The trawlfunctions package for R

Using trawlfunctions.R

The easiest method is simply to read the file trawlfunctions.R into your R session. This is done from the File menu > Source R code… (If you save the R workspace then the workspace will retain the functions.)

A number of R functions are defined in trawlfunctions.R. Only three, `ccfit`, `ttfit`, and `Rep.ttfit` are intended to be called directly by the user.

References

Millar, R. B., and S. J. Walsh. 1992. Analysis of trawl selectivity studies with an application to trouser trawls. *Fish. Res*. 13: 205-220

Millar, R. B. 1992. Estimating the size-selectivity of fishing gear by conditioning on the total catch. *J. Amer. Stat. Assoc*. 87: 962-968.

Millar, R. B., M. K. Broadhurst, and W. G. MacBeth. 2004. Modelling between-haul variability in the size selectivity of trawls. *Fish. Res*. 67:171-181.

`ccfit` *Function for fitting logistic or Richards curves to covered-codend data*

Description

`ccfit` fits a selection curve to data from covered-codend experiments using maximum likelihood. The selection curve can be the symmetric logistic, or the asymmetric Richards curve. Parameter estimates, standard errors and model deviances are produced, and plots of the fitted selection curve and deviance residuals are produced.

The selection curve is fitted using R's built-in numerical optimizer `nlm`.

Usage

```
ccfit(catch=catchdat,type="logit",probs=c(0.25,0.5,0.75),
   x0=c(-10,0.3),plots=T,suff.big=3,error.bars=F,plotlens=NULL,
   details=F)
```

Arguments

`catch`	Matrix containing the catch data. If no name is provided then it defaults to `catchdat.` The first column must contain the lengthclasses. The second column must contain the numbers caught in the experimental gear, and the last column contains the numbers caught in the cover.

`type`	Specifies the type of selection curve to be fitted. Takes the value “`logit`” or “`rich`”. Default is “`logit`”.
`probs`	Specifies the retention probabilities for which the corresponding fish length is required.
`x0`	Specifies start values for the `nlm` optimizer.
`delta`	Specifies start value of the asymmetry parameter for the `nlm` optimizer. Only used if `type=`“`rich`”.
`plots`	If true, produces a plot of data (with fit overlaid) and a plot of residuals. Default is `TRUE`.
`suff.big`	Model goodness of fit statistics are calculated over all lengthclasses, and again over only those lengthclasses with “sufficient” data. To be considered “sufficient”, the predicted catches in the codend and cover must both exceed `suff.big`.
`error.bars`	If true, approximate error bars are added to the plot of the data.
`plotlens`	Vector of lengths for which retention probabilities are required. If not specified then retention probabilities will be calculated for the lengthclasses in the data.
`details`	If true, provides a more extensive output including parameter covariances, fitted selection curve, and deviance residuals. Default is `FALSE`.

Value

`converged`	Return code from the `nlm` optimizer. Takes the value 1 or 2 if successfully converged .
`x`	Vector containing the fitted MLE estimates.
`l`	Matrix with two columns. First column gives the log-likelihoods for the fitted model, null model, and full model, respectively. Second column gives the associated dof (number of lengthclasses minus number of parameters).
`lens`	Matrix with two columns. The first column gives the estimated lengths corresponding to the retention probabilities specified in argument `probs`. The default gives the lengths of 25%, 50% and 75% retention. The second column gives the approximate standard errors.
`sr`	Vector giving the estimate of the difference between the lengths of 75% and 25% retention, and its approximate standard error.

If `details=T` then also

`xcovar`	Approximate covariance matrix of the MLE estimates.
`lensr.covar`	Approximate covariance matrix of `c(lens,sr)`.
`r`	Estimated retention probabilities, calculated for the lengthclasses in the data by default. See `plotlens` argument.

`devres`	Vector containing the deviance residuals.
`suff.dat`	Logical vector. Value is `TRUE` if the lengthclass was `suff.big` (see above).

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Examples

```
ccfit() #Logistic fit to data in matrix catchdat

ccfit(seldat) #Logistic fit to data in matrix seldat

ccfit(seldat,type=”rich”) #Richards fit

ccfit(seldat,x0=c(-20,0.5)) #Changing initial start values

#To get estimates of 10%, 25%, 50%, 75% and 90% retention lengths
ccfit(seldat,probs=c(0.1,0.25,0.5,0.75,0.9))

#To get retention probs for lengths from 20 to 40 in steps of 0.1
ccfit(seldat,plotlens=seq(20,40,0.1))
```

`ttfit`

Function for fitting logistic or Richards curves to data from alternate haul or trouser trawl type selectivity experiments

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Description

`ttfit` fits a selection curve to data from alternate haul or trouser trawl type experiments using maximum likelihood (i.e., the SELECT method). The selection curve can be the symmetric logistic, or the asymmetric Richards curve. The relative efficiency of the experimental and control gears can be estimated or specified. Parameter estimates, standard errors and model deviances are produced, and plots of the fitted curve and deviance residuals are produced.

The selection curve is fitted using R’s built-in numerical optimizer `nlm.`

Usage

```
ttfit(catch=catchdat,type="logit",probs=c(0.25,0.5,0.75),
      psplit=NULL,x0=c(10,0.3,0.5),delta=1.0,plots=T,
      suff.big=3,error.bars=F,plotlens=NULL,details=F)
```

Arguments

`catch`	Matrix containing the catch data. If no name is provided then it defaults to `catchdat.` The first column must contain the lengthclasses. The second column must contain the numbers caught in the experimental gear, and the last column contains the numbers caught in the control.
`type`	Specifies the type of selection curve to be fitted. Takes the value "`logit`" or "`rich`". Default is "`logit`".
`psplit`	If specified, the relative efficiency of the experimental codend is fixed at the value of `psplit`.
`probs`	Specifies the retention probabilities for which the corresponding fish length is required.
`x0`	Specifies start values of the selection curve parameters for the `nlm` optimizer.
`delta`	Specifies start value of the asymmetry parameter for the `nlm` optimizer. Only used if `type=`"`rich`".
`plots`	If true, produces a plot of data (with fit overlaid) and a plot of residuals. Default is `TRUE.`
`suff.big`	Model goodness of fit statistics are calculated over all lengthclasses, and again over only those lengthclasses with "sufficient" data. To be considered "sufficient", the predicted catches in the experimental and control gears must both exceed `suff.big`.
`error.bars`	If true, approximate error bars are added to the plot of the data.
`plotlens`	Vector of lengths for which retention probabilities are required. If not specified then retention probabilities will be calculated for the lengthclasses in the data.
`details`	If true, provides a more extensive output including parameter covariances, fitted selection curve, and deviance residuals. Default is `FALSE.`

Value

`converged`	Return code from the `nlm` optimizer. Takes the value 1or 2 if successfully converged.
`x`	Vector containing the fitted MLE estimates.
`l`	Matrix with two columns. First column gives the log-likelihoods for the fitted model, null model, and full model, respectively. Second column gives the associated dof (number of lengthclasses minus number of parameters).
`lens`	Matrix with two columns. The first column gives the estimated lengths corresponding to the retention probabilities specified in argument `probs`. The default gives the lengths of 25%, 50% and 75% retention. The second column gives the approximate standard errors.

`sr`	Vector giving the estimate of the difference between the lengths of 75% and 25% retention, and its approximate standard error.
p	Vector giving the estimate of relative efficiency, and its approximate standard error.

If `details=T` then also

`xcovar`	Approximate covariance matrix of the MLE estimates.
`lensr.covar`	Approximate covariance matrix of `c(lens,sr)`.
`r`	Estimated retention probabilities, calculated for the lengthclasses in the data by default. See `plotlens` argument.
`devres`	Vector containing the deviance residuals.
`suff.dat`	Logical vector. Value is `TRUE` if the lengthclass was `suff.big` (see above).

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Examples

```
#Fit a logistic curve to data in matrix seldat
ttfit(seldat)

#Fit a logistic curve, with relative efficiency of the
#experimental and control codends fixed at 0.5.
ttfit(seldat,psplit=0.5)
```

`Rep.ttfit` *Function for estimating the replicate estimate of dispersion from "stacked" trouser trawl or alternate haul data.*

Description

`Rep.ttfit` is similar to `ttfit`, but is specifically designed to calculate the replication estimate of overdispersion from stacked individual haul data arising from trouser trawl or alternate haul experiments. It uses a combined hauls selection curve, but ignores between-haul variability in the relative fishing efficiency parameter by calculating a separate efficiency parameter for each haul. (The method used is approximate for non-logistic selection curves.) See Millar et al. (2004) for details. If a common efficiency parameter is specified then the REP estimate is the same as that obtained from using `ttfit` on the stacked individual haul data.

Usage

```
Rep.ttfit(catch=catchdat,ntows,numlens,type="logit",
     x0=c(10,0.3,0.5),ind.psplit=T,suff.big=3,details=F)
```

Arguments

`catch`	Matrix containing the stacked individual haul catch data. If no name is provided then it defaults to `catchdat.` The first column must contain the lengthclasses. The second column must contain the numbers caught in hauls of the experimental gear, and the last column contains the numbers caught in the hauls of the control. It is assumed that all hauls use the same lengthclasses.
`ntows`	The number of tows.
`numlens`	The number of lengthclasses per tow. The number of rows in the `catch` matrix must equal `ntows` times `numlens`.
`type`	Specifies the type of selection curve to be fitted. Takes the value “`logit`” or “`rich`”. Default is “`logit`”.
`x0`	Specifies start values of the selection curve parameters for the `nlm` optimizer.
`delta`	Specifies start value of the asymmetry parameter for the `nlm` optimizer. Only used if `type=`“`rich`”.
`ind.psplit`	If true, individual haul relative efficiencies are used. If false, a common efficiency is used and the REP estimate is the same as would be obtained by using `ttfit` (on the stacked data).
`suff.big`	Model goodness of fit statistics are calculated over all lengthclasses, and again over only those lengthclasses with “sufficient” data. To be considered “sufficient”, the predicted catches in the experimental and control gears must both exceed `suff.big`.
`details`	If true, returns the individual haul efficiency parameters. Default is `FALSE.`

Value

In addition to printing summary output on the screen, `Rep.ttfit` returns a list containing a single numeric value, the REP correction factor.

If `details=T` then also

`psplits`	Vector of estimates of the individual haul efficiency parameters.

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