

Package ‘fishmethods’

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R topics documented:

fishmethods-package	3
agesurv	3
agesurvcl	4
alkD	6
alkdata	7
alkprop	8
alkss	9
baglimit	10
bheq1	12
bheq2	13
bhnoneq	15
bonito	16
buffalo	17
catch	18
catchpertrip	18

catchseries	20
clusmean	22
codcluslen	23
codlengths	24
codstrcluslen	24
combinevar	25
convmort	26
darter	27
deltadist	27
deplet	28
extractMRFSS	30
Gerking	31
goosefish	32
haddock	32
herring	33
Hoenig	34
irm_cr	34
irm_h	38
Jensen	40
Jiang	41
Kimura	42
lengthfreq	42
LengthIncr	44
lfclus	47
lfstrclus	49
lifetable	52
M.empirical	54
mrN.single	55
opt_slot	56
opt_trophy	58
powertrend	59
pstrat	60
rockbass	62
sbpr	63
schnabel	64
Shepherd	65
slca	66
surveyfit	68
surveyref	69
tag_model_avg	70
vblrt	72
wolffish	73
yellowtail	74
ypr	75

 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
 Type: Package
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Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries, Gloucester, MA.

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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

<code>age</code>	the vector of ages. Each row represents the age of an individual.
<code>full</code>	the fully-recruited age
<code>last</code>	the maximum age to include in the calculation. If not specified, the oldest age is used.
<code>estimate</code>	argument to select estimate type: "s" for annual survival, "z" for instantaneous total mortality. Default is both.
<code>method</code>	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

<code>results</code>	list element containing table of parameters and standard errors.
<code>data</code>	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 A1 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 (LI 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

<code>intdir</code>	the path and main directory (in quotes) under which raw intercept sub-directories are stored.
<code>estdir</code>	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
<code>species</code>	10-digit NODC species code. A complete list of species codes is provided at the MRFSS website
<code>state</code>	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 <code>c()</code> . North Atlantic= <code>c(9, 23, 25, 33, 44)</code> , Mid Atlantic= <code>c(10, 24, 34, 36, 51)</code> , South Atlantic= <code>c(13, 37, 45, 121)</code> , Gulf of Mexico= <code>c(1, 22, 28, 122)</code> .
<code>wave</code>	bimonthly wave(s) of data to include. Bimonthly 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 <code>c()</code> .
<code>mode</code>	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 <code>c()</code> .
<code>styr</code>	the starting year of data to include.
<code>endyr</code>	the ending year of data to include.
<code>bag</code>	the bag limit(s) to simulate. If multiple bag limits, separate values by commas in <code>c()</code> .

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

<code>No Bag Limit</code>	list element containing the table of catch, trip, intercept and harvest information with no bag limit.
<code>Bag Limit i</code>	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.
<code>Results</code>	the percent reduction in harvest associated with each bag limit.
<code>Details</code>	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 $\geq L_c$ is calculated automatically. Missing data are removed prior to calculation. Estimates of standard error are made by bootstrapping length data $\geq L_c$ using package `boot`.

Value

Dataframe of length 1 containing mean length $\geq L_c$, sample size $\geq L_c$, 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

<code>len</code>	the vector of length data. Each row represents one record per individual fish.
<code>K</code>	the growth coefficient from a von Bertalanffy growth model.
<code>Linf</code>	the L-infinity coefficient from a von Bertalanffy growth model.
<code>Lc</code>	the length at first capture.
<code>La</code>	the largest length of the largest size class.
<code>nboot</code>	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 $\geq Lc$ is calculated automatically. Missing data are removed prior to calculation. Estimates of standard error are made by bootstrapping length data $\geq Lc$ using package `boot`.

Value

Dataframe of length 1 containing mean length $\geq Lc$, sample size $\geq Lc$, Z estimate and standard error.

Author(s)

Gary A. Nelson, Massachusetts Division of Marine Fisheries [⟨gary.nelson@state.ma.us⟩](mailto: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)
```

bhoneq

*Length-based Beverton-Holt Nonequilibrium Z Estimator***Description**

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

Usage

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

Arguments

<code>year</code>	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.
<code>mlen</code>	the vector of mean lengths for lengths $\geq L_c$. One record for each year.
<code>ss</code>	the vector of numbers of observations associated with the mean length.
<code>K</code>	the growth coefficient from a von Bertalanffy growth model.
<code>Linf</code>	the L-infinity coefficient from a von Bertalanffy growth model.
<code>Lc</code>	the length at first capture.
<code>nbreaks</code>	the number of times (breaks) mortality is thought to change over the time series. Must be 1 or greater
<code>styrs</code>	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 concatenation function and should be within the range of years present in the data.
<code>stZ</code>	the starting guesses of Z values enclosed within the concatenation function. There should be $nbreaks+1$ values provided.
<code>stsigma</code>	the starting guess of sigma.

Details

The mean lengths for each year for lengths $\geq L_c$. 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 $\geq L_c$, 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

<code>results</code>	list element containing table of parameters with estimates, standard errors, and t-values.
<code>obs</code>	list element containing year, mean length of lengths $\geq L_c$, and sample size.
<code>pred</code>	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⟩](mailto: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)
```

bonito

Data from an age and growth study of the pacific bonito.

Description

Growth increment data derived from tagging experiment on Pacific bonito (*Sarda chiliensis*) used to illustrate Francis's maximum likelihood method estimation of growth and growth variability (1988), often referred to as GROTAG.

Usage

```
data(bonito)
```

Format

A data frame with 138 observations on the following 4 variables.

T1 a numeric vector describing the release date

T2 a numeric vector describing the recovery date

L1 a numeric vector describing the length at release in millimeters

delta.L a numeric vector describing the length increment, in millimeters

Details

Note that Francis (1988) has discarded 2 records from the original dataset collected by Campbell et al. (1975).

Source

- 1 Francis, R.I.C.C., 1988. Maximum likelihood estimation of growth and growth variability from tagging data. *New Zealand Journal of Marine and Freshwater Research*, 22, p.42–51.
- 2 Campbell, G. & Collins, R., 1975. The age and growth of the Pacific bonito, *Sarda chiliensis*, in the eastern north Pacific. *Calif. Dept. Fish Game*, 61(4), p.181-200.

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	<i>Number of cod captured in 10 standardized bottom trawl hauls from Massachusetts, 1985</i>
-------	--

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	<i>Catch-Per-Trip Analysis for Marine Recreational Fisheries Statistics Survey Data</i>
--------------	---

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

<code>intdir</code>	the path and main directory (in quotes) under which raw intercept sub-directories are stored.
<code>estdir</code>	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
<code>species</code>	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	bimonthly wave(s) of data to include. Bimonthly 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, 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	<i>Summary of Catch Estimates from the Marine Recreational Fisheries Statistics Survey</i>
-------------	--

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	bimonthly wave(s) of data to include. Bimonthly 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	<i>Estimation of Population Attributes and Effective Sample Size for Fishes Collected Via Cluster Sampling</i>
----------	--

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 obtain 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 ($\text{var}R$), variance of population attribute (s^2x), and effective sample size (m_{eff}).

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	<i>Lengths of Atlantic cod caught during Massachusetts Division of Marine Fisheries bottom trawl survey, spring 1985.</i>
------------	---

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	<i>Individual lengths of Atlantic cod from cooperative trawling in winter of 2000, Massachusetts Bay</i>
------------	--

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	<i>Lengths of Atlantic cod caught during Massachusetts Division of Marine Fisheries stratified random bottom trawl survey, spring 1985.</i>
---------------	---

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

`combinevar`*Combining Mean and Variances from Multiple Samples*

Description

This function takes multiple mean and sample variance estimates and combines them.

Usage

```
combinevar(xbar = NULL, s_squared = NULL, n = NULL)
```

Arguments

<code>xbar</code>	vector of means
<code>s_squared</code>	vector of sample variances
<code>n</code>	vector of number of observations

Details

If a Monte Carlo simulation is run over 1000 loops and then again over another 1000 loops, one may wish to update the mean and variance from the first 1000 loops with the second set of simulation results.

Value

Vector containing the combined mean and sample variance.

Author(s)

John M. Hoenig, Virginia Institute of Marine Science <hoenig@vims.edu>

Examples

```
xbar <- c(5,5)
s<-c(2,4)
n <- c(10,10)
combinevar(xbar,s,n)
```

`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

<code>value</code>	mortality rate
<code>fromto</code>	conversion direction: 1=from F to mu; 2 = from mu to F. Default is 1.
<code>type</code>	type of fishery following Ricker (1975): 1=Type I; 2=Type II. Default is 2.
<code>M</code>	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", "wh"), kwh=NULL, 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. <i>Variable Effort Models</i> : 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). <i>Constant Effort Model</i> : wh= the generalized removal method of Otis et al. (1978).
kwh	the number of capture parameters (p) to fit in method wh. NULL for all possible capture parameters.
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. Three removals are required to use the Leslie, Delury, and Gould and Pollock methods.

The constant effort model is the generalized removal method of Otis et al. 1978 reviewed in White et al. (1982: 109-114). If only two removals, the two-pass estimator of N in White et al. (1982:105) and the variance estimator of Otis et al. (1978: 108) are used.

Note: Calculation of the standard error using the ml method may take considerable time.

For the Delury method, zero catch values are not allowed because the log-transform is used.

For the generalized removal models, if standard errors appear as NAs but parameter estimates are provided, the inversion of the Hessian failed. If parameter estimates and standard errors appear as NAs, then model fitting failed.

For the Chao and Chang models, if the last catch value is zero, it is deleted from the data. Zero values between positive values are permitted.

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 K. 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.

Otis, D. L., K. P. Burnham, G. C. White, and D. R. Anderson. 1978. Statistical inference from capture data on closed animal populations. *Wildl. Monogr.* 62: 1-135.

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
```

extractMRFSS	<i>Extraction of Marine Recreational Fisheries Statistics Survey Data from SAS Transport Files</i>
--------------	--

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 sub-directories 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 concatenation function. If data from all states are desired, do not include the <code>state=</code> 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	<i>Mean Length and Numbers of Lengths for Northern Goosefish, 1963-2002</i>
-----------	---

Description

The `goosefish` data frame has 40 rows and 3 columns. The mean lengths (`mten`) by year and number (`ss`) of observations for length \geq 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

mten 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	<i>Biological data for haddock (Melanogrammus aeglefinus)</i>
---------	---

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	<i>Total length data for alewife (Alosa pseudoharengus) from Massachusetts waters</i>
---------	---

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

Hoenig

Tag Data from Hoenig et al. (1998)

Description

The `Hoenig` list containing 8 components of data. Data were obtained from the Hoenig et al.(1998).

Usage

`Hoenig`

Format

This list contains the following components:

relyrs vector of start and end years of release years

recapyrs vector of start and end years of recapture years

N vector of number of tags released in each release year

recapharv recapture matrix of harvested fish

lambda vector of reporting rates (one for each recapture year)

phi vector of initial tag loss (one for each recapture year)

Fyr vector of years to estimate fishing mortality

Myr vector of years to estimate natural mortality

Source

Hoenig, J. M, N. J. Barrowman, W. S. Hearn, and K. H. Pollock. 1998. Multiyear tagging studies incorporating fishing effort data. *Canadian Journal of Fisheries and Aquatic Sciences* 55: 1466-1476.

irm_cr

*Age-Independent Instantaneous Rates Model of Jiang et al. (2007)
Incorporating Catch and Release Tag Returns*

Description

The age-independent instantaneous rates model of Jiang et al. (2007) for estimating fishing and natural mortality from catch-release tag returns is implemented assuming known values of initial tag loss (ϕ) and reporting rate (λ)

Usage

```
irm_cr(relyrs = NULL, recapyrs = NULL, N = NULL, recapharv = NULL, recaprel = NULL,
hlambda = NULL, rlambda = NULL, hphi = NULL, rphi = NULL, hmrate = NULL, Fyr = NULL,
FAyr = NULL, Myr = NULL, initial = c(0.1,0.05,0.1), lower = c(0.0001,0.0001,0.0001),
upper=c(5,5,5),maxiter=10000)
```

Arguments

relyrs	vector containing the start and end year of the entire release period (e.g., c(1992,2006)).
recapyrs	vector containing the start year and end year of entire recapture period (e.g., c(1992,2008)).
N	vector of total number of tagged fish released in each release year (one value per year).
recapharv	matrix of the number of tag recoveries of harvested fish by release year (row) and recovery year (column). The lower triangle (blank cells) may be filled with -1s as place holders. Missing values in the upper triangle (release/recovery cells) are not allowed.
recaprel	matrix of the number of tag recoveries of fish recaptured and re-released with the tag removed by release year (row) and recovery year (column). The lower triangle (blank cells) may be filled with -1s as place holders. Missing values in the upper triangle (release/recovery cells) are not allowed.
hlambda	vector of reporting rate estimates (lambda) for harvested fish. One value for each recovery year.
rlambda	vector of reporting rate estimates (lambda) for recaptured fish re-released with tag removed. One value for each recovery year.
hphi	vector of initial tag loss estimates (phi) for harvested fish. One value for each recovery year.
rphi	vector of initial tag loss estimates (phi) for recaptured fish re-released with tag removed fish. One value for each recovery year.
hmrate	vector of hooking mortality rates. One value for each recovery year.
Fyr	vector of year values representing the beginning year of a period over which to estimate a constant fishing mortality rate (F). If estimation of F for each recovery year is desired, enter the year value for each year. The first year value must be the start year for the recovery period.
FAyr	vector of year values representing the beginning year of a period over which to estimate a constant tag mortality rate (FA). If estimation of FA for each recovery year is desired, enter the year value for each year. The first year value must be the start year for the recovery period.
Myr	vector of year values representing the beginning year of a period over which to estimate a constant natural mortality rate (M). If estimation of M for each recovery year is desired, enter the year value for each year. The first year value must be the start year for the recovery period.
initial	vector of starting values for fishing, tag, and natural mortality estimates. First position is the starting value for all Fs, second position is the starting value for all FAs, and the third position is the starting value for all Ms (e.g., c(0.1,0.1,0.2)).

lower	vector of lower bounds of F, FA, and M estimates used in optimization routine. First position is the lower value for all Fs, second position is the lower value for all FAs, and the third position is the lower value for all Ms.
upper	vector of upper bounds of F, FA, and M estimates used in optimization routine. First position is the upper value for all Fs, second position is the upper value for all FAs, and the third position is the upper value for all Ms.
maxiter	maximum number iterations used in the optimization routine.

Details

Jiang et al (2007) provides an extension of the Hoenig et al. (1998) instantaneous tag return model to account for catch/release of tagged fish. The benefits of this instantaneous rates model are that data from tagged fish that are recaptured and released alive are directly incorporated in the estimation of fishing and natural mortality. Jiang et al. models mortality of harvested fish and the mortality experienced by the tag because fish are often released after the tag has been removed. Therefore, additional tag mortality parameters are estimated in the model. The age-independent model of Jiang et al. is implemented here and initial tag loss and reporting rates are assumed known. This model assumes that tagged fish are fully-recruited to the fishery and that fishing took place throughout the year. Similar to Hoenig et al. (1998), observed recovery matrices from the harvest and catch/release fish with removed tags are compared to expected recovery matrices to estimate model parameters. Asymmetric recovery matrices are allowed (recovery years > release years). All summary statistics follow Burnham and Anderson (2002). Model degrees of freedom are calculated as the number of non-zero cells from the harvested and released recovery matrices minus the number of estimated parameters. Total chi-square is calculated by summing cell chi-square values for all non-zero observed cells of the harvest, released, and not seen matrices. C-hat, a measure of overdispersion, is estimated by dividing the total chi-square value by the model degrees of freedom. Pooling of cells to achieve an expected cell value of 1 is performed and pooled chi-square and c-hat metrics are additionally calculated. Pearson residuals are calculated by subtracting the observed numbers of recoveries in each cell from the predicted numbers of recoveries and dividing each cell by the square-root of the predicted cell value. The variance of instantaneous total mortality (Z) is calculated by $\text{var}F + \text{hmrate}^2 * \text{var}FA + \text{var}M + 2 * \text{sum}(\text{cov}(F, M) + \text{hmrate}^2 * \text{cov}(F, FA) + \text{hmrate}^2 * \text{cov}(FA, M))$, and the variance of survival (S) is calculated from Z using the delta method. The `optim` routine is used to find the parameters that minimize the $-1 * \text{negative log-likelihood}$.

The program allows the configuration of different model structures (biological realistic models) for the estimation of fishing, natural, and tag mortalities. Consider the following examples:

Example 1

Release years range from 1991 to 2003 and recovery years from 1991 to 2003. One model structure might be constant fishing mortality estimates over the recovery years of 1991-1994 and 1995-2003, one constant estimate of tag mortality and one constant estimate of natural mortality for the entire recovery period. To designate this model structure, the beginning year of each interval is assigned to the `Fyr` vector (e.g., `Fyr<-c(1991, 1995)`), and the beginning year of the recovery period is assigned to the `FAYr` vector and the `MYr` vector (e.g., `FAYr<-c(1991); MYr<-c(1991)`). The first value of each vector must always be the beginning year of the recovery period regardless of the model structure.

Example 2

Release years range from 1991 to 2003 and recovery years from 1991 to 2003. One model might be fishing and tag mortality estimates for each year of recovery years and two constant estimates of natural mortality for 1991-1996 and 1997-2003. To designate this model structure, one value for each year is assigned to the `Fyr` and `FAyr` vectors (e.g., `Fyr<-c(1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003)`), and the beginning years of the natural mortality intervals are assigned to the `Myr` vector (e.g., `Myr<-c(1991, 1997)`).

Averaging of model results can be accomplished using the function `tag_model_avg`.

Value

List containing summary statistics for the model fit, model convergence status, parameter correlation matrix, estimates of fishing mortality, natural mortality, tag mortality, total instantaneous mortality (Z), and survival (S) and their variances and standard errors by year, observed and predicted recoveries for harvested, released, and "not-seen" fish, cell chi-square and Pearson values for harvested, released, and "not seen" fish, and a model configuration label (type) used in the `tag_model_avg` function.

Author(s)

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

References

- Burnham, K. P. and D. R. Anderson. 2002. Model selection and multimodel inference : A Practical Information-Theoretic Approach, 2nd edition. Springer-Verlag, New York, NY. 488 p.
- Hoenig, J. M, N. J. Barrowman, W. S. Hearn, and K. H. Pollock. 1998. Multiyear tagging studies incorporating fishing effort data. *Canadian Journal of Fisheries and Aquatic Sciences* 55: 1466-1476.
- Jiang, H. 2005. Age-dependent tag return models for estimating fishing mortality, natural mortality and selectivity. Doctoral dissertation. North Carolina State University, Raleigh.
- Jiang, H., K. H. Pollock, C. Brownie, J. M. Hoenig, R. J. Latour, B. K. Wells, and J. E. Hightower. 2007. Tag return models allowing for harvest and catch and release: evidence of environmental and management impacts on striped bass fishing and natural mortality rates. *North American Journal of Fisheries Management* 27:387-396.

See Also

[irm_h](#) [tag_model_avg](#)

Examples

```
# Data come from Appendix Table A2 and model structure from model (a) in Table 3.2 of Jiang
data(Jiang)
modell<-irm_cr(relyrs = Jiang$relyrs, recapyrs = Jiang$recapyrs, N = Jiang$N, recapharv = Jian
  recaprel = Jiang$recaprel, hlambd = Jiang$hlambd, rlambd = Jiang$rlambd, hphi = Jian
  hmrate = Jiang$hmrate, Fyr = Jiang$Fyr, FAyr = Jiang$FAyr, Myr = Jiang$Myr, initial = c(
    lower = c(0.0001, 0.0001, 0.0001), upper=c(5, 5, 5), maxiter=10000)
```

irm_h	<i>Age-Independent Instantaneous Rates Tag Return Model of Hoenig et al. (1998)</i>
-------	---

Description

The age-independent instantaneous rates model of Hoenig et al. (1998) for estimating fishing and natural mortality from tag returns of harvested fish is implemented assuming known values of initial tag loss (ϕ) and reporting rate (λ)

Usage

```
irm_h(relyrs = NULL, recapyrs = NULL, N = NULL, recapharv = NULL, lambda = NULL, phi = NULL,
      Fyr = NULL, Myr = NULL, initial = NULL, lower = c(0.0001, 0.0001), upper = c(5, 5), ma
```

Arguments

relyrs	vector containing the start and end year of the entire release period (e.g., c(1992,2006)).
recapyrs	vector containing the start year and end year of entire recapture period (e.g., c(1992,2008)).
N	vector of total number of tagged fish released in each release year (one value per year).
recapharv	matrix of the number of tag recoveries of harvested fish by release year (row) and recovery year (column). The lower triangle (blank cells) may be filled with -1s as place holders. Missing values in the upper triangle (release/recovery cells) are not allowed.
lambda	vector of reporting rate estimates for harvested fish. One value for each recovery year.
phi	vector of initial tag loss estimates (ϕ) for harvested fish. One value for each recovery year.
Fyr	vector of year values representing the beginning year of a period over which to estimate a constant fishing mortality rate (F). If estimation of F for each recovery year is desired, enter the year value for each year. The first year value must be the start year for the recovery period.
Myr	vector of year values representing the beginning year of a period over which to estimate a constant natural mortality rate (M). If estimation of M for each recovery year is desired, enter the year value for each year. The first year value must be the start year for the recovery period.
initial	vector of starting values for fishing, and natural mortality estimates. First position is the starting value for all Fs and second position is the starting value for all Ms (e.g., c(0.1,0.2)).
lower	vector of lower bounds of F and M estimates used in optimization routine. First position is the lower value for all Fs and second position is the lower value for all Ms. Default = 0.0001.

upper	vector of upper bounds of F and M estimates used in optimization routine. First position is the upper value for all Fs and second position is the upper value for all Ms. Default = 5
maxiter	maximum number iterations used in the optimization routine.

Details

The instantaneous tag return model of Hoening et al. (1998) assuming known initial tag loss and reporting rates is implemented. This model assumes that tagged fish are fully-recruited to the fishery and that fishing took place throughout the year. The observed recovery matrices are compared to expected recovery matrices to estimate model parameters. Asymmetric recovery matrices are allowed (recovery years > release years). All summary statistics follow Burnham and Anderson (2002). Model degrees of freedom are calculated as the number of non-zero cells from the harvested and released recovery matrices minus the number of estimated parameters. Total chi-square is calculated by summing cell chi-square values for all non-zero observed cells of the harvest, released, and not seen matrices. C-hat, a measure of overdispersion, is estimated by dividing the total chi-square value by the model degrees of freedom. Pooling of cells to achieve an expected cell value of 1 is performed and pooled chi-square and c-hat metrics are additionally calculated. Pearson residuals are calculated by subtracting the observed numbers of recoveries in each cell from the predicted numbers of recoveries and dividing each cell by the square-root of the predicted cell value. The `optim` routine is used to find the parameters that minimize the $-1 \times \text{negative log-likelihood}$. The variance of instantaneous total mortality (Z) is calculated by $\text{varF} + \text{varM} + 2\text{cov}(F, M)$, and the variance of survival (S) is estimated from the variance of Z using the delta method.

The program allows the configuration of different model structures (biological realistic models) for the estimation of fishing and natural mortalities. Consider the following examples:

Example 1

Release years range from 1991 to 2003 and recovery years from 1991 to 2003. One model structure might be constant fishing mortality estimates over the recovery years of 1991-1994 and 1995-2003, and one constant estimate of natural mortality for the entire recovery period. To specify this model structure, the beginning year of each interval is assigned to the `Fyr` vector (e.g., `Fyr<-c(1991, 1995)`), and the beginning year of the recovery period is assigned to the `Myr` vector (e.g., `Myr<-c(1991)`). The first value of each vector must always be the beginning year of the recovery period regardless of the model structure.

Example 2

Release years range from 1991 to 2003 and recovery years from 1991 to 2003. One model might be fishing mortality estimates for each year of recovery years and two constant estimates of natural mortality for 1991-1996 and 1997-2003. To specify this model structure, one value for each year is assigned to the `Fyr` vector (e.g., `Fyr<-c(1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003)`) and the beginning years of the natural mortality intervals are assigned to the `Myr` vector (e.g., `Myr<-c(1991, 1997)`).

Averaging of model results can be accomplished using the function `tag_model_avg`.

Value

List containing summary statistics for the model fit, model convergence status, parameter correlation matrix, estimates of fishing mortality, natural mortality, total instantaneous mortality (Z), and survival (S) and their variances and standard errors by year, observed and predicted recoveries for

harvested, released, and "not-seen" fish, cell chi-square and Pearson values for harvested, released, and "not seen" fish and a model configuration label (type) used in the `tag_model_avg` function.

Author(s)

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

References

Burnham, K. P. and D. R. Anderson. 2002. Model selection and multimodel inference : A Practical Information-Theoretic Approach, 2nd edition. Springer-Verlag, New York, NY. 488 p.

Hoenig, J. M, N. J. Barrowman, W. S. Hearn, and K. H. Pollock. 1998. Multiyear tagging studies incorporating fishing effort data. Canadian Journal of Fisheries and Aquatic Sciences 55: 1466-1476.

See Also

[irm_cr tag_model_avg](#)

Examples

```
# Data come from Table 4 and model structure from Table 5 under "year-specific F, constant M
data(Hoenig)
modell<-irm_h(relyrs = Hoenig$relyrs, recapyrs = Hoenig$recapyrs, N = Hoenig$N, recapharv =
lambda = Hoenig$lambda, phi = Hoenig$phi, Fyr = Hoenig$Fyr, Myr = Hoenig$Myr, initial = c(0.1
lower = c(0.0001,0.0001), upper = c(5,5), maxiter = 10000)
```

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.

Jiang

Tag Data from Jiang (2005)

Description

The `Jiang` list containing 13 components of data. Data were obtained from the Jiang (2005).

Usage

`Jiang`

Format

This list contains the following components:

relyrs vector of start and end years of release years

recapysr vector of start and end years of recapture years

N vector of number of tags released in each release year

recapharv recapture matrix of harvest fish

recaprel recapture matrix of recaptured and re-released fish with tag removed

hlambda vector of reporting rates of harvested fish (one value for each recapture year)

rlambda vector of reporting rates of recaptured and re-released fish (one value for each recapture year)

hphi vector of initial tag loss of harvested fish (one value for each recapture year)

rphi vector of initial tag loss of harvested fish (one value for each recapture year)

hmrate vector of hooking mortality rates (one value for each recapture year)

Fyr vector of years to estimate fishing mortality

FAyr vector of years to estimate tag mortality

Myr vector of years to estimate natural mortality

Source

Jiang, H. 2005. Age-dependent tag return models for estimating fishing mortality, natural mortality and selectivity. Doctoral dissertation. North Carolina State University, Raleigh.

 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

<code>intdir</code>	the path and main directory (in quotes) under which raw intercept sub-directories are stored.
<code>estdir</code>	the path and main directory (in quotes) under which catch/effort sub-directories are stored.
<code>species</code>	10-digit NODC species code. A complete list of species codes is provided at the MRFSS website
<code>state</code>	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 <code>c()</code> . North Atlantic= <code>c(9, 23, 25, 33, 44)</code> , Mid Atlantic= <code>c(10, 24, 34, 36, 51)</code> , South Atlantic= <code>c(13, 37, 45, 121)</code> , Gulf of Mexico= <code>c(1, 22, 28, 122)</code> .
<code>wave</code>	bimonthly wave(s) of data to include. Bimonthly 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 <code>c()</code> .
<code>mode</code>	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 <code>c()</code> .
<code>area</code>	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 <code>c()</code> .
<code>conveq</code>	logical to indicate whether a length conversion equation will be provided. If TRUE, provide the intercept and slope in <code>parms</code> argument below. Conversion equation is used to convert MRFSS fork length (mm) to other length measurements.
<code>parms</code>	vector containing the intercept (position 1) and slope (position 2) of the conversion equation
<code>styr</code>	the starting year of data to include.
<code>endyr</code>	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 frequency 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)
```

LengthIncr

Re-parameterized Von Bertalanffy growth function (GROTAG) from Francis (1988) developed in the context of analysis of tagging data

Description

This function calculates the expected growth increment of a fish of length L1 over a time period of delta.T, assuming the knowledge of the mean annual growth rates (g.alpha and g.beta) of fish of arbitrary length alpha and beta.

Usage

```
LengthIncr(gr.alpha, gr.beta, L1, delta.T, alpha = 35, beta = 55)
```

Arguments

gr.alpha	A numeric value giving the mean annual growth rate of fish of arbitrary length alpha
gr.beta	A numeric value giving the mean annual growth rate of fish of arbitrary length beta
L1	A vector giving the length at release of a tagged fish
delta.T	A vector giving the time at liberty of a fish after tagging
alpha	A numeric value giving an arbitrary length alpha
beta	A numeric value giving an arbitrary length beta (NB: beta > alpha)

Details

Use this function to fit the models of Francis (1988). Examples of how this is accomplished are given below in the EXAMPLES section.

Note

It is assumed that the arbitrary length alpha > beta

Author(s)

Marco.Kienzle@gmail.com

References

Francis, R.I.C.C., 1988. Maximum likelihood estimation of growth and growth variability from tagging data. *New Zealand Journal of Marine and Freshwater Research*, 22, p.42–51.

Examples

```
data(bonito)

##### Example of implementation of Francis (1988) model 1

# Plot the data
plot(bonito$L1, bonito$delta.L, xlab = "Length at tagging", ylab = "Length increment", las=1,

# function
f1 <- function(p) {
  sum(dnorm(x=bonito$delta.L, mean = LengthIncr(p[1], p[2], bonito$L1, delta.T = bonito$T2 - b
})

# Get initial values for g35 and g55
# by calculating average growth from data with T2-T1 superior to 0.1 year
g35.init = with(subset(bonito, L1 > 30 & L1 < 40 & (T2-T1) > 0.1), mean(delta.L/ (T2 - T1))
g55.init = with(subset(bonito, L1 > 50 & L1 < 60 & (T2-T1) > 0.1), mean(delta.L / (T2 - T1))

# Fit the model - maximum likelihood parameters estimation
mod1 = optim(par = c(g35 = g35.init, g55 = g55.init, s = 0.5), fn = f1,
```

```
lower = c(max(g35.init - 5, 0), max(g55.init - 5, 0), 0), upper =
c(g35.init + 5, g55.init + 5, 5), method = "L-BFGS-B", hessian = TRUE,
control = list(fnscale = -1))
```

```
##### Example of implementation of Francis (1988) model 2
```

```
##### model with g.alpha, g.beta, standard deviation of error measurement s and growth varia
```

```
# function - Assume standard deviation of delta.L is proportional to length increment but re
f2 <- function(p){
std.dev = LengthIncr(p[1], p[2], bonito$L1, delta.T = bonito$T2 - bonito$T1, alpha = 35, bet
std.dev = replace(std.dev, which(std.dev < 0), p[4])
sum(dnorm(x = bonito$delta.L, mean = LengthIncr(p[1], p[2], bonito$L1, delta.T = bonito$T2 -
})
```

```
# Get first hint on g35 and g55 by estimating the average growth using the data that have T2
g35.init = with(subset(bonito, L1 > 30 & L1 < 40 & (T2-T1) > 0.1), mean(delta.L/ (T2 - T1))
g55.init = with(subset(bonito, L1 > 50 & L1 < 60 & (T2-T1) > 0.1), mean(delta.L / (T2 - T1))
```

```
# Fit the model - maximum likelihood parameters estimation
```

```
mod2 = optim(c(g35 = g35.init, g55 = g55.init, factor = 0.5, s = 0.5), f2, lower = c(max(g35
```

```
##### Example of implementation of Francis (1988) model 3
```

```
##### model with g.alpha, g.beta, mean and standard deviation of error measurement s and gro
```

```
# function - Assume standard deviation of delta.L is proportional to length increment but re
f3 = function(p){
std.dev = LengthIncr(p[1], p[2], bonito$L1, delta.T = bonito$T2 - bonito$T1, alpha = 35, bet
std.dev = replace(std.dev, which(std.dev < 0), p[5])
sum(dnorm(x = bonito$delta.L, mean = LengthIncr(p[1], p[2], bonito$L1, delta.T = bonito$T2 -
})
```

```
# Get first hint on g35 and g55 by estimating the average growth using the data that have T2
g35.init = with(subset(bonito, L1 > 30 & L1 < 40 & (T2-T1) > 0.1), mean(delta.L/ (T2 - T1))
g55.init = with(subset(bonito, L1 > 50 & L1 < 60 & (T2-T1) > 0.1), mean(delta.L / (T2 - T1))
```

```
# Fit the model - maximum likelihood parameters estimation
```

```
mod3 = optim(c(g35 = g35.init, g55 = g55.init, factor = 1, m = -1, s = 0.5), f3, lower = c(m
```

```
##### Example of implementation of Francis (1988) model 5
```

```
##### Model with 4 parameters: g.alpha, g.beta, measurement error and outliers
```

```
# function
f5 = function(p){
# Calculate range of growth increment
R = range(bonito$delta.L)[2] - range(bonito$delta.L)[1]
# Likelihood function
sum(log((1-p[3])) * dnorm(x = bonito$delta.L, mean = LengthIncr(p[1], p[2], bonito$L1, delta.
})
```

```
# Get first hint on g35 and g55 by estimating the average growth using the data that have T2
```

```

g35.init = with(subset(bonito, L1 > 30 & L1 < 40 & (T2-T1) > 0.1), mean(delta.L/ (T2 - T1))
g55.init = with(subset(bonito, L1 > 50 & L1 < 60 & (T2-T1) > 0.1), mean(delta.L / (T2 - T1))

# Fit the model - maximum likelihood parameters estimation
mod5 = optim(c(g35 = g35.init, g55 = g55.init, p = 0, s = 2), f5, lower
= c(max(g35.init - 5, 0), max(g55.init - 5,0),0,0), upper = c(g35.init +
5, g55.init + 5,1,5), method = "L-BFGS-B", hessian = TRUE, control =
list(fnscale = -1))

##### Generate a table formatted in the same way as Francis (1988) Tab. 3, p.47

# Header
result = as.data.frame(matrix(NA, ncol=1, nrow = 9))
dimnames(result)[[1]] = c("Log likelihood", "Mean growth rates g35", "Mean growth rates g55",

# mod1
result = cbind(result[,-1], model1 = c(round(mod1$value,1), round(mod1$par[1],1), round(mod1$par[2],1), round(mod1$par[3],1), round(mod1$par[4],1), round(mod1$par[5],1)))

# mod2
result = cbind(result, model2 = c(round(mod2$value,1), round(mod2$par[1],1), round(mod2$par[2],1), round(mod2$par[3],1), round(mod2$par[4],1), round(mod2$par[5],1)))

# mod3
result = cbind(result, model3 = c(round(mod3$value,1), round(mod3$par[1],1), round(mod3$par[2],1), round(mod3$par[3],1), round(mod3$par[4],1), round(mod3$par[5],1)))

# mod5
result = cbind(result, model5 = c(round(mod5$value,1), round(mod5$par[1],1), round(mod5$par[2],1), round(mod5$par[3],1), round(mod5$par[4],1), round(mod5$par[5],1)))
print(result)

```

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.

<code>haul</code>	vector containing the variable used to identify the sampling unit (e.g., haul) of length data. Identifier can be numeric or character.
<code>len</code>	vector containing the length class data. There should be one record for each length class by group and haul.
<code>number</code>	vector containing the numbers of fish in each length class.
<code>binsize</code>	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 $\text{trunc}(\text{len}/\text{binsize}) * \text{binsize} + \text{binsize}/2$. If use of the raw length classes is desired, then <code>binsize=0</code> .
<code>resamples</code>	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 Kolmogorov-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 (D_s) under a two-tailed test:

$$D_s = \max|S_1(X) - S_2(X)|$$

where $S_1(X)$ and $S_2(X)$ are the observed cumulative length frequency distributions of group 1 and group 2 in the paired comparisons. $S_1(X)$ and $S_2(X)$ 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 D_s , the proportion of all randomized D values that were greater than or equal to D_s , including the occurrence of D_s 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	<i>Statistical Comparison of Length Frequencies from Stratified Random Cluster Sampling</i>
-----------	---

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 $\text{trunc}(\text{len}/\text{binsize}) * \text{binsize} + \text{binsize}/2$. If use of the raw length classes is desired, then <code>binsize=0</code> .
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 Kolmogorov-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 (D_s) under a two-tailed test:

$$D_s = \max|S_1(X) - S_2(X)|$$

where $S_1(X)$ and $S_2(X)$ 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 D_s 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 D_s , the proportion of all randomized D values that were greater than or equal to D_s , including the occurrence of D_s 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 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, n_x =number of individuals of a cohort alive at the start of age interval X , l_x = proportion of individuals surviving at the start of age interval X , d_x = number of individuals of a cohort dying during the age interval X , q_x =finite rate of mortality during the age interval X to $X+1$, p_x =finite rate of survival during the age interval X to $X+1$, e_x =mean expectation of life for individuals alive at start of age X . For method 5, d_x is corrected for population growth by $d_x' = d_x * \exp(r * x)$ and in method 6, n_x is corrected for the same by $n_x * e(r * x)$. 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= Petersen 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)

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_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	<i>Post-stratification of Marine Recreational Fisheries Statistics Survey Estimates of Catch</i>
--------	--

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 <i>pestyear</i> .
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_yyyyww.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)

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

[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

<code>catch</code>	A vector containing the number of animal caught in each mark-recapture experiment.
<code>recaps</code>	A vector containing the number of animal recaptured in each mark-recapture experiment.
<code>newmarks</code>	A vector containing the newly marked animals in each mark-recapture experiment.
<code>alpha</code>	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⟩](mailto: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	<i>A Weakly Parametric Method for the Analysis of Length Composition Data</i>
------	---

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= <i>explore</i> , 2= <i>evaluate</i> .
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 concatenation 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 be 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 concatenation function, e.g. c(100,120,10).
Krange	the K range and increment to explore. If type=1, then values must be 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 concatenation 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)

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

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)
```

 surveyfit

Estimating the Relative Abundance of Fish From a Trawl Survey

Description

This function applies the time series method of Pennington (1986) for estimating relative abundance to a survey series of catch per tow data

Usage

```
surveyfit(year = NULL, index = NULL, logtrans = TRUE)
```

Arguments

year	vector containing the time series of numeric year labels.
index	vector containing the time series of mean catch per tow data.
logtrans	a logical value indicating whether the natural log-transform should be applied to the mean catch per tow values. Default is TRUE.

Details

Parameters for a first difference, moving average model of order 1 are estimated from the trawl time series using function `arima`. Following Equation 4 in Pennington (1986), fitted values are calculated from the model residuals and the estimate of theta.

Value

List containing summary statistics (sample size (n), the first three sample autocorrelations (r1-r3) for the first differenced logged series) and parameter estimates (theta, theta standard error, and sigma2), the observed log-transformed index and fitted values, and the ARIMA function output.

Author(s)

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

References

Pennington, M. P. 1986. Some statistical techniques for estimating abundance indices from trawl surveys. *Fishery Bulletin* 84(3): 519-525.

See Also

[surveyref](#)

Examples

```
data(yellowtail)
surveyfit(year=yellowtail$year, index=yellowtail$index)
```

surveyref	<i>Quantitative reference points from stock abundance indices based on research surveys</i>
-----------	---

Description

This function implements the methodology of Helser and Hayes (1995) for generating quantitative reference points from relative abundance indices based on research surveys

Usage

```
surveyref(x = NULL, refpt = 25, comyear = NULL, reffix = FALSE,
          refrange = NULL, nboot = 1000, allboots = FALSE)
```

Arguments

<code>x</code>	output object from function <code>surveyfit</code> .
<code>refpt</code>	the lower quantile (percentile) of the fitted time series used as the reference point.
<code>comyear</code>	the index year to compare to the reference point. Multiple years can be included in the comparison using the <code>c()</code> function.
<code>reffix</code>	a logical value specifying whether the lower quantile should be determined from a fixed set of years. Default = <code>FALSE</code> .
<code>refrange</code>	If <code>reffix = TRUE</code> , the beginning and ending year of the time series to include in determination of the lower quantile. The values should be enclosed within <code>c()</code> (e.g., <code>c(1963,1983)</code>).
<code>nboot</code>	the number of bootstrap replicates.
<code>allboots</code>	a logical value specifying whether the fitted values for the bootstrap replicates should be included in the output. Default = <code>FALSE</code> .

Details

Using the output object from function `surveyfit`, the methodology of Helser and Hayes (1995) is applied to generate the probability distribution that the abundance index value for a given year lies below the value of a lower quantile (reference point). The procedure is : 1) add to the original fitted time series residuals randomly selected with replacement from the Pennington model fit, 2) repeat this `nboot` times to create new time series, 3) fit the Pennington model to each new time series using the original theta estimate to get `nboot` replicates of new fitted time series, 4) determine the lower quantile for each new fitted time series and 5) calculate and integrate the joint probability density between the selected index year and lower quantile.

If comparisons between the current year's index and the reference point will be made year-after-year, Helser and Hayes (1995) recommend using a fixed set of years to select the lower quantile. This procedure will avoid a change in reference point over time as a survey time series is updated. Use arguments `reffix` and `refrange` to accomplish this.

Value

list containing the lower quantile of the original fitted time series and the mean quantile of the fitted bootstrap replicates (`comp_refpt`), the original fitted time series values versus the mean of the fitted bootstrap time series values (`comp_fitted`), the empirical distribution of the selected index (`emp_dist_index`), the empirical distribution of the lower quantile (`emp_dist_refpt`), the probability distribution that the index value lies below the reference point (`prob_index`), and, if argument `allboots` is TRUE, the fitted values of the bootstrap replicates (`boot_runs`).

Author(s)

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

References

Helser, T. E. and D. B. Hayes. 1995. Providing quantitative management advice from stock abundance indices based on research surveys. *Fishery Bulletin* 93: 290-298.

See Also

[surveyfit](#)

Examples

```
data(wolffish)
out<-surveyfit(year=wolffish$year,index=wolffish$index,logtrans=TRUE)
surveyref(out,refpt=25,compyear=c(1990))
```

tag_model_avg

Model Averaging for Instantaneous Rates Tag Return Models

Description

Calculates model averaged estimates of instantaneous fishing, natural and total mortality, and survival rates for instantaneous rates tag return models (Hoenig et al. (1998) and Jiang et al. (2007)).

Usage

```
tag_model_avg(..., global = NULL)
```

Arguments

... model object names separated by commas

global specify global model name in quotes. If the global model is the first model included in the list of candidate models, this argument can be ignored.

Details

Model estimates are generated from functions `irm_cr` and `irm_h`. Averaging of model estimates follows the procedures in Burnham and Anderson (2002). Variances of parameters are adjusted for overdispersion using the \hat{c} estimate from the global model: $\sqrt{\text{var} * \hat{c}}$. If \hat{c} of the global model is < 1 , then \hat{c} is set to 1. The \hat{c} is used to calculate the quasi-likelihood AIC and AICc metrics for each model (see page 69 in Burnham and Anderson(2002)). QAICc differences among models are calculated by subtracting the QAICc of each model from the model with the smallest QAICc value. These differences are used to calculate the Akaike weights for each model following the formula on page 75 of Burnham and Anderson (2002). The Akaike weights are used to calculate the weighted average and standard error of parameter estimates by summing the product of the model-specific Akaike weight and parameter estimate across all models. An unconditional standard error is also calculated by $\sqrt{\text{sum}(\text{QAICc wgt of model } i * (\text{var of estimate of model } i + (\text{estimate of model } i - \text{avg of all estimates})^2))}$.

Value

List containing model summary statistics, model-averaged estimates of fishing, natural, tag, and total mortality, and survival and their weighted and unconditional standard errors .

Author(s)

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

References

Burnham, K. P. and D. R. Anderson. 2002. Model selection and multimodel inference : A Practical Information-Theoretic Approach, 2nd edition. Springer-Verlag, New York, NY. 488 p.

See Also

[irm_h_irm_cr](#)

Examples

```
## This is a typical specification, not a working example
## Not run:
tag_model_avg(model1,model2,model3,model4,model5,model6,model7,global="model7")
## End(Not run)
```

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 <i>lijs</i> ; 2= constant variance for all mean lengths at age; 3=var of <i>lij</i> 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 <i>L-infinity</i> , <i>K</i> , and <i>t0</i> . 1=automatic selection, 2=user-specified. If <i>select</i> =1, initial starting values of <i>L-infinity</i> , <i>K</i> , and <i>t0</i> 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 <i>select</i> =2, the user must specified the values of <i>L-infinity</i> , <i>K</i> , and <i>t0</i> .
Linf	if <i>select</i> =2, the starting value for <i>L-infinity</i> of the von Bertalanffy equation.
K	if <i>select</i> =2, the starting value for <i>K</i> of the von Bertalanffy equation.
t0	if <i>select</i> =2, the starting value for <i>t0</i> 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 (Lin1=Lin2).
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 (Lin1=Lin2, 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)

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

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)
```

wolffish	<i>Spring untransformed mean catch per tow for wolffish (Anarhichas lupus)</i>
----------	--

Description

The wolffish data frame has 25 rows and 2 columns. The mean catch per tow values were digitized from Figure 4 of Helser and Hayes (1995) and back-transformed to the original scale.

Usage

```
wolffish
```

Format

This data frame contains the following columns:

year survey year of catch per tow

index mean catch per tow value (untransformed)

Source

Helser, T. E. and D. B. Hayes. 1995. Providing quantitative management advice from stock abundance indices based on research surveys. *Fishery Bulletin* 93: 290-298.

yellowtail	<i>Fall average catch per tow for southern New England yellowtail flounder</i>
------------	--

Description

The `yellowtail` data frame has 22 rows and 2 columns. The average catch per tow values were digitized from Figure 4 of Pennington (1986)

Usage

```
yellowtail
```

Format

This data frame contains the following columns:

year survey year of catch per tow

index average catch per tow value (untransformed)

Source

Pennington, M. P. 1986. Some statistical techniques for estimating abundance indices from trawl surveys. *Fishery Bulletin* 84(3): 519-525.

ypr

*Yield-Per-Recruit Analysis***Description**

Yield-per-recruit (YPR) analysis is conducted following the modified Thompson-Bell algorithm. Reference points F_{max} and $F_{0.1}$ 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 F_{max} and $F_{0.1}$ 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 F_{max} and $F_{0.1}$
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

*Topic **datasets**

- alkdata, 6
- bonito, 15
- buffalo, 16
- catch, 16
- codcluslen, 21
- codlengths, 22
- codstrcluslen, 23
- darter, 25
- Gerking, 30
- goosefish, 30
- haddock, 31
- herring, 31
- Hoening, 32
- Jensen, 38
- Jiang, 39
- Kimura, 40
- rockbass, 60
- Shepherd, 63
- wolffish, 71
- yellowtail, 72

*Topic **htest**

- lfstrclus, 47
- vblrt, 70

*Topic **misc**

- agesurv, 2
- agesurvcl, 3
- alkD, 4
- alkprop, 7
- alkss, 8
- baglimit, 9
- bheq1, 11
- bheq2, 12
- bhnoneq, 13
- catchpertrip, 17
- catchseries, 18
- clusmean, 20
- combinevar, 23
- convmort, 24

- deltadist, 26
- deplet, 27
- extractMRFSS, 28
- irm_cr, 33
- irm_h, 36
- lengthfreq, 40
- LengthIncr, 42
- lfclus, 45
- lfstrclus, 47
- lifetable, 50
- M.empirical, 52
- mrN.single, 53
- opt_slot, 54
- opt_trophy, 56
- powertrend, 57
- pstrat, 58
- sbpr, 61
- schnabel, 62
- slca, 64
- surveyfit, 66
- surveyref, 67
- tag_model_avg, 68
- vblrt, 70
- ypr, 73

*Topic **package**

- fishmethods-package, 1

- agesurv, 2, 4
- agesurvcl, 3
- alkD, 4, 7, 9
- alkdata, 6
- alkprop, 5, 7, 9
- alkss, 5, 7, 8
- baglimit, 9
- bheq1, 11, 13
- bheq2, 12, 12, 14
- bhnoneq, 12, 13, 13
- bonito, 15
- buffalo, 16

- catch, 16
- catchpertrip, 17
- catchseries, 18
- clusmean, 20
- codcluslen, 21
- codlengths, 22
- codstrcluslen, 23
- combinevar, 23
- convmort, 24

- darter, 25
- deltadist, 26
- deplet, 27

- extractMRFSS, 10, 18, 20, 28, 42, 60

- fishmethods
 - (*fishmethods-package*), 1
- fishmethods-package, 1

- Gerking, 30
- goosefish, 30

- haddock, 31
- herring, 31
- Hoenig, 32

- irm_cr, 33, 38, 69
- irm_h, 36, 36, 69

- Jensen, 38
- Jiang, 39

- Kimura, 40

- lengthfreq, 40
- LengthIncr, 42
- lfclus, 45, 50
- lfstrclus, 47, 47
- lifetable, 50

- M.empirical, 52
- mrN.single, 53

- opt_slot, 54, 56
- opt_trophy, 55, 56

- powertrend, 57
- pstrat, 58

- rockbass, 60

- sbpr, 61, 74
- schnabel, 62
- Shepherd, 63
- slca, 64
- surveyfit, 66, 68
- surveyref, 66, 67

- tag_model_avg, 36, 38, 68

- vblrt, 70

- wolffish, 71

- yellowtail, 72
- ypr, 62, 73