The gillnetfunctions **package for R**

Using **gillnetfunctions.R**

The easiest method is simply to read the file gillnetfunctions.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.)

The `gillnetfunctions.R` file defines the function `gillnetfit`. It also defines three additional functions (one for calculating the fitted relative retention curves, and two for plotting the curves and the deviance residuals) that are called by `gillnetfit`. These three additional functions are not intended to be called directly by the user.

`gillnetfit`   *Function for fitting relative retention curves to gillnet data. Relative fishing efficiencies (or unequal fishing effort) of the meshes can be specified.*

Description

`gillnetfit` fits relative retention curves to data from gillnet selectivity experiments using maximum likelihood. The retention curves can be normal shaped (with fixed spread, or spread proportional to mesh size), gamma shaped, or log-normal shaped. Plots of the fitted curves and deviance residuals are produced by default.

The curves are fitted using the R function `glm` for fitting log-linear models. The methodology, and definition of parameters, is given in

Millar, R. B., and Holst, R. (1997). Estimation of gillnet and hook selectivity using log-linear models. ICES J. Mar. Sci. 54: 471-477.

Usage

```
gillnetfit(data,meshsizes,type="norm.loc",rel=NULL,
                    plots=c(T,T),plotlens=NULL,details=F)
```

Arguments

The first two arguments are required.

`data`	Matrix containing the catch data. The first column must contain the lengthclasses. The second and subsequent columns must contain the numbers caught in the different sized meshes used. These columns are assumed to be in order of increasing mesh size. See file `holt.dat`
`meshsizes`	A vector containing the mesh sizes in increasing order.
`type`	Character value specifying the type of retention curve to be fitted. Possible values are "`norm.loc`" (normal shaped with common spread), "`norm.sca`" (normal shaped with spread proportional to mesh size), "`gamma`" (gamma shaped), "`lognorm`" (lognormal shaped).

`rel`	Vector of relative efficiencies (or fishing efforts) of the different sized meshes. The meshes are assumed to fish with equal efficiency (and effort) if not specified.
`plots`	Logical vector of length 2. If first element is true then a plot of fitted curves is produced. If second element is true then a plot of deviance residuals is produced. Default is both.
`plotlens`	Vector of lengths for which values of relative retention are required. If not specified then relative retention values will be calculated and plotted for the lengthclasses in the data.
`details`	If true, the returned object also includes the values of the fitted retention curves and deviance residuals. Default is `FALSE`.

Value

`fit.type`	Character value returning the fit type.
`gear.pars`	Vector of length 4. The first two elements are the MLE's of the parameters as specified in Millar and Holst (1997). The second two elements provide the mode and standard deviation of the retention curve of the smallest mesh.
`g.o.f`	Vector of length 3 containing the goodness of fit statistics. Elements are the model deviance, degrees of freedom, and null model deviance, respectively.

If `details=T` then also

`devres`	Matrix containing the deviance residuals.
`rselect`	Matrix containing the values of the fitted relative retention curves. See `plotlens`.

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Examples

```
#Read in catch data and specify mesh sizes
holt.dat=matrix(scan("holt.dat"),byrow=T,ncol=9)
meshsizes=c(13.5,14.0,14.8,15.4,15.9,16.6,17.8,19.0)

#Fit normal-shaped curves with common spread
gillnetfit(holt.dat,meshsizes)

#Fit gamma-shaped curves and use lengths from 40 to 100 in plot
gillnetfit(holt.dat,meshsizes,type="gamma",plotlens=40:100)

#Fit lognormal-shaped curves, with relative efficiency proportional to
#mesh size
gillnetfit(holt.dat,meshsizes,type="lognorm",rel=meshsizes)
```