Package 'FlexParamCurve'

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Title Tools to Fit Flexible Parametric Curves

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Description Model selection tools and 'selfStart' functions to fit parametric curves in 'nls', 'nlsList' and 'nlme' frameworks.

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Contents

`FlexParamCurve-package`

Tools to Fit Flexible Parametric Curves

Description

selfStart functions and model selection tools to fit parametric curves in

`nls`, `nlsList` and `nlme` frameworks.

Details

General approach for using package (also see examples below)

1) Run $modpar$ to produce initial parameter estimates and estimates of parameter bounds for your dataset.

These are used to accomodate fixed parameters and are saved in user-specified `list` object

All parameters and options in this list can be edited manually or using $change.pnparameters$. The

list could be created manually given that the elements were labelled sufficiently. Note that this step is

unnecessary when using the model selection routines $pn.mod.compare$ and $pn.modselect.step$ as they

will automatically call $modpar$ if parameter estimates are missing.

2) Determine most appropriate model (number of necessary parameters) for your data

using $pn.mod.compare$ or $pn.modselect.step$ (these rank competing model and then compare nested models using

$extraF$). This may take some time as many $nlsList$ objects are fitted.

Note that if you perform this step, then you do not need to perform step 1.

If you are sure of your model (e.g. it is a simple logistic) Step 2 may be unnecessary.

3) Fit nls or $nlsList$ or $nlme$ models using $SSposnegRichards$ specifying

the appropriate model number and the list of parameters and options (specified pn.options object).

Note if required model is monotonic (i.e. contains no recession parameters, modno= 12 or 32) recessional parameters

will be ignored unless "force.nonmonotonic" option is TRUE in the specified pn.options list

object (see $modpar$) in which case they will be included as fixed values from the list object.

Parameter bounds can be refinedto improve fits by altering this list, either manually or using

change.pnparameters.

4) Plot your curves using $posnegRichards.eqn$ specifying the appropriate model number and list of parameters/options.

User level functions include:

$pn.mod.compare$

all-model selection for positive-negative Richards nlsList models

$pn.modselect.step$

backward stepwise model selection for positive-negative Richards nlsList models

$SSposnegRichards$

selfStart function for estimating parameters of 36 possible reductions of the 8-parameter positive-negative Richards model (double-Richards)

$posnegRichards.eqn$

function for evaluating 36 possible reductions of the 8-parameter positive-negative Richards model (double-Richards)

$modpar$

estimates mean parameters (and parameter bounds) for 8-parameter positive-negative Richards models or 4-parameter Richards models and saves in objects pnmodelparams and pnmodelparamsbounds. (required prior to use of the above functions)

change.pnparameters

simple function to update pnmodelparams and pnmodelparamsbounds

with user specified values

extraF

performs extra sum-of-squares F test for two nested nlsList models

extaF.nls

performs extra sum-of-squares F test for two nested nls models

Note

Version 1.5 saves many variables, and internal variables in the package environment: FlexParamCurve:::FPCEnv. By default, the pn.options file is copied to the environment specified by the functions (global environment by default). Model selection routines also copy from FPCenv to the global environment all nlsList models fitted during model selection to provide backcompatibility with code for earlier versions. The user can redirect the directory to copy to by altering the Envir argument when calling the function.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

References

Oswald, S.A. et al. 2012. FlexParamCurve: R package for flexible

fitting of nonlinear parametric curves. Methods in Ecology and Evolution. 3(6): 1073-77.

doi: 10.1111/j.2041-210X.2012.00231.x (see also tutorial and introductory videos at:

http://www.methodsinecologyandevolution.org/view/0/podcasts.html

posted September 2012 - if no longer at this link, check the archived videos (and comments) at:

http://www.methodsinecologyandevolution.org/view/0/VideoPodcastArchive.html#allcontent)

See Also

nlme

SSlogis

Examples

```
#Code is provided here for an illustrative overview of using FlexParamCurve to select,

# fit, analyze and plot the most appropriate non-linear curves for a dataset.

# NOTE: autorun is disabled for these examples since more detailed examples are provided for the

# individual functions in their associated help files and runtime for this overview approximates

# 5 mins. To run, simply copy and paste code from this help file into the R GUI.


# run all-model selection for posneg.data object (Step 2) without need to run any previous functions

## Not run:

    modseltable <- pn.mod.compare(posneg.data$age, posneg.data$mass,

    posneg.data$id, existing = FALSE, pn.options = "myoptions")
## End(Not run)


# run backwards stepwise model selection (Step 2) for logist.data object

#without need to run any previous functions

## Not run:

    modseltable <- pn.modselect.step(logist.data$age, logist.data$mass,

    logist.data$id, existing = FALSE, pn.options = "myoptions")
## End(Not run)


# estimate fixed parameters use data object posneg.data (Step 1)
```

```
## Not run:

     modpar(posneg.data$age,posneg.data$mass, pn.options = "myoptions")
## End(Not run)



# change fixed values of M and constrain hatching mass to 45.5 in a growth curve (Step 1)

## Not run:

      change.pnparameters(M=1,RM=0.5,first.y=45.5, pn.options = "myoptions")
## End(Not run)



# fit nlsList object using 6 parameter model with values M and RM (Step 3)

# fixed to value in pnmodelparams and then fit nlme model

## Not run:

richardsR22.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

      Infl = Infl, RAsym = RAsym, Rk = Rk, Ri = Ri,

      modno = 22, pn.options = "myoptions"), data = posneg.data)

richardsR22.nlme <- nlme(richardsR22.lis, random = pdDiag(Asym + Infl ~ 1))
## End(Not run)



# fit reduced nlsList model and then compare performance with extraF (manual version of Step 2)

## Not run:

 richardsR20.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

      Infl = Infl, modno = 20, pn.options = "myoptions"), data = posneg.data)

 extraF(richardsR20.lis,richardsR22.lis)
## End(Not run)



# fit and plot a logistic curve (M=1) to data, note - all parameters set to 1 are ignored

# note code here forces \eqn{modpar} to only estimate 4 curve parameters (simple Richards curve)

#create list for fixed parameters

## Not run:
```

```
modpar(logist.data$age,logist.data$mass,force4par=TRUE, pn.options = "myoptions")

change.pnparameters(M=1, pn.options = "myoptions") # set M to 1 for subsequent fit

richardsR20.nls <- nls(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

      Infl = Infl, modno = 20, pn.options = "myoptions"), data = logist.data)

plot(logist.data$age , logist.data$mass, xlab = "age", ylab = "mass", pch = ".", cex = 0.7)

par <- coef( richardsR20.nls )
## End(Not run)



#(Step 4)

## Not run:

curve(posnegRichards.eqn(x, Asym = par[1], K = par[2], Infl = par[3], modno = 20

, pn.options = "myoptions"), add= TRUE)
## End(Not run)
```

`change.pnparameters` *Change Fixed Parameter Values*

Description

Function to alter values of parameters to be used by `SSposnegRichards`
or `posnegRichards.eqn`
as the fixed values in equations where parameters are fixed

Usage

```
change.pnparameters(Asym = NA,

K = NA,

Infl = NA,

M = NA,
```

```
    RAsym = NA,

    Rk = NA,

    Ri = NA,

    RM = NA,

    Amin = NA,

    Amax = NA,

    Kmin = NA,

    Kmax = NA,

    Imin = NA,

    Imax = NA,

    Mmin = NA,

    Mmax = NA,

    RAmin = NA,

    RAmax = NA,

    Rkmin = NA,

    Rkmax = NA,
```

```
    Rimin = NA,

    Rimax = NA,

    RMmin = NA,

    RMmax = NA,

    first.y = NA,

    x.at.first.y = NA,

    last.y = NA,

    x.at.last.y = NA,

    twocomponent.x = NA,

    verbose = NA,

    force4par = NA,

    pn.options,

    Envir = .GlobalEnv)
```

Arguments

Asym	a numeric value for the asymptote of the positive (increasing) curve
K	a numeric value for the rate parameter of the positive (increasing) curve
Infl	a numeric value for the point of inflection of the positive (increasing) curve
M	a numeric value for the shape parameter of the positive (increasing) curve

RAsym	a numeric value for the asymptote of the negative (decreasing) curve
Rk	a numeric value for the rate parameter of the negative (decreasing) curve
Ri	a numeric value for the point of inflection of the negative (decreasing) curve
RM	a numeric value for the shape parameter of the negative (decreasing) curve
Amin	a numeric value for the minimum bound of Asym
Amax	a numeric value for the maximum bound of Asym
Kmin	a numeric value for the minimum bound of K
Kmax	a numeric value for the maximum bound of K
Imin	a numeric value for the minimum bound of Infl
Imax	a numeric value for the maximum bound of Infl
Mmin	a numeric value for the minimum bound of M
Mmax	a numeric value for the maximum bound of M
RAmin	a numeric value for the minimum bound of RAsym
RAmax	a numeric value for the maximum bound of RAsym
Rkmin	a numeric value for the minimum bound of Rk
Rkmax	a numeric value for the maximum bound of Rk
Rimin	a numeric value for the minimum bound of Ri
Rimax	a numeric value for the maximum bound of Ri
RMmin	a numeric value for the minimum bound of RM
RMmax	a numeric value for the maximum bound of RM
first.y	the value of y at minimum x when it is required to be constrained
x.at.first.y	the final value of x - 0 value is used if not specified when last.y is not NA
last.y	the value of y at maximum x when it is required to be constrained
x.at.last.y	the final value of x - this is option is currently disabled
twocomponent.x	a numerical specifying the x-value (e.g. age) of intersection if a double model of two separate components is to be fitted. Alternatively a logical of value = TRUE if the same type of model is to be fitted but the x of intersection is unknown
verbose	logical indicating whether information on successful optimization and parameters should be returned during when using SSposnegRichards
force4par	logical specifying whether parameters of the negative Richards should be ignored - effectively using simple Richards curve
pn.options	required character string specifying the name of a list object currently populated with starting parameter estimates, fitting options and bounds to be modified
Envir	a valid R environment to find pn.options in, by default this is the global environment

Details

This function provides a simple way for the user to update
the a user-named list that holds fixed values and options
for fitting and solving positive-negative Richards curves with
SSposnegRichards and posnegRichards.eqn,
respectively. Running this function also concurrently updates the parameterbounds
in the same list which are the maximum and minimum values
for parameters to be used by optim and nls
during parameter estimation
in SSposnegRichards. The list is written automatically by the function but
it is also output as a return value for assignation in the usual way [myoptions<- change.pnparameters(...)].
The list specified by pn.options must exist before this function is called. Use modpar
to estimate values for all parameters and easily generate a suitable list. See modpar for details of bounding.

Value

a list of values for all above arguments,
with new values substituted where specified in the call

Note

Requires modpar to be have been run prior to execution
Version 1.5 saves many variables, and internal variables in the package environment:
FlexParamCurve:::FPCEnv. By default, the pn.options file is copied to the environment
specified by the functions (global environment by default). Model selection routines
also copy from FPCenv to the global environment all nlsList models fitted during
model selection to provide backcompatibility with code for earlier versions. The user
can redirect the directory to copy to by altering the Envir argument when calling the
function.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

See Also

modpar SSposnegRichards posnegRichards.eqn

Examples

```
# change all fixed values except K and Rk

    modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")

    change.pnparameters(Asym = 10000, Infl = 80, M = 5, RAsym = 10000,

        Ri = 240, RM = 5, pn.options = "myoptions")



# change fixed values of M and constrain hatching mass to 45.5 in a growth curve

    change.pnparameters(M = 1, RM = 0.5, first.y = 45.5, pn.options = "myoptions")
```

---

extraF *Compare Two $nlsList$ Models Using Extra Sum-of-Squares F-Tests*

Description

Function to compare two nested models using extra sum-of-squares F-Tests.

Usage

```
extraF(submodel = 1,

genmodel = 1,

warn = TRUE)
```

Arguments

submodel	$nlsList$ model with fewer curve parameters (reduced model)
genmodel	$nlsList$ model with more curve parameters (general model)
warn	logical specifying whether to report working R environment if previously exists

Details

Models must be entered in the correct order with the reduced model appearing
first in the call and the more general model appearing later. These must be nested models,
i.e. the general model must contain all of the curve parameters in the reduced model and more.
Entering models with the same number of parameters will produce NAs in the output, but
the function will produce seemingly adequate output with non-nested models. The user must
check that models are nested prior to use.
This function is primarily designed to be called by the model selection functions
`pn.modselect.step` and `pn.mod.compare` but can be used independently.
Extra sum-of-squares is obtained from:

```
F = (SS1 - SS2)/(df1 - df2) / (SS2 / df2)
```

where SS = sum-of-squares and df = degrees of freedom, for the more reduced model (1) and the
more general model (2), respectively.
If the F value is significant then the more general model provides a significant improvement
over the reduced model, but if the models are not significantly different then the reduced
parameter model is to be preferred.
In extraF (formulated especially for nlsList models), the root mean square error
(and sum of squares) is inflated to the value expected if all groups (levels) were
fitted [i.e. RSE = RSE* (sqrt(n1) / sqrt(n0)), where RSE is root mean square error, n0 is the sample size (total
number of data points used in fit) for the model with missing levels, and n1 is the inflated sample size (total number
of data points in dataset)]. This is based on RSE changing with the square root of sample size, as discussed in the help file for
`pn.mod.compare`. Degrees of freedom are then increased to the vaue if all individuals had been fitted successfully,
i.e. total df - (# curve parameters * # levels). Thus, RSE and df are enlarged for models with missing levels so all models are
compared based on the variability expected if all levels had been fitted . This allows the Fstat from extraF to be independent of missing levels
in either of the two models.

Value

A `data.frame` listing the names of the models compared, F,
numerator degrees of freedom,
demonimator degrees of freedom, P value and the residual sum of squares for both the general
and reduced models

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

References

Ritz, C. and Streibigg, J. C. (2008) $Nonlinear regression with R$.
Springer-Verlag, New York.

See Also

extraF.nls

nlsList

pn.modselect.step

pn.mod.compare

Examples

```
#compare two nested nlsList models (4 vs 8 parameter models)

modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")

# (only first 4 group levels in data used for example's sake)

subdata<-subset(posneg.data, as.numeric(row.names (posneg.data) ) < 53)

richardsR2.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

 Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri,modno = 2, pn.options = "myoptions")

                    , data = subdata)

richardsR12.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

  Infl = Infl, M = M, modno = 12, pn.options = "myoptions")

                    , data = subdata)

extraF(richardsR12.lis, richardsR2.lis)
```

`extraF.nls` *Compare Two nls Models Using Extra Sum-of-Squares F-Tests*

Description

Function to compare two nested `nls` models using extra sum-of-squares F-Tests.

Usage

```
extraF.nls(submodel,

genmodel)
```

Arguments

`submodel`	nls model with fewer curve parameters (reduced model)
`genmodel`	nls model with more curve parameters (general model)

Details

Models must be entered in the correct order with the reduced model appearing first in the call and the more general model appearing later. These must be nested models, i.e. the general model must contain all of the curve parameters in the reduced model and more. Entering models with the same number of parameters will produce NAs in the output, but the function will produce seemingly adequate output with non-nested models. The user must check that models are nested prior to use.

This function is not promoted for use in model selection as differences in curves of different grouping levels in the dataset may be obscured when curves are fitted to the entire dataset, as in `nls`.

Extra sum-of-squares is obtained from:

```
F = (SS1 - SS2)/(df1 - df2) / (SS2 / df2)
```

where SS = sum-of-squares and df = degrees of freedom, for the more reduced model (1) and the more general model (2), respectively. To account for missing individuals for different fits df are scaled in all models to the value they would be if all individuals fit successfully (note that if all individuals had the same fit, this would not influence extra sum of squares).
If the F value is significant then the more general model provides a significant improvement over the reduced model, but if the models are not significantly different then the reduced parameter model is to be preferred.

Value

A data.frame listing the names of the models compared, F,
numerator degrees of freedom,
demonimator degrees of freedom, P value and the residual sum of squares for both the general and reduced models

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

References

Ritz, C. and Streibigg, J. C. (2008) $Nonlinear regression with R$.
Springer-Verlag, New York.

See Also

extraF
nls
pn.modselect.step
pn.mod.compare

Examples

```
#fit and compare two nested nls models (7 vs 8 parameter models)

   #create list for fixed parameters

   modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")

   richardsR1.nls <- nls(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

  Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri, RM = RM, modno = 1, pn.options = myoptions)
```

```
                        , data = posneg.data)

richardsR2.nls <- nls(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri, modno = 2, pn.options = myoptions)

                        , data = posneg.data)

extraF.nls(richardsR2.nls, richardsR1.nls)
```

---

get.mod *Copy objects between R environments*

Description

Function to copy objects between R environments

Usage

```
get.mod(modelname = ls(FPCEnv, pattern=".lis" ),

 from.envir = FPCEnv, to.envir = .GlobalEnv,

 write.mod = FALSE, silent = FALSE)
```

Arguments

modelname	a character or character vector of object names
from.envir	R environment currently containing the object(s)
to.envir	destination R environment to copy the object(s) to
write.mod	logical specifying if single models should be assigned or simply returned
silent	logical specifying whether additional confirmation should be printed to the screen

Details

All arguments are optional. With defaults, this function copies any $nlsList$ models

from the FlexParamCurve working environment to the Global Environment. However, user could use

this function to move any objects between any environments.

Default behavior is to assign models to an environment if more than 1 modelname is provided but to

simply return the model from the function if only 1 modelname is given. Notes are printed to the screen to detail any models moved or any errors encountered.

Value

If only 1 modelname is provided, the contents of the object is returned. If more

more than 1 modelname is provided or if write.mod is FALSE then the object(s) will be assigned to the environment and no value is returned.

Note

The default function works by detecting the suffix .lis rather than object class, so will only return models with this suffix, not necessarily all $nlsList$ models if they have different suffixes.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

See Also

pn.mod.compare

pn.modselect.step

Examples

```
#transfer all nlsList models from the FlexParamCurve working environmment (FPCEnv)

  #to the Global Environment. Note: unless pn.mod.compare or

  #pn.modselect.step have been run, in which case this is default

  #1. subset data object (only 3 individuals) to expediate model selection

  subdata <- subset(posneg.data, as.numeric(row.names (posneg.data) ) < 40)

  #2. run model selection in FPCEnv using pn.mod.compare. Only two models (#1 and #5)

  #specified to be run here to reduce processing time. see pn.mod.compare

  modseltable <- pn.mod.compare(subdata$age, subdata$mass,

  subdata$id, existing = FALSE, pn.options = "myoptions", mod.subset = c(1,5)

  , Envir = FlexParamCurve:::FPCEnv)
```

```
#3. retrieve models from FlexParamCurve working environmment

get.mod()

#transfer an options file called myoptions from FPCEnv to the Global Environment

#note data are forced to fit a monotonic curve in this example

modpar(logist.data$age, logist.data$mass, pn.options = "myoptions.1", force4par = TRUE,

Envir = FlexParamCurve:::FPCEnv)

get.mod(modelname = "myoptions.1", write.mod = TRUE)
```

`logist.data` *Simulated growth of whiskered terns*

Description

The `logist.data` data frame has 1100 rows and 3 columns of records of the simulated masses for whiskered tern chicks between 0 and 21 days of age.

Usage

```
logist.data
```

Format

This object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

mass a numeric vector of chick masses (g).

age a numeric vector of chick ages (days).

id an ordered factor indicating unique id of each simulated individual, i.e. which data belongs to which individual.

Details

No published parameter estimates with associated variability are available for positive-negative growth curves. These data were simulated using an 3-parameter positive-negative Richards curve (`SSposnegRichards` (model 20)), using parameters drawn from normal distributions with the following means (standard deviations):

```
Asym=92.35 (15.65)
K=0.06 (0.138)
Infl=0.294 (1.72)
```

These values were taken from Pallisson et al. (2008) for 75 chicks reported. Each simulated individual had 11 measurements stratified through the development period, with 1-2 day random differences in timing of each measurement. This data object has methods for nlme grouped-data classes.

Source

Paillisson, J.-M., Latraube, F. & Reeber, S. (2008) Assessing growth and age of Whiskered Tern $Chlidoniashybrida$ chicks using biometrics. Ardea, 96, 271-277.

Examples

```
require(stats); require(graphics)
#view data
logist.data
#create list for fixed parameters
modpar(logist.data$age, logist.data$mass, force4par = TRUE, pn.options = "myoptions")
plot(mass ~ age, data = logist.data, subset = id == "0.002",
     xlab = "Chick age (day)", las = 1,
     ylab = "Chick mass (g)",
     main = "logist.data and fitted curve (Chick #2 only)")
change.pnparameters(M=1, pn.options = "myoptions") # set curve to logistic (M=1) in subsequent fit
fm1 <- nls(mass ~ SSposnegRichards(age,Asym=Asym,K=K,Infl=Infl,
           modno=20, pn.options = "myoptions"),
           data = logist.data, subset = id == "0.002")
age <- seq(0, 166, length.out = 101)
lines(age, predict(fm1, list(age = age)))
```

---

modpar *Estimate Values to be Used for Fixed FlexParamCurve Parameters*

Description

This function creates the object pnmodelparams

which holds estimates of values for all 8 FlexParamCurve

parameters used for fitting and solving positive-negative Richards curves with

SSposnegRichards and posnegRichards.eqn,

respectively.

Usage

```
modpar(x,

y,

pn.options = NA,
```

```
    first.y = NA,

    x.at.first.y = NA,

    last.y = NA,

    x.at.last.y = NA,

    twocomponent.x = NA,

    verbose = FALSE,

    force8par = FALSE,

    force4par = FALSE,

    suppress.text = FALSE,

    taper.ends = 0.45,

    width.bounds = 1,

    bounds.error = FALSE,

    Envir = .GlobalEnv,

    force.nonmonotonic = FALSE,

    ...)
```

Arguments

x	a numeric vector of primary predictor variable
y	a numeric vector of response variable
first.y	the value of y at minimum x when it is required to be constrained
x.at.first.y	the final value of x - 0 value is used if not specified when last.y is not NA
last.y	the value of y at maximum x when it is required to be constrained
x.at.last.y	the final value of x - must be specified if last.y is not NA
twocomponent.x	a numerical specifying the x-value (e.g. age) of intersection if a double model of two separate components is to be fitted. Alternatively a logical of value = TRUE if the same type of model is to be fitted but the x of intersection is unknown
verbose	logical indicating whether information on successful optimization and parameters should be returned during when using SSposnegRichards

force8par	logical specifying whether parameters of the negative Richards curve should be set to defaults if they cannot be estimated
force4par	logical specifying whether parameters of the negative Richards should be ignored - effectively using simple Richards curve
pn.options	character string specifying name of list object populated with starting parameter estimates, fitting options and bounds or the destination for modpar to write a new list
suppress.text	logical specifying whether modpar should return descriptive text to the screen during execution
taper.ends	numeric representing the proportion of the range of the x variable for which data are extended at the two ends of the data set. This is used in initial estimation (prior to optim and nls optimizations) and can speed up subsequent optimizations by imposing a more pronounced S-shape to both first and second curves. Defaults to 0.45.
width.bounds	a numeric indicating the proportion of the usual width of parameter bounds to be imposed during optimizations. Large values may slow or terminate computations, however they could better accomodate data in which different levels exhibit very different parameter values.
bounds.error	a logical. If true parameter estimation will terminate if initial estimation of parameters leads to values outside specified bounds in pn.options. If false, more appropriate bounds will be determined automatically.
Envir	a valid R environment to find pn.options in and export any output to, by default this is the global environment
force.nonmonotonic	if set to TRUE fixed recessional parameter estimates will be used for the two monotonic equations (modno #12 or #32), otherwise these two models will use RAsym = 0, Ri = 0, Rk = 1, RM = 1 to prevent non-monotonic relationships in these cases.
...	additional optional arguments to be passed to nlsList

Details

This function creates a formatted list object as named by the argument pn.options. This list holds estimates of values for all 8 FlexParamCurve parameters, fitting options and parameter bounds used for fitting and solving double-Richards curves with SSposnegRichards and posnegRichards.eqn, respectively. Parameter bounds are the maximum and minimum parameters values that can be used by optim and nls during parameter estimation. For definitions of parameters see either SSposnegRichards

or posnegRichards.eqn. The list is written automatically by the function (to ".pntemplist") but it is

also output as a return value for assignation and subsequent use in the usual way [myoptions<-change.pnparameters(...)].

Estimates are produced by fitting positive-negative or double Richards curves in

nls using

SSposnegRichards for the full 8 parameter model (R1).

If this fails, the function getInitial is called to

attempt to produce initial estimates using the same 8 parameter model.

If this also fails, estimates are attempted in the same way using the

4 parameter (positive only) model (R12). In this case, only the positive

parameters are returned (NAs are substituted for negative parameters)

unless argument force8par=TRUE, in which case negative parameters are

defaulted to: RAsym = 0.05*Asym, Rk = K, Ri = Infl, RM = M.

This function can now fit biphasic (and more generally

double-Richards) curves, where the final curve is effectively either two positive curves

or two negative curves, as well as negative-positive curves. This functionality is default

and does not need to be specified.

Parameter bounds estimated here for use in optim and nls

fits within SSposnegRichards are

applicable to a wide range of curves, although user may

change these manually in list object specified by pn.options.

Bounds are estimated by modpar by adding or subtracting multiples

of fixed parameter values to estimated mean parameter values:

-Asym*0.5 and +Asym*2.5,

-K*0.5 and +K*0.5,

-Infl*2.5 and +Infl*10

-M*2 and +M*2

-RAsym*0.5 and +RAsym*2.5,

-Rk*0.5 and +Rk*0.5,

-Ri*2.5 and +Ri*5

-RM*2 and +RM*2.

Use force8par = TRUE if initial call to modpar produces estimates for

only 4 parameters and yet an 8 parameter model is desired for SSposnegRichards

or posnegRichards.eqn.

Use force4par = TRUE if you desire to produces estimates only for the four parameters of

a single Richards curves. This should also be used if you wish to fit simple logistic

Gompertz or von Bertalanffy curves: see SSposnegRichards for more details. If

the specified model in subsequent $SSposnegRichards$, model selection or ploting calls

is monotonic (i.e. contains no recession parameters: modno= 12 or 32) recessional parameters

will not be included for these two models unless "force.nonmonotonic" option is TRUE,

in the specified pn.options list object, in which case parameters will be drawn from the specified

pn.options list object.

When specified, first.y and last.y are saved in list object specified by pn.options to instruct

SSposnegRichards to add this as the first or last value of the response, respectively,

during estimation.

To fit two-component double-curves, in which one curve equation is used up to (and including)

the x of intersection and a separate equation is used for x-values greater than the x of intersection

the argument twocomponent.x should be set to the value for the x of intersection. If this argument

is anything other than NA then a two-component model will be fitted when SSposnegRichards

is called. This option will be saved in list object specified by pn.options and can be changed at will.

taper.ends can be used to speed up optimization as it extends the dataset at maximum and minimum extremes

of x by repeatedly pasting the y values at these extremes for a specified proportion of the range of x.

taper.ends is a numeric value representing the proportion of the range of x values are extended for and

defaults to 0.45 (45

tend towards a zero slope this is a suitable values. If tapered ends are not desirable then choose taper.ends = 0.

If the argument verbose = TRUE then details concerning the optimization processes within

SSposnegRichards are printed on screen whenever SSposnegRichards is called.

These include whether optimization of the first or second parts of the curve or simultaneous optimizations

are successful, if these have been further refined by nls, whether default parameters were used or the

parameterization was aborted and what parameter values were finally exported by SSposnegRichards.

This option will be saved in the list object specified by pn.options and can be changed at will.

Value

a list of estimated fixed values for all

above arguments

Note

Version 1.5 saves many variables, and internal variables in the package environment: FlexParamCurve:::FPCEnv. By default, the pn.options file is copied to the environment specified by the functions (global environment by default). Model selection routines also copy from FPCenv to the global environment all nlsList models fitted during model selection to provide backcompatibility with code for earlier versions. The user can redirect the directory to copy to by altering the Envir argument when calling the function.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

Examples

```
# estimate fixed parameters use data object posneg.data

     modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")


# estimate fixed parameters use data object posneg.data (only first

# 4 group levels for example's sake) and specify a fixed hatching

# mass for curve optimization using \code{\link[FlexParamCurve]{SSposnegRichards}}

 modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")

     subdata <- subset(posneg.data,posneg.data$id == as.character(36)

     | posneg.data$id == as.character(9)

     | posneg.data$id == as.character(32)

     | posneg.data$id == as.character(43))

 richardsR22.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym,

         K = K, Infl = Infl, RAsym = RAsym, Rk = Rk, Ri = Ri,

          modno = 22, pn.options = "myoptions"), data = subdata)



# force an 8 parameter estimate on logistic data
```

```
modpar(logist.data$age,logist.data$mass,force8par=TRUE, pn.options = "myoptions")



# force an 4 parameter model on logistic data

modpar(logist.data$age,logist.data$mass,force4par=TRUE, pn.options = "myoptions")


# troubleshoot the fit of a model

modpar(posneg.data$age,posneg.data$mass,verbose=TRUE, pn.options = "myoptions")


# fit a two component model - enter your own data in place of "mydata"

        # this details an approach but is not run for want of appropriate data

        # if x of intersection unknown

        ## Not run:

  modpar(mydata$x,mydata$y,twocomponent.x=TRUE, pn.options = "myoptions")

        # if x of intersection = 75

  modpar(mydata$x,mydata$y,twocomponent.x=75, pn.options = "myoptions")

  richardsR1.nls <- nls(y~ SSposnegRichards(x, Asym = Asym, K = K,

                Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri, RM = RM,

                modno = 1, pn.options = "myoptions")

                , data = mydata)
## End(Not run)
```

---

penguin.data *Field data on growth of little penguins* $Eudyptula minor$

Description

The penguin.data data frame has 2244 rows and 11 columns of records of the measured masses for little penguin chicks between 13 and 74 days of age collected at Philip Island, Victoria, Australia in 2000 and 2002 (see Chiaradia & Nisbet 2006).

Usage

```
penguin.data
```

Format

This object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

site Three character factor for the site (only one site in dataset).

year A factor specifying the year of measurement.

bandid an ordered factor indicating unique id of each individual: the union of the laying date of the nest relative to the colony and the band combination

siteyear A factor specifying levels of year for different sites (only one site in dataset).

weight a numeric vector of chick masses (g).

ckage a numeric vector of chick ages (days).

Jdate a numeric vector of first egg-laying date of the nest(days), relative to the mean laying date for all nests in that year.

nest A factor of unique codes that identify each nest.

ck A factor of hatching order for each chick (A = first hatched, B = second hatched).

outcome A factor of codes for fate of each chick (F = fledged; only fledged chicks included).

clutch A factor of size of clutch/brood that each chick comes from (either 1- or 2-chick brood).

Details

Data were collected as outlined in Chiaradia & Nisbet (2006). Penguin chicks are generally considered to exhibit a double-Gompertz growth form.Please contact Andre Chiaradia (a.chiaradia@penguins.org.au) for use in collaborations.

Source

Chiaradia, A. & Nisbet, I.C.T. (2006) Plasticity in parental provisioning and chick growth in Little Penguins $Eudyptulaminor$ in years of high and low breeding success. Ardea, 94, 257-270.

Examples

```
require(stats); require(graphics)
#view data
penguin.data
modpar(penguin.data$ckage, penguin.data$weight, pn.options = "myoptions")
plot(weight ~ ckage, data = penguin.data, subset = bandid == penguin.data$bandid[1],
     xlab = "Chick age (day)", las = 1,
     ylab = "Chick mass (g)",
     main = "penguin.data and fitted curve (Chick #307 only)")
fm1 <- nls(weight ~ SSposnegRichards(ckage,Asym=Asym,K=K,Infl=Infl, RAsym=RAsym,
           modno=31, pn.options= "myoptions"),
           data = penguin.data, subset = bandid == penguin.data$bandid[1])
ckage <- seq(0, 74, length.out = 101)
lines(ckage, predict(fm1, list(ckage = ckage)))
```

pn.mod.compare *Compare All Possible Positive-Negative Richards nlslist Models*

Description

This function performs model selection for nlsList models fitted using SSposnegRichards.

Usage

```
pn.mod.compare(x,

y,

grp,

pn.options,

forcemod = 0,

existing = FALSE,

penaliz = "1/sqrt(n)",

taper.ends = 0.45,

mod.subset = c(NA),

Envir = .GlobalEnv,

...)
```

Arguments

x	a numeric vector of the primary predictor
y	a numeric vector of the response variable
grp	a factor of same length as x and y that distinguishes groups within the dataset
pn.options	required character string specifying name of list object populated with starting parameter estimates, fitting options and bounds
forcemod	optional numeric value to constrain model selection (see Details)
existing	optional logical value specifying whether some of the relevant models have already been fitted
penaliz	optional character value to determine how models are ranked (see Details)
taper.ends	numeric representing the proportion of the range of the x variable for which data are extended at the two ends of the data set. This is used in initial estimation (prior to optim and nls optimizations) and can speed up subsequent optimizations by imposing a more pronounced S-shape to both first and second curves. Defaults to 0.45.
mod.subset	optional vector containing modno of models that the user desires to be estimated. If not NA, only nlsList models in mod.subset will be fitted and ranked
Envir	a valid R environment to find pn.options in and export any output to, by default this is the global environment
...	additional optional arguments to be passed to nlsList

Details

First, whether parameter M should be fixed (see SSposnegRichards) is determined by fitting models 12 and 20 and comparing their perfomance using extraF. Note that model 20 is identical to model 32. If model 12 provides superior performance (variable values of M) then 16 models that estimate M are run (models 1 through 16), otherwise the models with fixed M are fitted (models 21 through 36). Fitting these nlsList models can be time-consuming (2-4 hours using the dataset posneg.data that encompasses 100 individuals) and if several of the relevant models are already fitted the option existing=TRUE can be used to avoid refitting models that already exist globally (note that a model object in which no grouping levels were successfully parameterized will be refitted, as will objects that are not of class nlsList). Specifying forcemod=3 will force model selection to only consider fixed M models and setting

forcemod=4 will force model selection to consider models with varying values of M only.

If fitting both models

12 and 20 fails, fixed M models will be used by default.

taper.ends can be used to speed up optimization as it extends the dataset at maximum and minimum extremes

of x by repeatedly pasting the y values at these extremes for a specified proportion of the range of x.

taper.ends is a numeric value representing the proportion of the range of x values are extended for and

defaults to 0.45 (45

tend towards a zero slope this is a suitable values. If tapered ends are not desirable then choose taper.ends = 0.

Models are ranked by modified pooled residual square error. By default residual standard error

is divided by the square root of sample size. This exponentially penalizes models for which very few

grouping levels (individuals) are successfully parameterized (the few individuals that are

parameterized in these models are fit unsuprisingly well) using a function based on the relationship

between standard error and sample size. However, different users may have different preferences

and these can be specified in the argument penaliz (which residual

standard error is multiplied by). This argument must be a character value

that contains the character n (sample size) and must be a valid right hand side (RHS) of a formula:

e.g. 1*(n), (n)^2. It cannot contain more than one n but could be a custom function, e.g. FUN(n).

Value

A list object with two components: $'Model rank table' contains the

statistics from `extraF` ranked by the modified residual standard error,

and $'P values from pairwise extraF comparison' is a matrix of P values from

`extraF` for legitimate comparisons (nested and successfully fitted models).

The naming convention for models is a concatenation of 'richardsR', the modno and '.lis'

which is shortened in the matrix output, where the number of parameters has been

pasted in parentheses to allow users to easily distinguish the more general model from

the more reduced model

(see `extraF` and `SSposnegRichards`).

For extra flexibility, mod.subset can specify a vector of modno values (a number of different models) that

can be fitted in `nlsList` and then evaluated by model selection. This prevents fitting of unwanted models or

attempts to fit models that are known to fail. If the `nlsList` model already exists it will not be refitted

and thus existing models can be included in the ranking table without adding noticeably to processing time.

Note

If appropriate bounds (or starting parameters) are not available in the list specified by the variable supplied

to pn.options, modpar will be called automatically prior to model selection.

During selection, text is output to the screen to inform the user of the progress of model selection

(which model is being fitted, which were fit successfully)

Version 1.5 saves many variables, and internal variables in the package environment:

FlexParamCurve:::FPCEnv. By default, the pn.options file is copied to the environment

specified by the functions (global environment by default). Model selection routines

also copy from FPCenv to the global environment all nlsList models fitted during

model selection to provide backcompatibility with code for earlier versions. The user

can redirect the directory to copy to by altering the Envir argument when calling the

function.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

See Also

extraF

SSposnegRichards

nlsList

Examples

```
#these examples will take a long while to run as they have to complete the 32 model comparison

#run model selection for posneg.data object (only first 3 group levels for example's sake)

   try(rm(myoptions),silent = TRUE)

   subdata <- subset(posneg.data, as.numeric(row.names (posneg.data) ) < 40)

   modseltable <- pn.mod.compare(subdata$age, subdata$mass,

      subdata$id, existing = FALSE, pn.options = "myoptions")
```

```
   modseltable



#fit nlsList model initially and then run model selection

#for posneg.data object when at least one model is already fit

#(only first 3 group levels for example's sake)

    richardsR22.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

      Infl = Infl, RAsym = RAsym, Rk = Rk, Ri = Ri , modno = 22, pn.options = "myoptions")

                        ,data = subdata)

   modseltable <- pn.mod.compare(subdata$age, subdata$mass,

      subdata$id, forcemod = 3, existing = TRUE, pn.options = "myoptions")

   modseltable



#run model selection ranked by residual standard error*(1/sample size)

    modseltable <- pn.mod.compare(subdata$age, subdata$mass,

      subdata$id, penaliz='1*(1/n)', existing = TRUE, pn.options = "myoptions")

    modseltable
```

pn.modselect.step *Backwards Stepwise Selection of Positive-Negative Richards $nlslist$ Models*

Description

This function performs backawards stepwise model selection for nlsList models fitted using SSposnegRichards.

Usage

```
pn.modselect.step(x,

y,

grp,

pn.options,

forcemod = 0,

existing = FALSE,

penaliz = "1/sqrt(n)",

taper.ends = 0.45,

Envir = .GlobalEnv,

...)
```

Arguments

x	a numeric vector of the primary predictor

y	a numeric vector of the response variable
grp	a factor of same length as x and y that distinguishes groups within the dataset
pn.options	required character string specifying name of list object populated with starting parameter estimates, fitting options and bounds
forcemod	optional numeric value to constrain model selection (see Details)
existing	optional logical value specifying whether some of the relevant models have already been fitted
penaliz	optional character value to determine how models are ranked (see Details)
taper.ends	numeric representing the proportion of the range of the x variable for which data are extended at the two ends of the data set. This is used in initial estimation (prior to optim and nls optimizations) and can speed up subsequent optimizations by imposing a more pronounced S-shape to both first and second curves. Defaults to 0.45.
Envir	a valid R environment to find pn.options in and export any output to, by default this is the global environment
...	additional optional arguments to be passed to nlsList

Details

First, whether parameter M should be fixed

(see SSposnegRichards) is determined by fitting models 12 and 32 and comparing

their perfomance using extraF.

If model 12 provides superior performance (variable values of M) then 16 models that estimate M

are run (models 1 through 16), otherwise the models with fixed M are fitted (models 21 through 36).

Model selection then proceeds by fitting the most general model (8-parameter, model 1 for variable M;

7-parameter, model 21 for fixed M). At each subsequent step reduced models are evaluated

by creating nlsList models through removal of a single parameter from the decreasing

section of the curve (i.e. RAsym, Rk, Ri or RM). This is repeated until all possible models with

one less parameter have been fitted and then these models are then ranked by modified pooled residual

standard error (see below) to determine which reduced parameter model provides the best fit. This ranking

esnures that in all cases subsequent extra sum-of-squares F-tests are only made between fully nested models.

The best ranked reduced parameter model is then compared with the more general model retained from the

the previous step using the function extraF to determine whether the more general model provides significant improvement over the best reduced model. The most appropriate model is then retained to be used as the general model in the next step. This process continues for up to six steps (all steps will be attempted even if the general model provides better performance to allow for much more reduced models to also be evaluated). The most reduced model possible to evaluate in this function contains only parameters for the positive section of the curve (4-parameters for variable M, 3-parameters for fixed M).

Fitting these nlsList models can be time-consuming (2-4 hours using the dataset posneg.data that encompasses 100 individuals) and if several of the relevant models are already fitted the option existing=TRUE can be used to avoid refitting models that already exist globally (note that a model object in which no grouping levels were successfully parameterized will be refitted, as will objects that are not of class nlsList).

Specifying forcemod=3 will force model selection to only consider fixed M models and setting forcemod=4 will force model selection to consider models with varying values of M only.

If fitting both models 12 and 32 fails, fixed M models will be used by default.

taper.ends can be used to speed up optimization as it extends the dataset at maximum and minimum extremes of x by repeatedly pasting the y values at these extremes for a specified proportion of the range of x.

taper.ends is a numeric value representing the proportion of the range of x values are extended for and defaults to 0.45 (45 tend towards a zero slope this is a suitable values. If tapered ends are not desirable then choose taper.ends = 0.

Competing non-nested models are ranked by modified pooled residual square error. By default this is residual standard error divided by the square root of sample size. This exponentially penalizes models for which very few grouping levels (individuals) are successfully parameterized (the few individuals that are parameterized in these models are fit unsuprisingly well) using a function based on the relationship between standard error and sample size. However, different users may have different preferences and these can be specified in the argument penaliz (which residual standard error is multiplied by). This argument must be a character value that contains the character n (sample size) and must be a valid right hand side (RHS) of a formula: e.g. 1*(n), (n)^2. It cannot contain more than one n but could be a custom function, e.g. FUN(n).

Value

A data.frame containing statistics produced by extraF

evaluations at each step, detailing the name of the general and best reduced model at each step. The overall best model evaluated by the end of the function is saved globally as $pn.bestmodel.lis$

The naming convention for models is a concatenation of 'richardsR', the modno and '.lis' (see SSposnegRichards).

Note

If appropriate bounds (or starting parameters) are not available in the list specified by the variable supplied

to pn.options, modpar will be called automatically prior to model selection.

During selection, text is output to the screen to inform the user of the progress of model selection (which model is being fitted)

Version 1.5 saves many variables, and internal variables in the package environment: FlexParamCurve:::FPCEnv. By default, the pn.options file is copied to the environment specified by the functions (global environment by default). Model selection routines also copy from FPCenv to the global environment all nlsList models fitted during model selection to provide backcompatibility with code for earlier versions. The user can redirect the directory to copy to by altering the Envir argument when calling the function.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

See Also

pn.mod.compare

extraF

SSposnegRichards

nlsList

Examples

```
#these examples will take a long while to run as they have to complete the 32 model comparison


#run model selection for posneg.data object (only first 3 group levels for example's sake)
```

```
    try( rm(myoptions), silent = TRUE)

    subdata <- subset(posneg.data, as.numeric(row.names (posneg.data) ) < 40)

    modseltable <- pn.modselect.step(subdata$age, subdata$mass,

       subdata$id, existing = FALSE, pn.options = "myoptions")

    modseltable



#fit nlsList model initially and then run model selection

#for posneg.data object when at least one model is already fit

#(only first 3 group levels for example's sake)

     richardsR22.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym, K = K,

      Infl = Infl, RAsym = RAsym, Rk = Rk, Ri = Ri , modno = 22, pn.options = "myoptions")

                          ,data = subdata)

    modseltable <- pn.modselect.step(subdata$age, subdata$mass,

       subdata$id, forcemod = 3, existing = TRUE, pn.options = "myoptions")

    modseltable



#run model selection ranked by residual standard error*sample size
```

```
#(only first 3 group levels for example's sake)

    modseltable <- pn.modselect.step(subdata$age, subdata$mass,

      subdata$id, penaliz='1*(n)', existing = TRUE, pn.options = "myoptions")

    modseltable
```

---

posneg.data *Simulated growth of black-browed albatrosses*

Description

The posneg.data data frame has 1300 rows and 3 columns of records of the simulated masses for black-browed albatross chicks between 0 and 166 days of age.

Usage

```
posneg.data
```

Format

This object of class c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame") containing the following columns:

mass a numeric vector of chick masses (g).

age a numeric vector of chick ages (days).

id an ordered factor indicating unique id of each simulated individual, i.e. which data belongs to which individual.

Details

No published parameter estimates with associated variability are available for positive-negative growth curves. These data were simulated using an 8-parameter positive-negative Richards curve (SSposnegRichards (model 1)), using parameters drawn from normal distributions with the following means (standard deviations):

```
Asym=4300 (180)
K=0.06 (0.01)
Infl=23 (0.4)
```

```
M=0.1 (0.05)
RAsym=1433.3 (540) #1/3 of Asym, more variable
Rk=0.108 (0.03) #1.8 times faster recession, more variable
Ri=Infl+87.259 (1.7) # more variable but linked to Infl
RM=M (0.15) #more variable
```

These values were chosen through comparison of growth curves with Huin and Prince (2000) Fig 2 and variability observed between individual chicks of little penguins in a 10 year dataset (Chiaradia and Nisbet unpublished data). Each simulated individual had 13 measurements stratified through the development period, with 1-13 day random differences in timing of each measurement. This data object has methods for nlme grouped-data classes.

Source

Huin, N. & Prince, P.A. (2000) Chick growth in albatrosses: curve fitting with a twist. Journal of Avian Biology, 31, 418-425.

Examples

```
require(stats); require(graphics)
#view data
posneg.data
#create list for fixed parameters
modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")
plot(mass ~ age, data = posneg.data, subset = id == "1",
     xlab = "Chick age (day)", las = 1,
     ylab = "Chick mass (g)",
     main = "posneg.data data and fitted curve (Chick #1 only)")
fm1 <- nls(mass ~ SSposnegRichards(age,Asym=Asym,K=K,Infl=Infl, RAsym=RAsym,
           Rk=Rk,Ri=Ri,modno=22, pn.options= "myoptions"),
           data = posneg.data, subset = id == "1")
age <- seq(0, 166, length.out = 101)
lines(age, predict(fm1, list(age = age)))
```

---

posnegRichards.calls *List of calls for fitting 33 SSposnegRichards models in* nlsList

---

Description

The posnegRichards.calls list has two components of 17 and 16 rows and 1 column, respectively, called 'Examples of calls for FlexParamCurve models that estimate parameter m' (models with 4 estimable first curve parameters) and "Examples of calls for FlexParamCurve models that fix parameter m" (models with 3 estimable second curve parameters, i.e. M is fixed to value in $pnmodelparams$. Individual calls can be accessed by indexing first the component number and then the model number - see examples below. Note that model 17 is formulated differently (see SSposnegRichards)

Usage

```
posnegRichards.calls
```

Format

This object of class `list` containing the components:

Examples of calls for FlexParamCurve models that estimate parameter m a list of 16 possible reductions (nos. 1-16) of the FlexParamCurve double-Richards model that estimate parameter m. Also includes a custom model (17; see `SSposnegRichards`).

Examples of calls for FlexParamCurve models that fix parameter m a list of 16 possible reductions (nos. 21-36) of the FlexParamCurve double-Richards model that do not estimate parameter m but instead fix it to a mean across the dataset or user-specified value.

Details

A list object to provide users with examples of how to fit 33 different `nlsList` models using the selfStart function `SSposnegRichards`.

Examples

```
# see all possible calls
posnegRichards.calls
# extract the call for fitting a nls model with 8-parameter double-Richards curve (model 1)
#for an example just fit a subset of the data, 3 group levels (individuals)
   data <- subset(posneg.data, as.numeric(row.names (posneg.data) ) < 40)
modtofit <- as.character(
            posnegRichards.calls [[2]] [row.names(posnegRichards.calls [[2]]) == "22",] )
#change the data source
modtofit <- sub("posneg.data","data",modtofit)
modtofit <- parse(text = modtofit)
#create list for fixed parameters
modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")
#create a new nlsList object called richards22.lis
eval(modtofit)
#view object
richardsR22.lis

# view call for model 1
posnegRichards.calls [[1]] [row.names(posnegRichards.calls [[1]]) == "1",]

# view call for model 21
posnegRichards.calls [[2]] [row.names(posnegRichards.calls [[2]]) == "21",]
```

`posnegRichards.eqn` *Equations of the FlexParamCurve Family*

Description

Function to solve any of the equations in the FlexParamCurve family,

depending on user-specified parameters and model choice

Usage

```
posnegRichards.eqn(x,

Asym = NA,

K = NA,

Infl = NA,

M = NA,

RAsym = NA,

Rk = NA,

Ri = NA,

RM = NA,

modno,

pn.options,

Envir = .GlobalEnv)
```

Arguments

x	a numeric vector of the primary predictor variable
Asym	a numeric value for the asymptote of the positive (increasing) curve
K	a numeric value for the rate parameter of the positive (increasing) curve
Infl	a numeric value for the point of inflection of the positive (increasing) curve
M	a numeric value for the shape parameter of the positive (increasing) curve
RAsym	a numeric value for the asymptote of the negative (decreasing) curve

Rk	a numeric value for the rate parameter of the negative (decreasing) curve
Ri	a numeric value for the point of inflection of the negative (decreasing) curve
RM	a numeric value for the shape parameter of the negative (decreasing) curve
modno	a numeric value (currently integer only) between 1 and 36 specifying the identification number of the equation to be fitted
pn.options	a character vector specifying a list of parameters and options for plotting
Envir	a valid R environment to find pn.options, by default this is the global environment

Details

This function fits 1 of 32 possible FlexParamCurve equations (plus custon model #17). Equations can fit both monotonic and non-monotonic curves (two different trajectories).

These equations have also been described as double-Richards curves, or positive-negative Richards curves.

From version 1.2 onwards this function can fit curves that exhibit negative followed by positive trajectories or double-positive or double-negative trajectories. This function can now also fit two component (biphasic) models, where the first curve is used up to the x-value (e.g. age) of intersection and the

second curve is used afterwards, thus the curves are not joined as in standard models (see SSposnegRichards for details.

The 32 possible equations are all based on the subtraction of one Richards curve from another, producing:

$y = A/([1+mexp(-k(t-i))]1/m) - A'/([1+m'exp(-k'(t-i'))]1/m')$, where A=Asym, k=K, i=Infl, m=M,

A'=RAsym, k'=Rk, i'=Ri, m'=RM; as described in the Arguments section above.

All 32 possible equations are simply reformulations of this equation, in each case fixing a parameter or

multiple parameters to (by default) the mean parameter across all individuals in the dataset (such as produced by a nls

model). All models are detailed in the SSposnegRichards help file. Any models that require parameter fixing

(i.e. all except model #1) extract appropriate values from the specified list passed by name to pn.options for the fixed parameters.

This object is most easily created by running modpar and can be adjusted manually or by using

change.pnparameters to user required specification.

If parameters are omitted in the call but required by the $modno$ specified in the call, then they will be automatically extracted

from the pn.options object supplied, with the appropriate warning. Thus, it is not necessary to list out parameters and modno but is

a useful exercise if you are unfamiliar or in doubt of exactly which model is being specified by $modno$, see SSposnegRichards

for a list. If a parameter is supplied separately with the call then this value will override those stored in for the same parameter in $modno$:

see examples below.

Value

the solution of the equation specified (by modno), given the user-entered parameters

Note

Any models that require parameter fixing (i.e. all except model #1) extract appropriate values from the specified

list passed to pn.options for the fixed parameters. This object is most easily created by running modpar

and can be adjusted manually or by using change.pnparameters to user required specification.

Version 1.5 saves many variables, and internal variables in the package environment:

FlexParamCurve:::FPCEnv. By default, the pn.options file is copied to the environment

specified by the functions (global environment by default). Model selection routines

also copy from FPCenv to the global environment all nlsList models fitted during

model selection to provide backcompatibility with code for earlier versions. The user

can redirect the directory to copy to by altering the Envir argument when calling the

function.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

See Also

SSposnegRichards

modpar

Examples

```
require(graphics)

# calculate y (dependent variable) for a given x for an 8-parameter double-Richards model

        #create pnmodelparams for fixed parameters

    modpar(posneg.data$age, posneg.data$mass, pn.options = "myoptions")
```

```
     x = 10

     y <- posnegRichards.eqn(x, 1000, 0.5, 25, 1, 100, 0.5, 125,

     1, modno = 1, pn.options = "myoptions")

     print( c(x = x, y = y) )



# plot 8-parameter model using saved parameter values from modpar

 plot(posneg.data$age, posneg.data$mass, pch = ".")

 curve(posnegRichards.eqn(x,modno = 1, pn.options = "myoptions"), add = TRUE, lwd = 3)



# plot 3-parameter model using saved parameter values from modpar

       curve(posnegRichards.eqn(x,modno = 32, pn.options = "myoptions"), add = TRUE, col =2

                , lwd = 3)



# tweak the plot of a 3-parameter model by user specifying a lower asymptote:

#      ie give some parameter values

# directly and others through pn.options by default

         curve(posnegRichards.eqn(x,modno = 32, Asym = 3200, pn.options = "myoptions"),
```

```
                add = TRUE, col = 5, lwd = 3)



# calculate y (dependent variable) for a given x for a 4-parameter Richards model

# (note that second curve parameters are unneeded) and replaced with value from pn.options.

# User-supplied variables over-ride those stored in pn.options object

 x = 10

     y <- posnegRichards.eqn(x, 1000, 0.5, 25, 1,

     1, modno = 12, pn.options = "myoptions")

     print( c(x = x, y = y) )



# plot a logistic curve (M=1),  note that second curve parameters are unneeded

         plot(1:200, posnegRichards.eqn(1:200, Asym = 1000, K = 0.5, Infl = 25, M = 1,

             modno = 12, pn.options = "myoptions"), xlim = c(1, 200), xlab = "x",

     ylab = "y", pch = 1, cex = 0.7)



# plot a double-logistic curve (M=1, RM=1),

#note that second curve parameters are unneeded

     plot(1:200, posnegRichards.eqn(1:200, Asym = 1000, K = 0.5, Infl = 25, M = 1,
```

```
        RAsym = -100, Rk = 0.5, Ri = 125, RM = 1,

        modno = 1, pn.options = "myoptions"), xlim = c(1, 200), xlab = "x",

    ylab = "y", pch = 1, cex = 0.7)
```

SSposnegRichards *Self-Starting Positive-Negative Richards Model (double-Richards)*

Description

This selfStart function evaluates a range of flexible logistic functions. It also has an initial attribute that creates initial estimates of the parameters for the model specified.

Usage

```
SSposnegRichards(x,

Asym = NA,

K = NA,

Infl = NA,

M = NA,

RAsym = NA,

Rk = NA,

Ri = NA,

RM = NA,

modno,

pn.options,

Envir = ".GlobalEnv")
```

Arguments

x	a numeric vector of the primary predictor variable at which to evaluate the model
Asym	a numeric value for the asymptote of the positive (increasing) curve
K	a numeric value for the rate parameter of the positive (increasing) curve
Infl	a numeric value for the point of inflection of the positive (increasing) curve
M	a numeric value for the shape parameter of the positive (increasing) curve
RAsym	a numeric value for the asymptote of the negative (decreasing) curve
Rk	a numeric value for the rate parameter of the negative (decreasing) curve
Ri	a numeric value for the point of inflection of the negative (decreasing) curve
RM	a numeric value for the shape parameter of the negative (decreasing) curve
modno	a numeric value (currently integer only) between 1 and 36 specifying the identification number of the equation to be fitted
pn.options	character string specifying name of list object populated with starting parameter estimates, fitting options and bounds
Envir	a character vector that represents the valid R environment in which to find pn.options in and write any output to, by default this is the global environment

Details

This selfStart function evaluates a range of flexible logistic functions. It also has an initial attribute that creates initial estimates of the parameters for the model specified. Equations can fit both monotonic and non-monotonic curves (two different trajectories). These equations have also been described as double-Richards curves, or positive-negative Richards curves. **From version 1.2 onwards this function can fit curves that exhibit negative followed by positive trajectories or double positive or double negative trajectories.***

The 32 possible equations (plus custom model #17) are all based on the subtraction of one Richards

curve from another, producing:
$y = A/([1 + mexp(-k(t - i))]1/m) + A'/([1 + m'exp(-k'(t - i'))]1/m')$,
where A=Asym, k=K, i=Infl, m=M,
A'=RAsym, k'=Rk, i'=Ri, m'=RM; as described in the Arguments section above.
All 32 possible equations are simply reformulations of this equation, in each
case fixing a parameter or multiple parameters to (by default) the mean parameter across
all individuals in the dataset (such as produced by a `nls`
model). Thus, a model in which one parameter is fixed has a 7-parameter equation,
and one in which four are fixed has a 4-parameter equation, thus reducing
complexity and computation and compensatory parameter changes when a parameter does not
vary across group levels (e.g individuals)
[the most appropriate equation can be determined using model selection in
`pn.modselect.step` or `pn.mod.compare`].
Any models that require parameter fixing (i.e. all except #1)
extract appropriate values from the list object specified by `pn.options` for the fixed
parameters. This object is most easily created by running
`modpar` and can be adjusted manually or by using
`change.pnparameters` to user-required specification.
Each of the 32 equations is identified by an integer value for modno (1 to 36).Models
21-36 are the same as 1-16 except that in the former the first curve parameter `m`
is fixed and not estimated. All equations (except 17 - see below) contain parameters Asym, K, and Infl.
The list below summarizes which of the other 5 parameters are contained in
which of the models (Y indicates that the parameter is estimated, blank indicates
it is fixed).

modno	M	RAsym	Rk	Ri	RM	NOTES
1	Y	Y	Y	Y	Y	8 parameter model
2	Y	Y	Y	Y		
3	Y			Y	Y	
4	Y	Y			Y	
5	Y				Y	
6	Y	Y		Y	Y	

```
 7       Y           Y    Y    Y
 8       Y     Y     Y         Y
 9       Y           Y         Y
 10      Y                Y
 11      Y     Y
 12      Y  4 parameter, standard Richards model
 13      Y     Y          Y
 14      Y           Y    Y
 15      Y     Y     Y
 16      Y           Y
 17      see below
 18      see below
 19      see below
 20      see below
 21            Y     Y    Y    Y    7 parameter model, 4 recession params
22       Y    Y   Y 6 parameter (double-logistic/double-Gompertz/double-Von Bertalannfy)
 23                       Y    Y
 24            Y               Y
 25                            Y
 26            Y          Y    Y
 27                 Y    Y    Y
 28            Y     Y         Y
 29                 Y         Y
 30                       Y
```

```
 31            Y

32 only 3 parameters (used for logistic, Gompertz or Von Bertalannfy - see below)

 33            Y          Y

 34                  Y    Y

 35            Y     Y

 36                  Y
```

modno 17 represents a different parameterization for a custom model:

(Asym/ 1 + exp(Infl - x)/ M) - (RAsym / 1 + exp(Ri - x)/ RM), in

which M and RM actually represent scale parameters not shape parameters. This model and a suite of reductions:

modno 17.1:

modno 17.2:

modno 17.3:

are designed for use in modeling migration, $sensu$. Bunnefeld et al. 2011, Singh et al. 2012.

modnos 18, 19 and 20 are reserved for internal use by `modpar`.

To access common 3 parameter sigmoidal models use modno = 32, fixing

parameters (using `change.pnparameters`) to M = 1 for logistic,

M = 0.1 for Gompertz, and M= -0.3 for von Bertalanffy. The same settings can be

used with modno = 2 to fit the double-logistic, double-Gompertz or double-Von Bertalannfy.

Note that to fit only 3 or 4 parameter curves, the option force4par = TRUE should be specified

when running `modpar`.

The call for `SSposnegRichards` only differs from

conventional selfStart models in that it requires a value for modno and a list of fitting options

and values from `modpar` to which to fix parameters in the reduced models.

Depending on the model chosen, different combinations of the 8 possible

parameters are required: if one is missing the routine will stop with an

appropriate error, if an extra one is added, it will be ignored (provided

that it is labelled, e.g. M = 1; this is good practice to prevent accidental

misassignments).

Here are two examples (7 parameter and 3 parameter):

```
richardsR2.lis <- nlsList(mass ~ SSposnegRichards(age,

        Asym = Asym, K = K, Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri,
```

```
          , modno = 2), data = posneg.data)

          #correct call includes all necessary parameters

richardsR20.lis <- nlsList(mass ~ SSposnegRichards(age,

          Asym = Asym, K = K, Infl = Infl, modno = 2), data = logist.data)

          #incorrect call missing required parameters,

          #function terminates and generates an error message
```

Examples for all models can be found in the list object
posnegRichards.calls.
If specified using modpar optional constraints
may be placed to specify response values at the minimum value and/or
maximum values of the predictor. Such constraint allows realistic fits for
datasets which are missing data
at either end of the curve (e.g. hatching weight for some growth curves).
Estimates are produced by splitting the two curves into separate positive
and negative curves and estimating parameters for each curve separately
in a similar manner to SSlogis. Each curve is fit first by
optim using the parameter bounds in pnmodelparamsbounds
(see modpar) and a subsequent refinement is attempted using
nls with more restrictive parameter bounds. Finally, both curves
are annealed
and parameters are again estimated using restrictive bounds and starting values
already determined during separate estimates. Equations for which the positive
curve was inestimable are not estimated further, but if negative curve estimation
or overall curve estimation fail, partial estimates are used: either default
negative parameters (RAsym = 0.05*Asym, Rk = K, Ri = Infl, RM = M) annealed to positive
curves or separate estimates annealed; both with compensation for interation
between asymptotes.
From version 1.2 onwards, this function can now fit two component models, where
the first curve is used up to the x-value (e.g. age) of intersection and the second curve is used
afterwards. Confusingly, these are also called "double Richards", "double Gompertz"
or "double logistic": see Murphy et al. (2009) or Ross et al. (1995) for examples.
To specify such models set twocomponent.x = TRUE (this will estimate the x of

intersection) when running modpar. Alternatively, if known, the
x of intersection can be set directly by setting
twocomponent.x = # (where # is the x of intersection). When modpar
is run this option will be saved in pnmodelparas and can be changed at will,
either manually or using change.pnparameters.
From version 1.2 onwards, this function can now fit bilogistic (and more generally
biRichards) curves, where the final curve is effectively either two positive curves
or two negative curves. See Meyer (1994) for examples. This functionality is default
and does not need to be specified.

Value

a numeric vector of the same length as x containing parameter
estimates for equation specified (fixed parameters
are not return but are substituted in calls to nls
nlsList and nlme with the fixed parameters
stored in pnmodelparams; see modpar

Note

Any models that require parameter fixing (i.e. all except #1)
extract appropriate values from the object pnmodelparams for the fixed
parameters. This object is created by running
modpar and can be adjusted manually or by using
change.pnparameters to user required specification.
Output may show errors and warnings especially during a nlsList
fit, in which the function is called repeatedly: once for each group level in the
dataset. Warnings indicate conditions for which default parameters or incomplete estimates
are used - see Details section - and errors occur from insufficient data or singularities.
As a result of possible interaction and correlation between the parameters in some models,
singularities may be common, but do not be alarmed by repeated error messages, as
examination of a fitted nlsList model may releave a large number of
well estimated group levels, thus the elimation of unsuitable outlying groups only. Also,
because very few of the 32 equations are likely to be suitable for the majority
of datasets, consideration of the model being fitted is crucial when examining the output. Functions
pn.modselect.step and pn.mod.compare provide the ability
for model selection of these equations through stepwise backward deletion or all
model comparison, respectively. These offer powerful ways to determine the
best equation for your dataset.

To increase the ability of optimization routines to deal with
a wide variety of values, particularly negative values for M or RM,
only real component of complex numbers are modelled and integer versions
of M and RM are used during estimation if floating values cause conversion
issues.
Speed of the function depends on the complexity of the data being fit.
Version 1.5 saves many variables, and internal variables in the package environment:
FlexParamCurve:::FPCEnv. By default, the pn.options file is copied to the environment
specified by the functions (global environment by default). Model selection routines
also copy from FPCenv to the global environment all nlsList models fitted during
model selection to provide backcompatibility with code for earlier versions. The user
can redirect the directory to copy to by altering the Envir argument when calling the
function.

Author(s)

Stephen Oswald <steve.oswald@psu.edu>

References

Oswald, S.A. et al. (2012) FlexParamCurve: R package for flexible
fitting of nonlinear parametric curves. Methods in Ecology and Evolution 3: 1073-1077.

doi: 10.1111/j.2041-210X.2012.00231.x

(see also tutorial and introductory videos at:

http://www.methodsinecologyandevolution.org/view/0/podcasts.html

(posted September 2012 - if no longer at this link, check the archived videos at:

http://www.methodsinecologyandevolution.org/view/0/VideoPodcastArchive.html#allcontent

#1# Nelder, J.A. (1962) Note: an alternative form of a generalized
logistic equation. Biometrics, 18, 614-616.
#2#
Huin, N. & Prince, P.A. (2000) Chick growth in albatrosses: curve fitting
with a twist. Journal of Avian Biology, 31, 418-425.
#3#
Meyer, P. (1994) Bi-logistic growth. Technological Forecasting and Social

Change. 47: 89-102
#4#
Murphy, S. et al. (2009) Importance of biological parameters in assessing
the status of Delphinus delphis. Marine Ecology Progress Series 388: 273-291.
#5#
Pinheiro, J. & Bates, D. (2000) Mixed-Effects Models in S and S-Plus.
Springer Verlag, Berlin.
#6#
Ross, J.L. et al. (1994) Age, growth, mortality, and reproductive biology
of red drums in North Carolina waters. Transactions of the American Fisheries
Society 124: 37-54.
#7#
Bunnefeld et al. (2011) A model-driven approach to quantify migration patterns:
individual, regional and yearly differences. Journal of Animal Ecology 80: 466-476.
#8#
Singh et al. (2012) From migration to nomadism: movement variability in a northern
ungulate across its latitudinal range. Ecological Applications 22: 2007-2020.

See Also

SSlogis
SSgompertz
posnegRichards.eqn

Examples

```
set.seed(3) #for compatability issues

require(graphics)

   # retrieve mean estimates of 8 parameters using getInitial

   # and posneg.data object

  modpar(posneg.data$age, posneg.data$mass,verbose=TRUE, pn.options = "myoptions", width.bounds=2)

   getInitial(mass ~ SSposnegRichards(age, Asym, K, Infl, M,

       RAsym, Rk, Ri, RM, modno = 1, pn.options = "myoptions"), data = posneg.data)


   # retrieve mean estimates and produce plot to illustrate fit for

   # curve with M, Ri and Rk fixed
```

```
    pars <- coef(nls(mass ~ SSposnegRichards(age,
        Asym = Asym, K = K, Infl = Infl, RAsym = RAsym,
         RM = RM, modno = 24, pn.options = "myoptions"), data = posneg.data,
         control=list(tolerance = 10)))
    plot(posneg.data$age, posneg.data$mass, pch=".")
    curve(posnegRichards.eqn(x, Asym = pars[1], K = pars[2],
        Infl = pars[3], RAsym = pars[4],
        RM = pars[5],  modno = 24, pn.options = "myoptions"), xlim = c(0,
        200), add = TRUE)



        # following example not run as appropriate data are not available in the package
        # retrieve mean estimates and produce plot to illustrate fit for custom model 17
     ## Not run:
     pars<-as.numeric( getInitial(mass ~ SSposnegRichards(age, Asym, K, Infl,
          M, RAsym, Rk, Ri, RM, modno = 17, pn.options = "myoptions"), data = datansd) )
     plot(datansd$jday21March, datansd$moosensd)
     curve( posnegRichards.eqn(x, Asym = pars[1], K = 1, Infl = pars[2],
            M = pars[3], RAsym = pars[4], Rk = 1, Ri = pars[5], RM = pars[6],
           modno = 17, pn.options = "myoptions"), lty = 3, xlim = c(0, 200) , add = TRUE)
## End(Not run)


    # fit nls object using 8 parameter model
    # note: ensure data object is a groupedData object


        richardsR1.nls <- nls(mass ~ SSposnegRichards(age, Asym = Asym,
```

```
    K = K, Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri,
    RM = RM, modno = 1, pn.options = "myoptions"), data = posneg.data)



# following example not run as it fits very few levels in these data - as noted
# such a comprehensive equation is rarely required
# fit nlsList object using 8 parameter model
# note: ensure data object is a groupedData object
# also note: not many datasets require all 8 parameters
     ## Not run:
     richardsR1.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym,
    K = K, Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri,
    RM = RM, modno = 1, pn.options = "myoptions"), data = posneg.data)
summary(richardsR1.lis)
## End(Not run)


# fit nlsList object using 6 parameter model with value M and RM
# fixed to value in pnmodelparams and then fit nlme model
# note data is subset to provide estimates for a few individuals
# as an example


subdata <- subset(posneg.data,posneg.data$id == as.character(26)
| posneg.data$id == as.character(1)
| posneg.data$id == as.character(32))
richardsR22.lis <- nlsList(mass ~ SSposnegRichards(age, Asym = Asym,
    K = K, Infl = Infl, RAsym = RAsym, Rk = Rk, Ri = Ri,
    modno = 22, pn.options = "myoptions"), data = subdata)
```

```
summary(richardsR22.lis )
richardsR22.nlme <- nlme(richardsR22.lis, random = pdDiag(Asym + Infl ~ 1) )
summary(richardsR22.nlme)

# fit nls object using simple logistic model, with
# M, RAsym, Rk, Ri, and RM fixed to values in pnmodelparams

modpar(logist.data$age, logist.data$mass ,force4par = TRUE, pn.options = "myoptions")
change.pnparameters(M = 1, pn.options = "myoptions") #set to logistic (M =1) prior to fit
richardsR32.nls <- nls(mass ~ SSposnegRichards(age, Asym = Asym,
    K = K, Infl = Infl, modno = 32, pn.options = "myoptions"), data = logist.data)
coef(richardsR32.nls)

# fit a two component model - enter your own data in place of "mydata"
# this is not run for want of an appropriate dataset
# if x of intersection unknown
## Not run:
modpar(mydata$x,mydata$y,twocomponent.x=TRUE, pn.options = "myoptions")
# if x of intersection = 75
modpar(mydata$x,mydata$y,twocomponent.x=75, pn.options = "myoptions")
richardsR1.nls <- nls(y~ SSposnegRichards(x, Asym = Asym, K = K,
  Infl = Infl, M = M, RAsym = RAsym, Rk = Rk, Ri = Ri, RM = RM,
  modno = 1, pn.options = "myoptions")
  , data = mydata)
coef(richardsR1.nls)
## End(Not run)
```

`tern.data` *Field data on growth of common terns* $Sternahirundo$

Description

The `tern.data` data frame has 1164 rows and 12 columns of records of the measured masses for common tern chicks between 1 and 30 days of age collected at at Grays Beach, MA, in 1973 (Nisbet 1975) and Monomoy, MA, in 1975 (Nisbet et al. 1978)

Usage

```
tern.data
```

Format

This object of class `c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame")` containing the following columns:

site Four character factor for the two sites (MYMA: Monomoy Island, MA; GBCT: Grays Beach, CT).

year A factor specifying the year of measurement: 1973 or 1976.

bandid an ordered factor indicating unique id of each individual: the union of the laying date of the nest relative to the colony and the band combination

siteyear A factor specifying levels of year for different sites (different years at each site).

weight a numeric vector of chick masses (g).

ckage a numeric vector of chick ages (days).

Jdate a numeric vector of first egg-laying date of the nest(days), relative to the mean laying date for all nests in that year.

nest A factor of unique codes that identify each nest.

ck A factor of hatching order for each chick (A = first hatched, B = second hatched C = third hatched).

outcome A factor of codes for fate of each chick (F = fledged; only fledged chicks included).

eggmass A numeric vector of the mass of the egg (from which the chick hatched) at laying.

clutch A factor of size of clutch/brood that each chick comes from (either 1- or 2-chick brood).

Details

Data were collected as outlined in Nisbet (1975)[Grays Beach, MA, 1973] and Nisbet et al.(1978) [Monomoy, MA, 1975]. Please contact Ian Nisbet <icnisbet@verizon.net> for use in collaborations.

Source

Nisbet, I.C.T. (1975) Selective effects of predation in a tern colony. Condor, 77, 221-226. Nisbet, I.C.T., Wilson, K.J. & Broad, W.A. (1978) Common Terns raise young after death of their mates. Condor, 80, 106-109.

Examples

```
require(stats); require(graphics)
#view data
tern.data
#create pnmodelparams for fixed parameters
modpar(tern.data$ckage, tern.data$weight, force4par = TRUE, pn.options = "myoptions")
plot(weight ~ ckage, data = tern.data, subset = bandid == tern.data$bandid[1],
     xlab = "Chick age (day)", las = 1,
     ylab = "Chick mass (g)",
     main = "tern.data and fitted curve (Chick #156 only)")
fm1 <- nls(weight ~ SSposnegRichards(ckage,Asym=Asym,K=K,Infl=Infl,modno=32,
           pn.options= "myoptions"),
           data = tern.data, subset = bandid == tern.data$bandid[1])
ckage <- seq(0, 30, length.out = 101)
lines(ckage, predict(fm1, list(ckage = ckage)))
```

Index