 34= NJ, 10= DE, 24= MD, 51= VA, 37= NC, 45= SC, 13= GA, 12= FL (121= East FL, 122= West FL), 1=AL, 28= MS, and 22= LA. Any combination of states can be included in c(). North Atlantic= c(9, 23, 25, 33, 44), Mid Atlantic= c(10, 24, 34, 36, 51), South Atlantic= c(13, 37, 45, 121), Gulf of Mexico= c(1, 22, 28, 122).
`stwave`	bimothly wave(s) of data to include. Bimothly Waves: 1= Jan-Feb, 2= Mar-Apr, 3= May-Jun, 4= Jul-Aug, 5= Sept-Oct, and 6= Nov-Dec. Any combination of waves can be included in c().
`endwave`	last bimonthly wave of data to include.
`psfactor`	name of dataframe with poststratification variable(s)

Details

Raw intercept data and catch/effort estimates must be extracted using function `extractMRFSS`. Post-stratification methodology follows the SAS post-stratification program available from MRFSS. A dataframe must be created that contains the MRFSS variable(s) linked to the variable AREA.G which identifies the post-stratification scheme.

As a first example, the State of Massachusetts post-stratifies catch estimates by county to examine regional fishing harvest. The MRFSS variable CNTY is used to group the regions. To code the post-stratification variable, a dataframe containing CNTY numbers and the associated grouping labels under variable `AREA.G` is created as follows:

```
post<-data.frame(CNTY=c(9,21,25,23,1,7,5,18,17,27),
AREA.G=c("A","B","C","D","E","F","G","H","Y","Y"))
```

Each `AREA.G` label is matched to a specific county. `AREA.G` must be the name of the grouping label. More than one variable (other than CNTY) can be used to parse the data into more specific strata by creating an additional column in the dataframe.

As a second example, the State of Florida post-stratifies catch estimates into four regions (Northeast, Southeast, Southwest and Northwest Florida) related to spotted seatrout (Cynoscion nebulosus) management. The coding for the four regions uses CNTY to create groupings:

```
post<-data.frame(CNTY=c(89,31,109,35,19,107,127,9,61,111,85,
                        99,11,25,87,21,51,71,15,27,115,81,
                        57,103,101,53,17,75,1,29,123,65,129,37,
                        77,45,5,133,131,91,113,33
                        ),
                       AREA.G=c("N","N","N","N","N","N",
                       "S","S","S","S","S","S","S",
                       "S","S","S","S","S","S","S",
                       "S","S","S","S","N","N","N",
                       "N","N","N","N","N","N","N",
                       "N","N","N","N","N","N","N",
                       "N"))
```

Notice that there are not four `AREA.G` labels for the different areas because post-stratification is automatically performed over the sub-region variable (Florida East Coast SUB.REG=6 and Florida West Coast is SUB.REG=7). For states with only one SUB.REG code, four `AREA.G`labels would need to be created.

The AREA.S variable, which is the AREA.G and AREA.X labels combined, is created in the output file and designates the post-stratification levels.

All variables coded found in the MRFSS Recreational Fisheries Data User's Manual.

Value

Post-stratified estimates from each year and wave are written to comma-delimited (.csv) files and are stored under the `pestdir` directory as AG_*yyyywv*`.csv` (e.g., `AG_20075.csv`).

Note

The MRFSS post-stratification program written in SAS by Gerry Gray et al. of the National Marine Fisheries Service was converted to R-code.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Marine Recreational Fisheries Statistics Survey - Recreational Fisheries Data User's Manual

`http://www.st.nmfs.noaa.gov/st1/recreational/SurveyMaterials.html`

See Also

`extractMRFSS`

Examples

```
## An example of code - not a working example
## Not run:
post<-data.frame(CNTY=c(9,21,25,23,1,7,5,18,17,27),
            AREA.G=c("A","B","C","D","E","F","G","H","Y","Y"))

pstrat(intdir="C:/Temp", estdir="C:/Temp",pstdir="C:/Temp",state=25,
  year=2007,stwave=2,endwave=6,psfactor=post)
## End(Not run)
```

`rockbass` *Age Frequency Data for Rock Bass*

Description

The `rockbass` data frame has 243 rows and 1 column. The age data are from a sample of rock bass trap-netted from Cayuga Lake, New York by Chapman and Robson, as reported by Seber (2002; page 417) and were expanded to individual observations from the age frequency table.

Usage

```
rockbass
```

Format

This data frame contains the following columns:

age age of individual rock bass in years

Source

Seber, G. A. F. 2002. *The Estimation of Animal Abundance and Related Parameters, Second Edition*. The Blackburn Press, Caldwell, New Jersey. 654 p.

`sbpr` *Spawning Stock Biomass-Per-Recruit Analysis*

Description

Spawning stock biomass-per-recruit(SBPR) analysis is conducted following Gabriel et al. (1989). Reference points of F and SBPR for a percentage of maximum spawning potential are calculated.

Usage

```
sbpr(age = NULL, ssbwgt = NULL, partial = NULL, pmat = pmat,
 M = NULL, pF = NULL, pM = NULL, MSP = 40, plus = FALSE,
 oldest = NULL, maxF = 2, incrF = 1e-04)
```

Arguments

`age`	vector of cohort ages. If the last age is a plus group, do not add a "+" to the age.
`ssbwgt`	vector of spawning stock weights for each age. Length of vector must correspond to the length of the age vector.
`partial`	partial recruitment vector applied to fishing mortality (F) to obtain partial F-at-age. Length of this vector must match length of the age vector.
`pmat`	proportion of mature fish at each age. Length of this vector must match the length of the age vector.
`M`	vector containing a single natural mortality (M) rate if M is assumed constant over all ages, or a vector of Ms, one for each age. If the latter, the vector length match the length of the age vector.
`pF`	the proportion of fishing mortality that occurs before spawning.
`pM`	the proportion of natural mortality that occurs before spawning.
`MSP`	the percentage of maximum spawning potential (percent MSP reference point) for which F and SBPR should be calculated.
`plus`	a logical value indicating whether the last age is a plus-group. Default is FALSE.
`oldest`	if plus=TRUE, a numeric value indicating the oldest age in the plus group.
`maxF`	the maximum value of F range over which SBPR will be calculated. SBPR is calculated for F = 0 to maxF.
`incrF`	F increment for SBPR calculation.

Details

Spawning stock biomass-per-recruit analysis is conducted following Gabriel et al. (1989). The F and SBPR for the percentage maximum spawning potential reference point are calculated. If the last age is a plus-group, the cohort is expanded to the `oldest` age and the `ssbwgt`, `partial`, `pmat`, and `M` values for the plus age are applied to the expanded cohort ages.

Value

`Reference_Points`	F and SBPR values for the percentage MSP
`SBPR_vs_F`	Spawning stock biomass-per-recruit values for each F increment

Author(s)

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References

Gabriel, W. L., M. P. Sissenwine, and W. J. Overholtz. 1989. Analysis of spawning stock biomass per recruit: an example for Georges Bank haddock. North American Journal of Fisheries Management 9: 383-391.

See Also

`ypr`

Examples

```
data(haddock)
sbpr(age=haddock$age,ssbwgt=haddock$ssbwgt,partial=haddock$partial,
pmat=haddock$pmat,M=0.2,pF=0.2, pM=0.1667,MSP=30,plus=FALSE,maxF=2,
incrF=0.001)
```

`schnabel` *Population Size Estimates from Repeated Mark-Recapture Experiments*

Description

Estimates of population abundance from Schnabel (1938) and Schumacher and Eschmeyer (1943) are calculated from repeated mark-recapture experiments following Krebs (1989).

Usage

```
schnabel(catch = NULL, recaps = NULL, newmarks = NULL,
 alpha = 0.05)
```

Arguments

`catch`	A vector containing the number of animal caught in each mark-recapture experiment.
`recaps`	A vector containing the number of animal recaptured in each mark-recapture experiment.
`newmarks`	A vector containing the newly marked animals in each mark-recapture experiment.
`alpha`	the alpha level for confidence intervals. Default = 0.05

Details

All computations follow Krebs (1989: p. 30-34). For the Schnabel method, the poisson distribution is used to set confidence intervals if the sum of all recaptures is <50,and the t distribution is used if the sum of all recaptures is >=50. For the Schumacher-Eschmeyer method, the t distribution is used to set confidence intervals.

Value

Dataframe containing the population estimates for the Schnabel and Schumacher & Eschmeyer methods (N), the inverse standard errors (invSE), lower (LCI) and upper (UCI) confidence intervals, and the type of distribution used to set confidence intervals (CI Distribution).

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Krebs, C. J. 1989. *Ecological Methodologies*. Harper and Row, New York, NY. 654 p.

Examples

```
data(Gerking)
schnabel(catch=Gerking$C,recaps=Gerking$R, newmarks=Gerking$nM,
 alpha=0.10)
```

`Shepherd` *Seasonal Length Frequencies for Raja clavata*

Description

The `Shepherd` data frame has 24 rows and 4 columns. The seasonal length frequency data of Raja clavata are from Shepherd's working document.

Usage

```
Shepherd
```

Format

This data frame contains the following columns:

length lower limit of length interval

f1 length frequency from first sampling event in year.

f2 length frequency from second sampling event in year.

f3 length frequency from third sampling event in year.

Source

Shepherd, J. G. 1987. *A weakly parametric method for the analysis of length composition data*. In: D. Pauly and G. Morgan, (eds). The Theory and Application of Length-Based Methods of Stock Assessment. ICLARM Conf. Ser. Manilla.

`slca` *A Weakly Parametric Method for the Analysis of Length Composition Data*

Description

Shepherd's method for the decomposition of seasonal length frequencies into age classes.

Usage

```
slca(x, type = 1, fryr=NULL, Linf = NULL, K = NULL, t0 = NULL,
 Lrange = NULL, Krange = NULL)
```

Arguments

`x`	the dataframe containing the seasonal length frequencies. The first column contains the lower limit of the length bin as a single numeric value, and the second and remaining columns contain the number of fish in each length bin for each seasonal length frequency. The increment of length frequencies should be constant, e.g. every 3 cm. Empty cells must be coded as zeros. Column headers are not required.
`type`	the analysis to be conducted: 1=*explore*, 2=*evaluate*.
`fryr`	the fraction of the year corresponding to when each seasonal length frequency was collected. Enter one numeric value for each length frequency separated by commas within the concatentation function, e.g. c(0.2,0.45). Values must be entered for type=1 and type=2.
`Linf`	the von Bertalanffy L-infinity parameter. If type=2, then value must be entered.
`K`	the von Bertalanffy growth parameter. If type=2, then value must be entered.
`t0`	the von Bertalanffy t-sub zero parameter. If type=2, the value must be entered.
`Lrange`	the L-infinity range (minimum and maximum) and increment to explore. If type=1, then values must by entered. The first position is the minimum value, the second position is the maximum value, and the third position is the increment. Values should be separated by commas within the concatentation function, e.g. c(100,120,10).
`Krange`	the K range and increment to explore. If type=1, then values must by entered. The first position is the minimum value, the second position is the maximum value, and the third position is the increment. Values should be separated by commas within the concatentation function, e.g. c(0.1,0.3,0.02).

Details

There are two analytical steps. In the "explore" analysis, a set of von Bertalanffy parameters that best describes the growth of the seasonal length groups is selected from a table of goodness-of-fit measures mapped over the range of specified K and L-infinity values. Once the best K and L-infinity parameters are selected, the corresponding t0 value is obtained off the second table. In the "evaluate" analysis, the selected parameters are used to 'slice' the seasonal length frequencies into age classes.

Value

If type=1, tables of goodness of fit measures versus L-infinity and K parameters, and t0 values versus L-infinity and K parameters. If type=2, table of age classes produced from slicing the length frequencies.

Note

Shepherd's Fortran code provided in his original working document was translated into R code.

Author(s)

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References

Shepherd, J. G. 1987. A weakly parametric method for the analysis of length composition data. In: D. Pauly and G. Morgan, (eds). The Theory and Application of Length-Based Methods of Stock Assessment. ICLARM Conf. Ser. Manilla.

Examples

```
#Data are from Shepherd working document - seasonal length frequencies
# for Raja clavata.
data(Shepherd)

#explore
slca(Shepherd,1,fryr=c(0.2,0.45,0.80),Lrange=c(100,150,10),
Krange=c(0.1,0.3,0.02))

#evaluate
slca(Shepherd,2,fryr=c(0.2,0.45,0.80),Linf=120,K=0.2,t0=0.57)
```

`vblrt` *Likelihood Ratio Tests for Comparing Two von Bertalanffy Growth Curves*

Description

Likelihood ratio tests for comparison of two von Bertalanffy growth curves following Kimura (1980).

Usage

```
vblrt(len = NULL, age = NULL, group = NULL, error = 1,
 select = 1, Linf = NULL, K = NULL, t0 = NULL)
```

Arguments

`len`	the vector of lengths of individual fish.
`age`	the vector of ages associated with the length vector.
`group`	the vector of character or numeric codes specifying group association.
`error`	the error variance assumption. 1= constant variance for all *lij*s; 2= constant variance for all mean lengths at age; 3=var of *lij* varies with age. See methods a-c in Kimura (1980: pp. 766). The required statistics for each type of error are calculated from the individual length-age observations.
`select`	the selection of starting values of *L-infinity*, *K*, and *t0*. 1=automatic selection, 2=user-specified. If *select*=1, initial starting values of *L-infinity*, *K*, and *t0* are calculated from Walford lines (Everhart et al. 1975), and ages represented as decimal values are truncated to the integer before linear regression is applied. If select=2, the user must specified the values of *L-infinity*, *K*, and *t0*.
`Linf`	if *select*=2, the starting value for *L-infinity* of the von Bertalanffy equation.
`K`	if *select*=2, the starting value for *K* of the von Bertalanffy equation.
`t0`	if *select*=2, the starting value for *t0* of the von Bertalanffy equation.

Details

Following Kimura (1980), the general model (6 parameters; one *L-infinity*, *K*, and *t0* for each group) and four sub models are fitted to the length and age data using function *nls* (nonlinear least squares). For each general model-sub model comparison, likelihood ratios are calculated by using the residual sum-of-squares and are tested against chi-square statistics with the appropriate degrees of freedom. Individual observations of lengths-at-age are required. If error variance assumptions 2 or 3, mean lengths and required statistics are calculated. A dummy vector called *cat*, containing 0s for the first group with lower alpha-numeric order and 1s for the second group, is used in the estimation of group parameters.

Value

`results`	list element with the likelihood ratio tests comparing von Bertalanffy models.
`model Ho`	list element with the `nls` fit for the general model.
`model H1`	list element with the `nls` for model H1 (Linf1=Linf2).
`model H2`	list element with the `nls` fit for model H2 (K1=K2).
`model H3`	list element with the `nls` fit for model H3 (t01=t02).
`model H4`	list element with the `nls` fit for model H4 (Linf1=Linf2, K1=K2, t01=t02).
`rss`	list element with the residual sum-of-squares from each model.
`residuals`	list element with the residuals from each model.

Author(s)

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References

Everhart, W. H., A. W. Eipper, and W. D. Youngs. 1975. Principles of Fishery Science. Cornell University Press.

Kimura, D. K. 1980. Likelihood methods for the von Bertalanffy growth curve. U. S. Fish. Bull. 77(4): 765-776.

Examples

```
## Normally, the length and age data will represent data for individuals.
## Kimura's data are mean lengths-at-age but are usable because error=2
## will calculate mean lengths-at-age from individual data. Since only
## one value is present for each age,the mean length will be calculated
## as the same value.
data(Kimura)
vblrt(len=Kimura$length,age=Kimura$age,group=Kimura$sex,error=2,select=1)
```

`ypr` *Yield-Per-Recruit Analysis*

Description

Yield-per-recruit (YPR) analysis is conducted following the modified Thompson-Bell algorithm. Reference points Fmax and F0.1 are calculated.

Usage

```
ypr(age = NULL, wgt = NULL, partial = NULL, M = NULL,
 plus = FALSE, oldest = NULL, maxF = 2, incrF = 0.001)
```

Arguments

`age`	the vector of cohort ages, e.g. c(1,2,3,4,5). If the last age is a plus group, do not add a "+" to the age.
`wgt`	the vector of catch weights for each age, e.g. c(0.2,0.4,0.7,1.0,1.2). Length of vector must correspond to the length of the age vector.
`partial`	the partial recruitment vector applied to fishing mortality (F) to obtain partial F-at-age. Length of the partial recruitment vector must correspond to the length of the age vector.
`M`	vector containing a single natural mortality (M) rate if M is assumed constant over all ages, or a vector of Ms, one for each age. If the latter, the vector length must correspond to the length of the age vector.
`plus`	a logical value indicating whether the last age is a plus-group. Default is FALSE.
`oldest`	if plus=TRUE, a numeric value indicating the oldest age in the plus group.
`maxF`	the maximum value of F range over which YPR will be calculated. YPR is calculated for F = 0 to maxF.
`incrF`	F increment for YPR calculation.

Details

Yield-per-recruit analysis is conducted following the modified Thompson-Bell algorithm. Reference points Fmax and F0.1 are calculated. If the last age is a plus-group, the cohort is expanded to the `oldest` age and the `wgt`, `partial`, and `M` values for the plus age are applied to the expanded cohort ages.

Value

`Reference_Points`	F and yield-per-recruit values for Fmax and F0.1
`F_vs_YPR`	Yield-per-recruit values for each F increment

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries ⟨gary.nelson@state.ma.us⟩

References

Gabriel, W. L., M. P. Sissenwine, and W. J. Overholtz. 1989. Analysis of spawning stock biomass per recruit: an example for Georges Bank haddock. North American Journal of Fisheries Management 9: 383-391.

See Also

`sbpr`

Examples

```
data(haddock)
ypr(age=haddock$age,wgt=haddock$ssbwgt,partial=haddock$partial,M=0.4,
plus=TRUE,oldest=100,maxF=2,incrF=0.001)
```

Index