

Package ‘phenology’

March 14, 2018

Type Package

Title Tools to Manage a Parametric Function that Describes Phenology

Version 7.0

Date 2018-03-14

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Depends numDeriv, parallel, optimx, lmf, HelpersMG (>= 2.0), R (>= 3.4)

Suggests shiny, fields, progress, car

Description Functions used to fit and test the phenology of species based on counts.

License GPL-2

LazyData yes

LazyLoad yes

URL http://max2.esse.u-psud.fr/epc/conservation/Girondot/Publications/Marine_Turtles_Nesting_Season.html

Encoding UTF-8

NeedsCompilation no

RoxygenNote 6.0.1

Repository CRAN

Date/Publication 2018-03-14 10:34:40 UTC

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phenology-package *Tools to Manage a Parametric Function that Describes Phenology*

Description

Functions used to fit and test the phenology of species based on counts.

Note that only the most significant changes are reported in the NEWS.

To do:

- * There are problems with SE for fitRMU().
- * Auto-scaling for optim during fitRMU search.

The latest version of this package can always be installed using:

```
install.packages("http://www.esu-psud.fr/epc/conservation/CRAN/HelpersMG.tar.gz", repos=NULL, type="source")
```

```
install.packages("http://www.esu-psud.fr/epc/conservation/CRAN/phenology.tar.gz", repos=NULL, type="source")
```

Details

Fit a parametric function that describes phenology

```

Package: phenology
Type: Package
Version: 7.0 build 576
Date: 2018-03-14
License: GPL (>= 2)
LazyLoad: yes

```

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Girondot, M. 2010. Estimating density of animals during migratory waves: application to marine turtles at nesting site. *Endangered Species Research*, 12, 85-105.

Girondot M. and Rizzo A. 2015. Bayesian framework to integrate traditional ecological knowledge into ecological modeling: A case study. *Journal of Ethnobiology*, 35, 339-355.

- Girondot, M. 2010. Editorial: The zero counts. *Marine Turtle Newsletter*, 129, 5-6.
- Girondot, M., 2017. Optimizing sampling design to infer marine turtles seasonal nest number for low-and high-density nesting beach using convolution of negative binomial distribution. *Ecological Indicators* 81, 83–89.
- Rivalan, P., Godfrey, M.H., Prévot-Julliard, A.-C., Girondot, M., 2005. Maximum likelihood estimates of tag loss in leatherback sea turtles. *Journal of Wildlife Management* 69, 540-548.

See Also

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- Briane J-P, Rivalan P, Girondot M (2007) The inverse problem applied to the Observed Clutch Frequency of Leatherbacks from Yalimapo beach, French Guiana. *Chelonian Conservation and Biology* 6:63-69
- Fossette S, Kelle L, Girondot M, Goverse E, Hilterman ML, Verhage B, Thoisy B, de, Georges J-Y (2008) The world's largest leatherback rookeries: A review of conservation-oriented research in French Guiana/Suriname and Gabon. *Journal of Experimental Marine Biology and Ecology* 356:69-82

Examples

```
## Not run:
library(phenology)
# Get the latest version at:
# install.packages("http://www.esu-psud.fr/epc/conservation/CRAN/phenology.tar.gz",
  repos=NULL, type="source")
# Read a file with data
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
  reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
  fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Plot the phenology and get some stats
output <- plot(result_Gratiot)

## End(Not run)
```

adapt_parameters	<i>Extract the parameters from a set of parameters to be used with another dataset.</i>
------------------	---

Description

The function "adapt_parameters" extracts the set of parameters to be used with a subset of data. All the unnecessary parameters are removed. It can be used when a set of beaches are fitted first and after only one of these beaches is fitted again.

Usage

```
adapt_parameters(data = stop("Datasets is mandatory for this function"),
  parameters = stop("Set of parameters is mandatory for this function"))
```

Arguments

data	A dataset of counts
parameters	A set of parameters

Details

adapt_parameters get the fitted parameters from a result object.

Value

Return the set of parameters

Author(s)

Marc Girondot

Examples

```
library(phenology)
# Read a file with data
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot<-add_phenology(Gratiot, name="Complete",
  reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Add unnecessary parameters to parg
parg <- c(parg, Max_dummybeach=2, Peak_dummybeach=123)
# Extract the fitted parameters
parg1<-adapt_parameters(data=data_Gratiot, parameters=parg)
```

 add_phenology

 Create a new dataset or add a timeserie to a previous dataset.

Description

To create a new dataset, the syntaxe is :

```
data <- add_phenology(add=newdata, name="Site", reference=as.Date('2001-12-31'), format='%d/%m/%y')
```

To add a dataset to a previous one, the syntaxe is :

```
data <- add_phenology(previous=previousdata, add=newdata, name='Site',
reference=as.Date('2001-01-01'), format="%Y-%m-%d")
```

To add several timeseries at the same time with '%d/%m/%y' or '%d/%m/%Y' date format:

```
data<-add_phenology(add=list(newdata1, newdata2), name=c('Site1', 'Site2'),
reference=as.Date('2001-01-01'), format=c('%d/%m/%y', '%d/%m/%Y'))
```

The dataset to be added must include 2 or 3 columns.

The first one is the date in the format specified by the parameter format=. If the number of nests is known for an exact data, then only one date must be indicated.

If the number of nests is known for a range of date, the first and last dates must be separated but a - (dash).

For example: 1/2/2000-10/2/2000

The second column is the number of nests observed for this date or this range of dates.

The third column is optional and is the name of the rookery.

If only two columns are indicated, the name can be indicated as a parameter of the function with name=. If no name is indicated, the default name Site will be used, but take care, only one rookery of this name can be used.

Several rookeries can be included in the same file but in this case the rookery name is obligatory at the third column.

The simplest use of this function is just:

```
phen <- add_phenology()
```

Some problems that can occur:

If a name is defined as a third column of a data.frame and a name is defined also with name=, the third column has priority.

Two different timeseries MUST have different name and character _ is forbidden in timeseries names.

Usage

```
add_phenology(add = file.choose(), name = NULL, reference = NULL,
month_ref = NULL, sep.dates = "-", header = NULL, format = NULL,
previous = NULL, silent = FALSE)
```

Arguments

add	The data to be added. It can be a set of several entities that uses the same reference and date format
name	The name of the monitored site
reference	as.Date('2001-12-31') The date used as 1st date
month_ref	If no reference date is given, use this month as a reference
sep.dates	Separator used to separate dates when incertitude is included
header	If the data is read from a file, can be used to force header or not
format	The format of the date in the file. Several format can be set and the last one that give compatible result is used
previous	Previous data formatted with add_phenology or NULL [default] if no previous data exist
silent	Does information about added timeseries is shown

Details

add_phenology creates a new dataset.

Value

Return a list of formatted data that can be used with fit_phenology()

Author(s)

Marc Girondot

Examples

```
## Not run:
# Get the latest version at:
# install.packages("http://www.esu-psud.fr/epc/conservation/CRAN/phenology.tar.gz",
  repos=NULL, type="source")
library(phenology)
# Read a file with data
Gratiot<-read.delim("http://max2.esu-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot <- add_phenology(Gratiot, name="Complete",
  reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot, fitted.parameters=parg,
  fixed.parameters=NULL)
data(result_Gratiot)
# Plot the phenology and get some stats
output <- plot(result_Gratiot)
```

```
## End(Not run)
```

add_SD	<i>Add SD for a fixed parameter.</i>
--------	--------------------------------------

Description

This function is used to add standard deviation for a fixed parameter.

Usage

```
add_SD(fixed.parameters = NULL, parameters = NULL, SD = NULL)
```

Arguments

fixed.parameters	Set of fixed parameters
parameters	Set of current parameters
SD	Standard deviation value to be added

Details

add_SD adds SD for a fixed parameter.

Value

The parameters set with the new SD value

Author(s)

Marc Giron dot

Examples

```
library(phenology)
# Generate a set of fixed parameter: Flat and Min
pfixed<-c(Flat=0, Min=0)
# Add SD for the Flat parameter
pfixed<-add_SD(fixed.parameters=pfixed, parameters="Flat", SD=5)
```

AutoFitPhenology *Automatic fit for phenology and tests*

Description

This function is used to test several combinations of fit at a time.

Usage

```
AutoFitPhenology(data = stop("A dataset must be provided"),
  progressbar = TRUE, ...)
```

Arguments

data	Dataset generated with add_phenology()
progressbar	If FALSE, do not show the progress bar
...	Parameters for fit_phenology()

Details

AutoFitPhenology runs fit for phenology and tests several combinations

Value

A list with 12 elements corresponding to the 12 tested models

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
# Read a file with data
Gratiot <- read.delim("http://max2.esse.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
  reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Run the optimisation
result_Gratiot_Auto <- AutoFitPhenology(data=data_Gratiot)
result_Gratiot_Auto <- AutoFitPhenology(data=data_Gratiot,
  control=list(trace=0, REPORT=100, maxit=500))

## End(Not run)
```

 BE_to_LBLE

Transform a set of parameters from Begin End to LengthB LengthE.

Description

This function is used to transform a set of parameters that uses Begin, Peak and End to a set of parameters that uses LengthB, Peak and LengthE.

Usage

```
BE_to_LBLE(parameters = NULL, help = FALSE)
```

Arguments

parameters	Set of current parameters
help	If TRUE, an help is displayed

Details

BE_to_LBLE transforms a set of parameters from Begin End format to LengthB LengthE.

Value

Return the set of modified parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
# Read a file with data
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt",
header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Change the parameters to Begin End format
parg1<-LBLE_to_BE(parameters=parg)
# And change back to LengthB LengthE.
parg2<-BE_to_LBLE(parameters=parg1)

## End(Not run)
```

ECFOCF_f

*Calculate a table of probabilities of ECF and OCF.***Description**

This function calculates a table of probabilities of ECF and OCF.

If p is lower or higher than $1E-100$ or $1-1E-100$, it is changed to $1E-100$ and $1-(1E-100)$ respectively.

Names for p vector elements should be p , or px (with $x=1:categories$), or $px.period$.

If mu_season and sd_season are equal to NA , the model is not temporalized.

If mu_season and sd_season are not NA , the model is temporalized.

Usage

```
ECFOCF_f(mu, sd, p, MaxNests = 15, mu_season = NA, sd_season = NA,
  MeanDaysBetween2Nests = 9.8,
  length_season = floor(365/MeanDaysBetween2Nests) + 1, parallel = TRUE)
```

Arguments

<code>mu</code>	The average of lognormal for clutch frequency.
<code>sd</code>	The sd parameter of lognormal for clutch frequency.
<code>p</code>	The capture probability for an individual nesting event.
<code>MaxNests</code>	Maximum number of nests by a female.
<code>mu_season</code>	The average of ordinal day for beginning of nesting season.
<code>sd_season</code>	The sd parameter of lognormal for ordinal day for beginning of nesting season.
<code>MeanDaysBetween2Nests</code>	Average number of days between two nests.
<code>length_season</code>	The total length of season based on groups of interclutch intervals.
<code>parallel</code>	If TRUE parallel computing is used.

Details

ECFOCF_f calculate a table of probabilities of ECF and OCF.

Value

Return a matrix of class TableECFOCF.

Author(s)

Marc Girondot

See Also

Other Model of Clutch Frequency: [TableECFOCF](#), [fitCF](#), [lnLCF](#), [logLik.ECFOCF](#), [plot.ECFOCF](#), [plot.TableECFOCF](#)

Examples

```
## Not run:
library(phenology)
# Example
modelECFOCF <- ECFOCF_f(mu=5.58013243236187,
                        sd=1.225581130238,
                        p=invlogit(1.3578137414575),
                        MaxNests=15)

plot(modelECFOCF)
modelECFOCF <- ECFOCF_f(mu=5.58013243236187,
                        sd=1.225581130238,
                        mu_season=12,
                        sd_season=2,
                        p=c(p1=invlogit(1.3578137414575)),
                        MaxNests=15,
                        MeanDaysBetween2Nests=9.8,
                        length_season=floor(365/9.8)+1
                        )
plot(modelECFOCF, period=2)

## End(Not run)
```

extract_result

Extract the set of parameters from a result object.

Description

The function "extract_result" permits to extract the set of parameters from a result object obtained after fit_phenology.

Usage

```
extract_result(result = NULL)
```

Arguments

result A result file

Details

extract_result get the fitted parameters from a result object.

Value

Return the set of fitted parameters

Author(s)

Marc Girondot

Examples

```
library(phenology)
## Not run:
# Read a file with data
Gratiot<-read.delim("http://max2.esse.u-psud.fr/epc/conservation/BI/Complete.txt", \cr
header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
# result_Gratiot<-fit_phenology(data=data_Gratiot, fitted.parameters=parg,
fixed.parameters=NULL)
data(result_Gratiot)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot)

## End(Not run)
```

fitCF

Fit a model of Clutch Frequency for marine turtles.

Description

This function fits a model of clutch frequency.

This model is an enhanced version of the one published by Briane et al. (2007).

Parameters are μ and σ being the parameters of a distribution used to model the clutch frequency.

This distribution is used only as a guide but has not statistical meaning.

The parameter p is the -logit probability that a female is seen on the beach for a particular nesting event. It includes both the probability that it is captured but also the probability that it uses that specific beach.

Several categories of females can be included in the model using index after the name of the parameter, for example μ_1 , σ_1 and μ_2 , σ_2 indicates that two categories of females with different clutch frequencies distribution are present. Similarly p_1 and p_2 indicates that two categories of females with different capture probabilities are present.

If more than one category is used, then it is necessary to include the parameter OTN to indicate the relative frequencies of each category. If two categories are used, one OTN parameter named ONT1 must be included. The OTN2 is forced to be 1. Then the relative frequency for category 1 is

OTN1/(OTN1+1) and for category 2 is $1/(OTN1+1)$. Same logic must be applied for 3 and more categories with always the last one being fixed to 1.

if p or a are equal to -Inf, the probability is 0 and if they are equal to +Inf, the probability is 1.

The best way to indicate capture probability for 3D model (OCF, ECF, Period) is to indicate p.period common for all categories and a1, a2, etc for each category. The capture probability for category 1 will be p.period * a1, and for category 2 will be p.period * a2, etc. In this case, the parameters p.period should be indicated in fitted parameters as well as a1, but a2 must be fixed to +Inf in fixed.parameters. Then the capture probability for category 2 will be p.period and for category 1 a1 * p.period.

Usage

```
fitCF(x = c(mu = 4, sd = 100, p = 0), fixed.parameters = NULL,
      data = stop("Data formatted with TableECFOCF() must be provided"),
      method = c("Nelder-Mead", "BFGS"), control = list(trace = 1, REPORT = 100,
      maxit = 500), itnmax = c(500, 100), hessian = TRUE, parallel = TRUE)
```

Arguments

x	Initial parameters to be fitted
fixed.parameters	Parameters that are fixed.
data	CMR data formatted using TableECFOCF()
method	Method to be used by optimx()
control	List of controls for optimx()
itnmax	A vector with maximum iterations for each method.
hessian	Logical to estimate SE of parameters
parallel	If TRUE, will use parallel computing for ECFOCF_f()

Details

fitCF fit a model of Clutch Frequency for marine turtles.

Value

Return a list of class ECFOCF with the fit information.

The list has the following items:

- data: The observations to be fitted
- par: The fitted parameters
- SE: The standard error of parameters if hessian is TRUE
- value: The -log likelihood of observations within the fitted model
- AIC: The AIC of fitted model
- mu: The vector of fitted mu values
- sd: The vector of fitted sd values

- prob: The vector of fitted capture probabilities
- a: The vector of fitted capture probabilities multiplier
- OTN: The vector of fitted relative probabilities of contribution
- period_categories: A list with the different period probabilities as named vectors for each category
- period: The combined period probabilities using OTN as named vector
- CF_categories: A list with the different CF probabilities as named vectors for each category
- CF: The combined CF probabilities using OTN as named vector
- ECFOCF_categories: A list with the different probability ECFOCF tables for each category
- ECFOCF: The combined table of ECFOCF using OTN probabilities tables
- ECFOCF_0: The combined table of ECFOCF probabilities tables using OTN without the OCF=0
- SE_df: A data.frame with SE and 95% confidence intervals for meanx and vx (mean and variance of clutch frequency for x category), OTNx (proportion for x category), and probx (capture probability for x category)

Author(s)

Marc Girondot

See Also

Briane J-P, Rivalan P, Girondot M (2007) The inverse problem applied to the Observed Clutch Frequency of Leatherbacks from Yalimapo beach, French Guiana. *Chelonian Conservation and Biology* 6:63-69

Fossette S, Kelle L, Girondot M, Goverse E, Hilterman ML, Verhage B, Thoisy B, de, Georges J-Y (2008) The world's largest leatherback rookeries: A review of conservation-oriented research in French Guiana/Suriname and Gabon. *Journal of Experimental Marine Biology and Ecology* 356:69-82

Other Model of Clutch Frequency: [ECFOCF_f](#), [TableECFOCF](#), [lnLCF](#), [logLik.ECFOCF](#), [plot.ECFOCF](#), [plot.TableECFOCF](#)

Examples

```
## Not run:
library(phenology)
# Example
data(MarineTurtles_2002)
ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002)

o_mulp1 <- fitCF(x = c(mu = 2.1653229641404539,
                      sd = 1.1465246643327098,
                      p = 0.25785366120357966),
                fixed.parameters=NULL,
                data=ECFOCF_2002, hessian = TRUE)

lnLCF(x = c(mu = 2.1653258860140556,
            sd = 1.1465243828331857,
```

```

      p = 0.25785578374593487),
fixed.parameters=NULL,
data=ECFOCF_2002)

o_mu2p1 <- fitCF(x = c(mu1 = 1.2190766766978423,
      sd1 = 0.80646454821956925,
      mu2 = 7.1886819592223246,
      sd2 = 0.18152887523015518,
      p = 0.29347220802963259,
      OTN = 2.9137627675219533),
fixed.parameters=NULL,
data=ECFOCF_2002, hessian = TRUE)

o_mu1p2 <- fitCF(x = c(mu = 5.3628701816871462,
      sd = 0.39390555498088764,
      p1 = 0.61159637544418755,
      p2 = -2.4212753004659189,
      OTN = 0.31898004668901009),
data=ECFOCF_2002, hessian = TRUE)

o_mu2p2 <- fitCF(x = c(mu1 = 0.043692606004492131,
      sd1 = 1.9446036983033428,
      mu2 = 7.3007868915644751,
      sd2 = 0.16109296152913491,
      p1 = 1.6860260469536992,
      p2 = -0.096816113083788985,
      OTN = 2.2604431232973501),
data=ECFOCF_2002, hessian = TRUE)

compare_AIC(mu1p1=o_mu1p1,
      mu2p1=o_mu2p1,
      mu1p2=o_mu1p2,
      mu2p2=o_mu2p2)

o_mu3p3 <- fitCF(x = c(mu1 = 0.24286312214288761,
      sd1 = 0.34542255091729313,
      mu2 = 5.0817174343025551,
      sd2 = 1.87435099405695,
      mu3 = 5.2009265101740683,
      sd3 = 1.79700447678357,
      p1 = 8.8961708614726156,
      p2 = 0.94790116453886453,
      p3 = -0.76572930634505421,
      OTN1 = 1.2936848663276974,
      OTN2 = 0.81164278235645926),
data=ECFOCF_2002, hessian = TRUE)

o_mu3p1 <- fitCF(x = structure(c(0.24387978183477,
      1.2639261745506,
      4.94288464711349,

```



```

1.945082889758,
4.9431672350811,
1.287663104591,
0.323636536050397,
1.37072039291397,
9.28055412564559e-06),
.Names = c("mu1", "sd1", "mu2",
            "sd2", "mu3", "sd3",
            "p", "OTN1", "OTN2")),
data=ECFOCF_2002, hessian = TRUE)

o_mu1p3 <- fitCF(x = structure(c(4.65792402108387,
1.58445909785,
-2.35414198317177,
0.623757854800649,
-3.62623634029326,
11.6950204755787,
4.05273728846523),
.Names = c("mu", "sd",
            "p1", "p2", "p3",
            "OTN1", "OTN2")),
data=ECFOCF_2002, hessian = TRUE)

compare_AIC(mu1p1=o_mu1p1,
            mu2p1=o_mu2p1,
            mu1p2=o_mu1p2,
            mu2p2=o_mu2p2,
            mu3p3=o_mu3p3,
            mu1p3=o_mu1p3,
            mu3p1=o_mu3p1)

# 3D model for (ECF, OCF, period)

ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))

fp <- rep(0, dim(ECFOCF_2002)[3])
names(fp) <- paste0("p1.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
par <- c(mu = 2.6404831115214353,
        sd = 0.69362774786433479,
        mu_season = 12.6404831115214353,
        sd_season = 1.69362774786433479)
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]]:
        attributes(ECFOCF_2002)$table["end"]])

fp <- rep(-Inf, dim(ECFOCF_2002)[3])
names(fp) <- paste0("p1.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
fixed.parameters <- fp[-c(attributes(ECFOCF_2002)$table["begin"]):
        attributes(ECFOCF_2002)$table["end"]])

lnLCF(x=par, data=ECFOCF_2002, fixed.parameters=fixed.parameters)

ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))

```

```

fp <- rep(0, dim(ECFOCF_2002)[3])
names(fp) <- paste0("p1.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
par <- c(mu = 2.6404831115214353,
        sd = 0.69362774786433479,
        mu_season = 12.6404831115214353,
        sd_season = 1.69362774786433479)
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]]:
        attributes(ECFOCF_2002)$table["end"]])
names(fp) <- paste0("p2.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]]:
        attributes(ECFOCF_2002)$table["end"]])
fixed.parameters <- c(p1=-Inf, p2=-Inf)

lnLCF(x=par, data=ECFOCF_2002, fixed.parameters=fixed.parameters)

ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))
fp <- rep(0, dim(ECFOCF_2002)[3])
names(fp) <- paste0("p.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
par <- c(mu = 2.6404831115214353,
        sd = 0.69362774786433479,
        mu_season = 12.6404831115214353,
        sd_season = 1.69362774786433479,
        a1=10,
        a2=0)
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]]:
        attributes(ECFOCF_2002)$table["end"]])
names(fp) <- paste0("p2.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
fixed.parameters <- c(p=-Inf)

lnLCF(x=par, data=ECFOCF_2002, fixed.parameters=fixed.parameters)

ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))
par <- c(mu = 2.6404831115214353,
        sd = 0.69362774786433479,
        mu_season = 12.6404831115214353,
        sd_season = 1.69362774786433479,
        a1=10,
        a2=0)
fixed.parameters <- c(p=-Inf)

lnLCF(x=par, data=ECFOCF_2002, fixed.parameters=fixed.parameters)

o_mu1season1a2 <- fitCF(x=par, fixed.parameters=fixed.parameters,
                      data=ECFOCF_2002)

ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002,
                          date0=as.Date("2002-01-01"),
                          MeanDaysBetween2Nest = 9.8,
                          MaxNests=15
                          )
par <- c(mu = 2.6404831115214353,
        sd = 0.69362774786433479,
        mu_season = 12.6404831115214353,

```

```

sd_season = 1.69362774786433479,
a2=0)
fp <- rep(0, dim(ECFOCF_2002)[3])
names(fp) <- paste0("p.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]]:
        attributes(ECFOCF_2002)$table["end"]])
fixed.parameters <- c(a1=Inf, p=-Inf)

lnLCF(x=par, data=ECFOCF_2002, fixed.parameters=fixed.parameters)

o_mu1season1a2p <- fitCF(x=par, fixed.parameters=fixed.parameters,
                        data=ECFOCF_2002)

## End(Not run)

```

fitRMU

Adjust incomplete timeseries with various constraints.

Description

The data must be a data.frame with the first column being years and two columns for each beach: the average and the se for the estimate.

The correspondance between mean and se for each rookery are given in the RMU.names data.frame. In the result list, the mean proportions for each rookeries are in \$proportions, \$proportions.CI.0.05 and \$proportions.CI.0.95.

The names of beach columns must not begin by T_, SD_, a0_, a1_ or a2_ and cannot be r.

A RMU is the acronym for Regional Management Unit. See:

Wallace, B.P., DiMatteo, A.D., Hurley, B.J., Finkbeiner, E.M., Bolten, A.B., Chaloupka, M.Y., Hutchinson, B.J., Abreu-Grobois, F.A., Amorocho, D., Bjorndal, K.A., Bourjea, J., Bowen, B.W., Dueñas, R.B., Casale, P., Choudhury, B.C., Costa, A., Dutton, P.H., Fallabrino, A., Girard, A., Girondot, M., Godfrey, M.H., Hamann, M., López-Mendilaharsu, M., Marcovaldi, M.A., Mortimer, J.A., Musick, J.A., Nel, R., Seminoff, J.A., Troëng, S., Witherington, B., Mast, R.B., 2010. Regional management units for marine turtles: a novel framework for prioritizing conservation and research across multiple scales. PLoS One 5, e15465.

Standard deviation for each value is supposed to be additive based on both the observed SE (in the RMU.data object) and a constant value dependent on the rookery if model.SD is equal to Constant. This value is fixed to zero for model.SD="Zero".

The support for optimx is still experimental. It has been fully tested only with BFGS and Nelder-Mead method. Several methods can be used in a single run for optimx. In this case the best likelihood is used.

Usage

```

fitRMU(RMU.data = stop("data parameter must be provided"), RMU.names = NULL,
      model.trend = "Constant", model.rookeries = "Constant",
      model.SD = "Zero", parameters = NULL, fixed.parameters = NULL,
      SE = NULL, method = "BFGS", replicate.CI = 1000,
      colname.year = "Year", control = list(trace = 1, REPORT = 100, maxit =
      500), optim = "optim", maxL = 1e+09)

```

Arguments

RMU.data	A data.frame with a column Year (the name is defined in colname.year) and two columns per rookery defined in RMU.names
RMU.names	A dataframe with two columns indicating name of columns for mean and standard error for rookerys
model.trend	Can be Constant, Exponential or Year-specific
model.rookeries	Description temporal change in rookeries proportion. It be Constant, First-order or Second-order
model.SD	Can be Zero or Constant. See description.
parameters	Parameters to fit
fixed.parameters	Parameters that are fixed
SE	Parameters SE for example from fitRMU_MHmcmc()
method	Method of optimization, default is BFGS
replicate.CI	Number of replicates to estimate CI of proportion for each rookery
colname.year	Name of the column to be used as time index
control	List for control parameters of optim
optim	Function to be called for optimization, default is optim but it could be optimx
maxL	If an error is produced during the estimation of likelihood, replace -Ln L by this value

Details

fitRMU is used to estimate missing information when several linked values are observed along a timeseries

Value

Return a list with the results from optim and synthesis for proportions and numbers

Author(s)

Marc Girondot

See Also

Other Fill gaps in RMU: [fitRMU_MHmcmc_p](#), [fitRMU_MHmcmc](#), [logLik.fitRMU](#), [plot.fitRMU](#)

Examples

```

## Not run:
library("phenology")
RMU.names.AtlanticW <- data.frame(mean=c("Yalimapo.French.Guiana",
                                       "Galibi.Suriname",
                                       "Irakumpapy.French.Guiana"),
                                 se=c("se_Yalimapo.French.Guiana",
                                       "se_Galibi.Suriname",
                                       "se_Irakumpapy.French.Guiana"))

data.AtlanticW <- data.frame(Year=c(1990:2000),
                             Yalimapo.French.Guiana=c(2076, 2765, 2890, 2678, NA,
                                                         6542, 5678, 1243, NA, 1566, 1566),
                             se_Yalimapo.French.Guiana=c(123.2, 27.7, 62.5, 126, NA,
                                                           230, 129, 167, NA, 145, 20),
                             Galibi.Suriname=c(276, 275, 290, NA, 267,
                                                  542, 678, NA, 243, 156, 123),
                             se_Galibi.Suriname=c(22.3, 34.2, 23.2, NA, 23.2,
                                                    4.3, 2.3, NA, 10.3, 10.1, 8.9),
                             Irakumpapy.French.Guiana=c(1076, 1765, 1390, 1678, NA,
                                                         3542, 2678, 243, NA, 566, 566),
                             se_Irakumpapy.French.Guiana=c(23.2, 29.7, 22.5, 226, NA,
                                                            130, 29, 67, NA, 15, 20))

cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
              colname.year="Year", model.trend="Constant",
              model.SD="Zero")

cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
              colname.year="Year", model.trend="Constant",
              model.SD="Zero",
              control=list(trace=1, REPORT=100, maxit=500, parscale = c(3000, -0.2, 0.6)))

# Example with optimx
require("optimx")
cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
              colname.year="Year", model.trend="Constant",
              model.SD="Zero", optim="optimx", method=c("Nelder-Mead","BFGS"),
              control = list(trace = 0, REPORT = 100, maxit = 500,
                             parscale = c(3000, -0.2, 0.6)))

expo <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
               colname.year="Year", model.trend="Exponential",
               model.SD="Zero", optim="optimx", method=c("Nelder-Mead","BFGS"),
               control = list(trace = 0, REPORT = 100, maxit = 500,
                              parscale = c(6000, -0.05, -0.25, 0.6)))

YS <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
             colname.year="Year", model.trend="Year-specific", method=c("Nelder-Mead","BFGS"),
             optim="optimx", model.SD="Zero")

YS1 <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
              colname.year="Year", model.trend="Year-specific", method=c("Nelder-Mead","BFGS"),
              optim="optimx", model.SD="Zero", model.rookeries="First-order")

YS1_cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
                  colname.year="Year", model.trend="Year-specific",
                  model.SD="Constant", model.rookeries="First-order",

```

```

      optim="optimx", parameters=YS1$par, method=c("Nelder-Mead", "BFGS"))
YS2 <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
      colname.year="Year", model.trend="Year-specific",
      model.SD="Zero", model.rookeries="Second-order",
      optim="optimx", parameters=YS1$par, method=c("Nelder-Mead", "BFGS"))
YS2_cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
      colname.year="Year", model.trend="Year-specific",
      model.SD="Constant", model.rookeries="Second-order",
      optim="optimx", parameters=YS1_cst$par, method=c("Nelder-Mead", "BFGS"))

compare_AIC(Constant=cst, Exponential=expo,
YearSpecific=YS)

compare_AIC(YearSpecific_ProportionsFirstOrder_Zero=YS1,
YearSpecific_ProportionsFirstOrder_Constant=YS1_cst)

compare_AIC(YearSpecific_ProportionsConstant=YS,
      YearSpecific_ProportionsFirstOrder=YS1,
      YearSpecific_ProportionsSecondOrder=YS2)

compare_AIC(YearSpecific_ProportionsFirstOrder=YS1_cst,
      YearSpecific_ProportionsSecondOrder=YS2_cst)

barplot_errbar(YS1_cst$proportions[1, ], y.plus = YS1_cst$proportions.CI.0.95[1, ],
y.minus = YS1_cst$proportions.CI.0.05[1, ], las=1, ylim=c(0, 0.7),
main="Proportion of the different rookeries in the region")

plot(cst, main="Use of different beaches along the time", what="total")
plot(expo, main="Use of different beaches along the time", what="total")
plot(YS2_cst, main="Use of different beaches along the time", what="total")

plot(YS1, main="Use of different beaches along the time")
plot(YS1_cst, main="Use of different beaches along the time")
plot(YS1_cst, main="Use of different beaches along the time", what="numbers")

## End(Not run)

```

fitRMU_MHmcmc

Run the Metropolis-Hastings algorithm for RMU.data

Description

Run the Metropolis-Hastings algorithm for RMU.data.

The number of iterations is $n.iter+n.adapt+1$ because the initial likelihood is also displayed.

I recommend $thin=1$ because the method to estimate SE uses resampling.

As initial point is maximum likelihood, $n.adapt = 0$ is a good solution.

The parameters `intermediate` and `filename` are used to save intermediate results every '`intermediate`' iterations (for example 1000). Results are saved in a file of name `filename`.

The parameter previous is used to indicate the list that has been save using the parameters intermediate and filename. It permits to continue a mcmc search.

These options are used to prevent the consequences of computer crash or if the run is very very long and computer processes at time limited.

Usage

```
fitRMU_MHmcmc(result = stop("An output from fitRMU_MHmcmc() must be provided"),
  n.iter = 10000,
  parametersMCMC = stop("A model generated with fitRMU_MHmcmc_p() must be provided"),
  n.chains = 4, n.adapt = 0, thin = 1, trace = FALSE,
  intermediate = NULL, filename = "intermediate.Rdata", previous = NULL)
```

Arguments

result	An object obtained after a SearchR fit
n.iter	Number of iterations for each step
parametersMCMC	A set of parameters used as initial point for searching with information on priors
n.chains	Number of replicates
n.adapt	Number of iterations before to store outputs
thin	Number of iterations between each stored output
trace	True or False, shows progress
intermediate	Period for saving intermediate result, NULL for no save
filename	If intermediate is not NULL, save intermediate result in this file
previous	Previous result to be continued. Can be the filename in which intermediate results are saved.

Details

fitRMU_MHmcmc runs the Metropolis-Hastings algorithm for RMU.data (Bayesian MCMC)

Value

A list with resultMCMC being mcmc.list object, resultLnL being likelihoods and parametersMCMC being the parameters used

Author(s)

Marc Girondot

See Also

Other Fill gaps in RMU: [fitRMU_MHmcmc_p](#), [fitRMU](#), [logLik.fitRMU](#), [plot.fitRMU](#)

Examples

```
## Not run:
library("phenology")
RMU.names.AtlanticW <- data.frame(mean=c("Yalimapo.French.Guiana",
                                       "Galibi.Suriname",
                                       "Irakumpapy.French.Guiana"),
                                 se=c("se_Yalimapo.French.Guiana",
                                       "se_Galibi.Suriname",
                                       "se_Irakumpapy.French.Guiana"))

data.AtlanticW <- data.frame(Year=c(1990:2000),
                             Yalimapo.French.Guiana=c(2076, 2765, 2890, 2678, NA,
                                                         6542, 5678, 1243, NA, 1566, 1566),
                             se_Yalimapo.French.Guiana=c(123.2, 27.7, 62.5, 126, NA,
                                                         230, 129, 167, NA, 145, 20),
                             Galibi.Suriname=c(276, 275, 290, NA, 267,
                                                  542, 678, NA, 243, 156, 123),
                             se_Galibi.Suriname=c(22.3, 34.2, 23.2, NA, 23.2,
                                                    4.3, 2.3, NA, 10.3, 10.1, 8.9),
                             Irakumpapy.French.Guiana=c(1076, 1765, 1390, 1678, NA,
                                                         3542, 2678, 243, NA, 566, 566),
                             se_Irakumpapy.French.Guiana=c(23.2, 29.7, 22.5, 226, NA,
                                                            130, 29, 67, NA, 15, 20))

cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
              colname.year="Year", model.trend="Constant",
              model.SD="Zero")

pMCMC <- fitRMU_MHmcmc_p(result=cst, accept=TRUE)
fitRMU_MCMC <- fitRMU_MHmcmc(result = cst, n.iter = 10000,
                             parametersMCMC = pMCMC, n.chains = 1, n.adapt = 0, thin = 1, trace = FALSE)

## End(Not run)
```

fitRMU_MHmcmc_p

Generates set of parameters to be used with fitRMU_MHmcmc()

Description

Interactive script used to generate set of parameters to be used with phenology_MHmcmc().

Usage

```
fitRMU_MHmcmc_p(result = stop("An output from fitRMU() must be provided"),
               accept = FALSE)
```

Arguments

result	An object obtained after a fitRMU() fit
accept	If TRUE, does not wait for user interaction

Details

fitRMU_MHmcmc_p generates set of parameters to be used with fitRMU_MHmcmc()

Value

A matrix with the parameters

Author(s)

Marc Girondot

See Also

Other Fill gaps in RMU: [fitRMU_MHmcmc](#), [fitRMU](#), [logLik.fitRMU](#), [plot.fitRMU](#)

Examples

```
## Not run:
library("phenology")
RMU.name.AtlanticW <- data.frame(mean=c("Yalimapo.French.Guiana",
                                       "Galibi.Suriname",
                                       "Irakumpapy.French.Guiana"),
                                se=c("se_Yalimapo.French.Guiana",
                                       "se_Galibi.Suriname",
                                       "se_Irakumpapy.French.Guiana"))

data.AtlanticW <- data.frame(Year=c(1990:2000),
                              Yalimapo.French.Guiana=c(2076, 2765, 2890, 2678, NA,
                                                         6542, 5678, 1243, NA, 1566, 1566),
                              se_Yalimapo.French.Guiana=c(123.2, 27.7, 62.5, 126, NA,
                                                         230, 129, 167, NA, 145, 20),
                              Galibi.Suriname=c(276, 275, 290, NA, 267,
                                                  542, 678, NA, 243, 156, 123),
                              se_Galibi.Suriname=c(22.3, 34.2, 23.2, NA, 23.2,
                                                  4.3, 2.3, NA, 10.3, 10.1, 8.9),
                              Irakumpapy.French.Guiana=c(1076, 1765, 1390, 1678, NA,
                                                         3542, 2678, 243, NA, 566, 566),
                              se_Irakumpapy.French.Guiana=c(23.2, 29.7, 22.5, 226, NA,
                                                            130, 29, 67, NA, 15, 20))

cst <- fitRMU(data=data.AtlanticW, RMU.name=RMU.name.AtlanticW,
              colname.year="Year", model.trend="Constant",
              model.SD="Zero")
pMCMC <- fitRMU_MHmcmc_p(result=cst, accept=TRUE)

## End(Not run)
```

fit_phenology

*Fit the phenology parameters to timeseries of counts.***Description**

Function of the package phenology to fit parameters to timeseries.

To fit data, the syntaxe is :

```
Result <- fit_phenology(data=dataset, fitted.parameters=par, fixed.parameters=pfixed, trace=1, method_incertitude=2, zero_counts=TRUE, hessian=TRUE)
```

or if no parameter is fixed :

```
Result <- fit_phenology(data=dataset, fitted.parameters=par)
```

Add trace=1 [default] to have information on the fit progression or trace=0 to hide information on the fit progression.

zero_counts = c(TRUE, TRUE, FALSE) indicates whether the zeros have been recorded for each of these timeseries. Defaut is TRUE for all.

hessian = FALSE does not estimate se of parameters.

If the parameter Theta is fixed to +Inf, a Poissonian model of daily nest distribution is implemented.

Usage

```
fit_phenology(data = file.choose(), fitted.parameters = NULL,
  fixed.parameters = NULL, method_incertitude = "convolution",
  infinite = 200, zero_counts = TRUE, hessian = TRUE, silent = FALSE,
  growlnotify = TRUE, cofactors = NULL, add.cofactors = NULL,
  zero = 1e-09, control = list(trace = 1, REPORT = 100, maxit = 500))
```

Arguments

data	A dataset generated by add_format
fitted.parameters	Set of parameters to be fitted
fixed.parameters	Set of fixed parameters
method_incertitude	'combinatory' estimates likelihood of all combinations for nest numbers; 'convolution' [default] uses the exact likelihood of the sum of negative binomial distribution.
infinite	Number of iterations for dSnbinom() used for method_incertitude='sum'
zero_counts	example c(TRUE, TRUE, FALSE) indicates whether the zeros have been recorded for each of these timeseries. Defaut is TRUE for all.
hessian	If FALSE does not estimate se of parameters
silent	If TRUE does not show any message
growlnotify	If FALSE, does not send growl notification (only in MacOSX)
cofactors	data.frame with a column Date and a column for each cofactor

add.cofactors Names of the column of parameter cofactors to use as a cofactor
 zero If the theoretical nest number is under this value, this value will be used
 control List for control parameters for optimx

Details

fit_phenology fits parameters to timeseries.

Value

Return a list of with data and result

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
# Read a file with data
Gratiot <- read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt",
header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Plot the phenology and get some stats
output <- plot(result_Gratiot)
# Use fit with co-factor
# First extract tide information for that place
td <- tide.info(year=2001, latitude=4.9167, longitude=-52.3333, tz="America/Cayenne")
td2 <- td[td$Tide=="High Tide", ]
td3 <- cbind(td2, Date=as.Date(td2$Date.Time))
td4 <- td3[(as.POSIXlt(td3$Date.Time)$hou<6) | (as.POSIXlt(td3$Date.Time)$hou>18), ]
with(td4, plot(Date.Time, Level, type="l"))
data_Gratiot$Complete$Date
td5 <- merge(data_Gratiot$Complete, td4, by.x="Date", by.y="Date")
td6 <- td5[, c("Date", "Level")]
parg <- par_init(data_Gratiot, fixed.parameters=NULL, add.cofactors="Level")
result_Gratiot_CF <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL, cofactors=td6,
add.cofactors="Level")
compare_AIC(WithoutCF=result_Gratiot, WithCF=result_Gratiot_CF)
plot(result_Gratiot_CF)
```

```

# Example with two series fitted with different peaks but same Length of season

Gratiot2 <- Gratiot
Gratiot2[, 2] <- floor(Gratiot2[, 2]*runif(n=nrow(Gratiot2)))
data_Gratiot <- add_phenology(Gratiot, name="Complete",
                             reference=as.Date("2001-01-01"), format="%d/%m/%Y")
data_Gratiot <- add_phenology(Gratiot2, name="Complete2",
                             reference=as.Date("2001-01-01"),
                             format="%d/%m/%Y", previous=data_Gratiot)

pfixed=c(Min=0)
p <- par_init(data_Gratiot, fixed.parameters = pfixed)
p <- c(p, Peak_Complete=175, Peak_Complete2=175)
p <- p[-4]
p <- c(p, Length=90)
p <- p[-(3:4)]
result_Gratiot <- fit_phenology(data=data_Gratiot, fitted.parameters=p,
                                fixed.parameters=pfixed)

## End(Not run)

```

Gratiot

Leatherback nest counts from Gratiot et al. (2006) Figure 1

Description

Leatherback nest counts from Gratiot et al. (2006) Figure 1. These data have been collected by the ONG Kwata in French Guiana.

The data have been obtained from the graph of the publication (see reference).

Usage

Gratiot

Format

data.frame with the morning date in the first column and the nest counts on the second one.

Details

Leatherback nest counts from Gratiot et al. (2006) Figure 1

Author(s)

KWATA ONG

References

Gratiot, N., Gratiot, J., de Thoisy, B. & Kelle, L. 2006. Estimation of marine turtles nesting season from incomplete data ; statistical adjustment of a sinusoidal function. *Animal Conservation*, 9, 95-102.

Examples

```

library(phenology)
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)

```

LBLE_to_BE

Transform a set of parameters from LengthB LengthE to Begin End.

Description

This function is used to transform a set of parameters that uses LengthB, Peak and LengthE to a set of parameters that uses Begin, Peak and End.

Usage

```
LBLE_to_BE(parameters = NULL, help = FALSE)
```

Arguments

parameters	Set of current parameters
help	If TRUE, an help is displayed

Details

LBLE_to_BE transforms a set of parameters from LengthB LengthE to Begin End.

Value

Return a set of modified parameters

Author(s)

Marc Girondot

Examples

```

# Read a file with data
# Gratiot<-read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt", , header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot<-add_phenology(Gratiot, name="Complete", reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)

```

```
# Change the parameters to Begin End format
parg1<-LBLE_to_BE(parameters=parg)
# And change back to LengthB LengthE
parg2<-BE_to_LBLE(parameters=parg1)
```

LBLE_to_L

Transform a set of parameters from LengthB LengthE format to Length

Description

This function is used to transform a set of parameters that uses LengthB and LengthE to a set of parameters uses Length.

Usage

```
LBLE_to_L(parameters = stop("Set of parameters must be given"))
```

Arguments

parameters Set of current parameters

Details

LBLE_to_L transforms a set of parameters from LengthB LengthE format to Length.

Value

Return the set of modified parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
# Read a file with data
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt",
header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot<-add_phenology(Gratiot, name="Complete", reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Change the parameters to Begin End format
parg1<-LBLE_to_L(parameters=parg)
# And change back to LengthB LengthE.
parg2<-L_to_LBLE(parameters=parg1)
```

likelihood_phenology *Estimate the likelihood of timeseries based on a set of parameters.*

Description

This function is used to estimate the likelihood based on a set of parameters.

Usage

```
likelihood_phenology(data = NULL, fitted.parameters = NULL,
  fixed.parameters = NULL, zero_counts = NULL, method_incertitude = NULL,
  result = NULL, cofactors = NULL, add.cofactors = NULL, infinite = 200,
  zero = 1e-09)
```

Arguments

data	Dataset generated with add_format
fitted.parameters	Set of parameters to be fitted
fixed.parameters	Set of fixed parameters
zero_counts	example c(TRUE, TRUE, FALSE) indicates whether the zeros have been recorder for each of these timeseries. Default is TRUE for all.
method_incertitude	2 [default] is the correct one from a statistical point of view; 0 is an aproximate method more rapid; 1 is an alternative more rapid but biased.
result	An object obtained after fit_phenology()
cofactors	data.frame with a column Date and a column for each cofactor
add.cofactors	Names of the column of parameter cofactors to use as a cofactor
infinite	Number of iterations for dSnbinom() used for method_incertitude='sum'
zero	If the theoretical nest number is under this value, this value wll be used

Details

likelihood_phenology estimate likelihood for a set of parameters.

Value

The likelihood of the data with the parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
# Read a file with data
Gratiot<-read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Estimate likelihood with this initial set of parameters
likelihood_phenology(data=data_Gratiot, fitted.parameters=parg, fixed.parameters=NULL)
# Or directly from a result object
likelihood_phenology(result=result_Gratiot)

## End(Not run)
```

InLCF

Calculate the -log likelihood of data within a model.

Description

Calculate the -log likelihood of data within a model.

Usage

```
InLCF(x, data, fixed.parameters = NULL, parallel = TRUE)
```

Arguments

x	A named vector of parameters (mu, sd, mu_season, sd_season, a, p and OTN).
data	CMR database formatted using TableECFOCF().
fixed.parameters	Parameters that are fixed.
parallel	If TRUE, parallel computing in ECFOCF_f is used.

Details

InLCF calculate the -log likelihood of data within a model.

Value

Return the -log likelihood of data within a model.

Author(s)

Marc Girondot

See Also

Other Model of Clutch Frequency: [ECFOCF_f](#), [TableECFOCF](#), [fitCF](#), [logLik.ECFOCF](#), [plot.ECFOCF](#), [plot.TableECFOCF](#)

Examples

```
## Not run:
library(phenology)
# Example
ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002)
lnLCF(x=c(mu=4.71768454279272,
          sd=1.075711951667,
          p=-1.79746277312909),
      data=ECFOCF_2002)

ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))
fp <- rep(0, dim(ECFOCF_2002)[3])
names(fp) <- paste0("p.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
par <- c(mu1 = 0.6404831115214353,
        sd1 = 0.69362774786433479,
        mu2 = 5.6404831115214353,
        sd2 = 5.69362774786433479,
        mu_season = 12.6404831115214353,
        sd_season = 1.69362774786433479,
        OTN=1)
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]:attributes(ECFOCF_2002)$table["end"]])
fixed.parameters <- c(p=-Inf)

lnLCF(x=par, data=ECFOCF_2002, fixed.parameters=fixed.parameters)

## End(Not run)
```

logLik.ECFOCF

Return Log Likelihood of a fit done using fitCF

Description

Return Log Likelihood of a fit generated by fitCF.

Usage

```
## S3 method for class 'ECFOCF'
logLik(object, ...)
```

Arguments

object A result file generated by fitCF
 ... Not used

Details

logLik.ECFOCF return Log Likelihood of a fit done using fitCF

Value

The Log Likelihood value for the fitted model with data

Author(s)

Marc Girondot

See Also

Other Model of Clutch Frequency: [ECFOCF_f](#), [TableECFOCF](#), [fitCF](#), [lnLCF](#), [plot.ECFOCF](#), [plot.TableECFOCF](#)

Examples

```
## Not run:
library(phenology)
# Example
ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))
par <- c(mu = 2.6404831115214353,
        size = 0.69362774786433479,
        mu_season = 12.6404831115214353,
        size_season = 1.69362774786433479,
        a2=0)
fp <- rep(0, dim(ECFOCF_2002)[3])
names(fp) <- paste0("p.", formatC(1:(dim(ECFOCF_2002)[3]), width=2, flag="0"))
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]:attributes(ECFOCF_2002)$table["end"]])
fixed.parameters <- c(a1=Inf, p=-Inf)

lnLCF(x=par, data=ECFOCF_2002, fixed.parameters=fixed.parameters)

o_mu1season1a2p <- fitCF(x=par, fixed.parameters=fixed.parameters,
                        data=ECFOCF_2002)

logLik(o_mu1season1a2p)
AIC(o_mu1season1a2p)

## End(Not run)
```

logLik.fitRMU	<i>Return Log Likelihood of a fit generated by fitRMU</i>
---------------	---

Description

Return Log Likelihood of a fit generated by fitRMU

Usage

```
## S3 method for class 'fitRMU'
logLik(object, ...)
```

Arguments

object	A result file generated by fitRMU
...	Not used

Details

logLik.fitRMU Return Log Likelihood of a fit for fitRMU

Value

The Log Likelihood value for the fitted model with data

Author(s)

Marc Girondot

See Also

Other Fill gaps in RMU: [fitRMU_MHmcmc_p](#), [fitRMU_MHmcmc](#), [fitRMU](#), [plot.fitRMU](#)

Examples

```
## Not run:
library(phenology)
RMU.name.AtlanticW <- data.frame(mean=c("Yalimapo.French.Guiana",
                                       "Galibi.Suriname",
                                       "Irakumpapy.French.Guiana"),
                                se=c("se_Yalimapo.French.Guiana",
                                      "se_Galibi.Suriname",
                                      "se_Irakumpapy.French.Guiana"))
data.AtlanticW <- data.frame(Year=c(1990:2000),
                             Yalimapo.French.Guiana=c(2076, 2765, 2890, 2678, NA,
                                                         6542, 5678, 1243, NA, 1566, 1566),
                             se_Yalimapo.French.Guiana=c(123.2, 27.7, 62.5, 126, NA,
                                                         230, 129, 167, NA, 145, 20),
                             Galibi.Suriname=c(276, 275, 290, NA, 267,
```

```

                    542, 678, NA, 243, 156, 123),
se_Galibi.Suriname=c(22.3, 34.2, 23.2, NA, 23.2,
                    4.3, 2.3, NA, 10.3, 10.1, 8.9),
Irakumpapy.French.Guiana=c(1076, 1765, 1390, 1678, NA,
                           3542, 2678, 243, NA, 566, 566),
se_Irakumpapy.French.Guiana=c(23.2, 29.7, 22.5, 226, NA,
                              130, 29, 67, NA, 15, 20))

cst <- fitRMU(data=data.AtlanticW, RMU.name=RMU.name.AtlanticW,
              colname.year="Year", model.trend="Constant",
              model.SD="Zero")

logLik(cst)
AIC(cst)

## End(Not run)

```

logLik.phenology	<i>Return Log Likelihood of a fit generated by fit_phenology</i>
------------------	--

Description

Return Log Likelihood of a fit generated by fit_phenology

Usage

```

## S3 method for class 'phenology'
logLik(object, ...)

```

Arguments

object	A result file generated by fit_phenology
...	Not used

Details

logLik.phenology Return Log Likelihood of a fit

Value

The Log Likelihood value of the fitted model and data

Author(s)

Marc Girondot

Examples

```
## Not run:  
library(phenology)  
data(result_Gratiot)  
logLik(result_Gratiot)  
AIC(result_Gratiot)  
  
## End(Not run)
```

logLik.Tagloss	<i>Return Log Likelihood of a fit generated by Tagloss_fit</i>
----------------	--

Description

Return Log Likelihood of a fit generated by Tagloss_fit

Usage

```
## S3 method for class 'Tagloss'  
logLik(object, ...)
```

Arguments

object	A result file generated by Tagloss_fit
...	Not used

Details

logLik.Tagloss returns Log Likelihood of a fit for tag loss

Value

The Log Likelihood value for the fitted model with data

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_L](#), [Tagloss_daymax](#), [Tagloss_fit](#), [Tagloss_format](#), [Tagloss_model](#), [Tagloss_simulate](#), [plot.Tagloss](#)

Examples

```
## Not run:
library(phenology)
# Example
data_f_21 <- Tagloss_format(outLR, model="21")
# Without the N20 the computing is much faster
data_f_21_fast <- subset(data_f_21, subset=(is.na(data_f_21$N20)))
par <- structure(c(48.8292784204825, 1039.02842229274, -89.3162940697861,
5.21817463244988, 8.00575451188548, 8.32971268127933, 161.265553603601,
602.935748681661, 2643.57415102633, 16.752815732218, 10.181616195839,
7.14279063312016), .Names = c("D1_2", "D2D1_2", "D3D2_2", "A_2",
"B_2", "C_2", "D1_1", "D2D1_1", "D3D2_1", "A_1", "B_1", "C_1"))
o <- Tagloss_fit(data=data_f_21_fast, fitted.parameters=par)
logLik(o)
AIC(o)

## End(Not run)
```

L_to_LBLE

Transform a set of parameters from Length format to LengthB LengthE

Description

This function is used to transform a set of parameters that uses Length to a set of parameters uses LengthB and LengthE.

Usage

```
L_to_LBLE(parameters = stop("Set of parameters must be given"))
```

Arguments

parameters Set of current parameters

Details

L_to_LBLE transforms a set of parameters from Length format to LengthB LengthE.

Value

Return the set of modified parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
# Read a file with data
Gratiot<-read.delim("http://max2.esse.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Change the parameters to Begin End format
parg1<-LBLE_to_L(parameters=parg)
# And change back to LengthB LengthE.
parg2<-L_to_LBLE(parameters=parg1)
```

map_Gratiot

Likelihood map of Leatherback nest counts

Description

Likelihood map of Leatherback nest counts from Gratiot et al. (2006) Figure 1. A intraseasonal periodic pattern was searched for varying Phi and Delta parameters.

Usage

```
map_Gratiot
```

Format

A list with Gratiot data and the result of the fit.

Details

Likelihood map of Leatherback nest counts from Gratiot et al. (2006) Figure 1

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Gratiot, N., Gratiot, J., de Thoisy, B. & Kelle, L. 2006. Estimation of marine turtles nesting season from incomplete data ; statistical adjustment of a sinusoidal function. *Animal Conservation*, 9, 95-102.

Examples

```
library(phenology)
# Read a file with likelihood map
data(map_Gratiot)
```

map_phenology	<i>Generate a likelihood map varying Phi and Delta.</i>
---------------	---

Description

This function generates a map of likelihood varying Phi and Delta.

Parameters are the same than for the fit_phenology() function except for trace that is disabled.

If Alpha, Beta or Tau are not indicated, Alpha and Tau are set to 0 and 1 and Beta is fitted.

Only one set of Alpha, Beta, Tau, Phi and Delta are used for all timeseries present in data.

Note that it is possible to fit or fixed Alpha[n], Beta[n], Tau[n], Phi[n] and Delta[n] with [n]=1 or 2 and then it is possible to use this function to establish the likelihood map for a second or third sinusoids added to the global pattern.

If Delta is not specified, it is estimated from Phi and the same precision as Phi is used.

Usage

```
map_phenology(data = NULL, fitted.parameters = NULL,
  fixed.parameters = NA, Phi = seq(from = 0.2, to = 20, length.out = 100),
  Delta = NULL, infinite = 50, method_incertitude = "convolution",
  zero_counts = TRUE, progressbar = TRUE, cofactors = NULL,
  add.cofactors = NULL, zero = 1e-09)
```

Arguments

data	dataset generated with add_format
fitted.parameters	Set of parameters to be fitted
fixed.parameters	Set of fixed parameters
Phi	Phi values to be analyzed
Delta	Delta value to be analyzed
infinite	Number of iterations for dmnbinom() used for method_incertitude='convolution'
method_incertitude	'combinatory' estimates likelihood of all combinations for nest numbers; 'convolution' [default] uses the exact likelihood of the sum of negative binomial distribution.
zero_counts	Example c(TRUE, TRUE, FALSE) indicates whether the zeros have been recorded for each of these timeseries. Default is TRUE for all.
progressbar	If FALSE, do not show the progress bar

cofactors data.frame with a column Date and a column for each cofactor
 add.cofactors Names of the column of parameter cofactors to use as a cofactor
 zero If the theoretical nest number is under this value, this value will be used

Details

map_phenology generates a likelihood map.

Value

Display a likelihood map

Author(s)

Marc Girondot

Examples

```
library("phenology")
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt",
header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
## Not run:
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)

## End(Not run)
data(result_Gratiot)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot)
# Add constant Alpha and Tau values
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
pfixed<-c(parg1, Alpha=0, Tau=1)
pfixed<-pfixed[-which(names(pfixed)=="Theta")]
# The only fitted parameter will be Beta
parg2<-c(Beta=0.5, parg1["Theta"])
# Generate a likelihood map
# [default Phi=seq(from=0.1, to=20, length.out=100) but it is very long]
# Take care, it takes 20 hours ! The data map_Gratiot has the result
## Not run:
map_Gratiot<-map_phenology(data=data_Gratiot, Phi=seq(from=0.1, to=20, length.out=100),
fitted.parameters=parg2, fixed.parameters=pfixed)
```

```
## End(Not run)
data(map_Gratiot)
# Plot the map
plot(map_Gratiot, col=heat.colors(128))
# Plot the min(-Ln L) for Phi varying at any delta value
plot_phi(map=map_Gratiot)
# Plot the min(-Ln L) for Delta varying with Phi equal to the value for maximum likelihood
plot_delta(map=map_Gratiot)
# Plot the min(-Ln L) for Delta varying with Phi the nearest to 15
plot_delta(map=map_Gratiot, Phi=15)
```

MarineTurtles_2002 *Database of tagged marine turtles in 2002*

Description

Extraction of 2002 PIT tagged marine turtles database

Usage

MarineTurtles_2002

Format

data.frame with 2 columns:

- Date: The date the female has been seen on the beach (morning date of the night)
- ID: The unique identifier of the female

Details

Database of tagged marine turtles in 2002

Author(s)

Marc Girondot

Examples

```
library(phenology)
data(MarineTurtles_2002)
```

MinBMinE_to_Min	<i>Transform a set of parameters from MinB and MinE to Min</i>
-----------------	--

Description

This function is used to transform a set of parameters that uses MinB and MinE to a set of parameters that uses Min.

Usage

```
MinBMinE_to_Min(parameters = stop("A set of parameters must be indicated"))
```

Arguments

parameters Set of current parameters

Details

MinBMinE_to_Min transforms a set of parameters from MinB and MinE to Min

Value

Return a set of modified parameters

Author(s)

Marc Girondot

Examples

```
# Read a file with data
# Gratiot<-read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt", , header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot<-add_phenology(Gratiot, name="Complete", reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot)
# Change the parameters to PMinB and PMinE
parg1<-MinBMinE_to_Min(parameters=parg)
```

outLR

Database of leatherback CMR in French Guiana

Description

Database of leatherback CMR in French Guiana

Usage

outLR

Format

A dataframe with database of leatherback CMR in French Guiana

Details

Database of leatherback CMR in French Guiana

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Rivalan, P., Godfrey, M.H., Prévot-Julliard, A.-C., Girondot, M., 2005. Maximum likelihood estimates of tag loss in leatherback sea turtles. *Journal of Wildlife Management* 69, 540-548.

Examples

```
## Not run:  
library(phenology)  
# Read a file with result  
data(outLR)  
data_f_21 <- Tagloss_format(outLR, model="21")  
  
## End(Not run)
```

par_init	<i>Calculate initial set of parameters.</i>
----------	---

Description

This function is used to generate an initial set of parameters for fitting that is expected to be not too far from the final.

The parameters can be:

- Min, MinE, MinB, PMin, PMinB, PMinE;
- Max;
- Begin, Peak, Flat, End;
- Length, LengthB, LengthE;
- Theta;
- Alpha, Beta, Tau, Phi, Delta;
- Alpha1, Beta1, Tau1, Phi1, Delta1;
- Alpha2, Beta2, Tau2, Phi2, Delta2;
- Alpha3, Beta3, Tau3, Phi3, Delta3;

And the name of level if a cofactor is used.

The parameters Max, Min, MinE, MinB, Length, LengthB, LengthE, and Peak can be followed with `_` and the name of the rookery.

Usage

```
par_init(data = stop("A dataset must be provided"), fixed.parameters = NULL,
         add.cofactors = NULL)
```

Arguments

data	Dataset generated with <code>add_phenology()</code>
fixed.parameters	Set of fixed parameters
add.cofactors	Names of cofactors that will be used (see <code>fit_phenology</code>)

Details

`par_init` calculates initial set of parameters.

Value

The initial set of parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
# Read a file with data
Gratiot <- read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt",
header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Plot the phenology and get some stats
output<-plot(result_Gratiot)

## End(Not run)
```

phenology

Run a shiny application for basic functions of phenology package

Description

Run a shiny application for basic functions of phenology package. Thanks to Adriana Cortés Gomés and Joana Hancock for their help with translation.

Usage

```
phenology()
```

Details

phenology runs a shiny application for basic functions of phenology package

Value

Nothing

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
phenology()

## End(Not run)
```

phenology_MHmcmc *Run the Metropolis-Hastings algorithm for data*

Description

Run the Metropolis-Hastings algorithm for data.
 The number of iterations is $n.iter+n.adapt+1$ because the initial likelihood is also displayed.
 I recommend $thin=1$ because the method to estimate SE uses resampling.
 As initial point is maximum likelihood, $n.adapt = 0$ is a good solution.
 The parameters `intermediate` and `filename` are used to save intermediate results every 'intermediate' iterations (for example 1000). Results are saved in a file of name `filename`.
 The parameter `previous` is used to indicate the list that has been save using the parameters `intermediate` and `filename`. It permits to continue a mcmc search.
 These options are used to prevent the consequences of computer crash or if the run is very very long and computer processes at time limited.

Usage

```
phenology_MHmcmc(result = stop("An output from fit_phenology() must be provided"),
  n.iter = 10000,
  parametersMCMC = stop("A model generated with phenology_MHmcmc_p() must be provided"),
  n.chains = 4, n.adapt = 0, thin = 1, trace = FALSE,
  adaptive = FALSE, adaptive.lag = 500, adaptive.fun = function(x) {
  ifelse(x > 0.234, 1.3, 0.7) }, intermediate = NULL,
  filename = "intermediate.Rdata", previous = NULL)
```

Arguments

<code>result</code>	An object obtained after a SearchR fit
<code>n.iter</code>	Number of iterations for each step
<code>parametersMCMC</code>	A set of parameters used as initial point for searching with information on priors
<code>n.chains</code>	Number of replicates
<code>n.adapt</code>	Number of iterations before to store outputs
<code>thin</code>	Number of iterations between each stored output
<code>trace</code>	TRUE or FALSE, shows progress
<code>adaptive</code>	Should an adaptive process for SDProp be used

adaptive.lag	Lag to analyze the SDProp value in an adaptive content
adaptive.fun	Function used to change the SDProp
intermediate	Period for saving intermediate result, NULL for no save
filename	If intermediate is not NULL, save intermediate result in this file
previous	Previous result to be continued. Can be the filename in which intermediate results are saved.

Details

phenology_MHmcmc runs the Metropolis-Hastings algorithm for data (Bayesian MCMC)

Value

A list with resultMCMC being mcmc.list object, resultLnL being likelihoods and parametersMCMC being the parameters used

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
  reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
  fitted.parameters=parg, fixed.parameters=NULL)
# Generate set of priors for Bayesian analysis
pmcmc <- phenology_MHmcmc_p(result_Gratiot, accept = TRUE)
result_Gratiot_mcmc <- phenology_MHmcmc(result = result_Gratiot, n.iter = 10000,
  parametersMCMC = pmcmc, n.chains = 1, n.adapt = 0, thin = 1, trace = FALSE)
# Get standard error of parameters
summary(result_Gratiot_mcmc)
# Make diagnostics of the mcmc results using coda package
mcmc <- as.mcmc(result_Gratiot_mcmc)
require(coda)
heidel.diag(mcmc)
raftery.diag(mcmc)
autocorr.diag(mcmc)
acf(mcmc[[1]][,"LengthB"], lag.max=200, bty="n", las=1)
acf(mcmc[[1]][,"Max_Gratiot"], lag.max=50, bty="n", las=1)
batchSE(mcmc, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmc)$statistics[,"Time-series SE"]
```



```
plot(result_Gratiot_mcmc, parameters=3, las=1, xlim=c(-10, 300))  
  
## End(Not run)
```

phenology_MHmcmc_p *Generates set of parameters to be used with phenology_MHmcmc()*

Description

Interactive script used to generate set of parameters to be used with phenology_MHmcmc().

Usage

```
phenology_MHmcmc_p(result = stop("An output from fit_phenology() must be provided"),  
accept = FALSE)
```

Arguments

result	An object obtained after a fit_phenology() fit
accept	If TRUE, does not wait for user interaction

Details

phenology_MHmcmc_p generates set of parameters to be used with MHmcmc()

Value

A matrix with the parameters

Author(s)

Marc Girondot

Examples

```
## Not run:  
library(phenology)  
data(Gratiot)  
# Generate a formatted list named data_Gratiot  
data_Gratiot<-add_phenology(Gratiot, name="Complete",  
reference=as.Date("2001-01-01"), format="%d/%m/%Y")  
# Generate initial points for the optimisation  
parg<-par_init(data_Gratiot, fixed.parameters=NULL)  
# Run the optimisation  
result_Gratiot<-fit_phenology(data=data_Gratiot,  
fitted.parameters=parg, fixed.parameters=NULL)  
# Generate set of priors for Bayesian analysis
```

```

pmcmc <- phenology_MHmcmc_p(result_Gratiot, accept = TRUE)
result_Gratiot_mcmc <- phenology_MHmcmc(result = result_Gratiot, n.iter = 10000,
parametersMCMC = pmcmc, n.chains = 1, n.adapt = 0, thin = 1, trace = FALSE)
# Get standard error of parameters
summary(result_Gratiot_mcmc)
# Make diagnostics of the mcmc results using coda package
mcmc <- as.mcmc(result_Gratiot_mcmc)
require(coda)
heidel.diag(mcmc)
raftery.diag(mcmc)
autocorr.diag(mcmc)
acf(mcmc[[1]][,"LengthB"], lag.max=200, bty="n", las=1)
acf(mcmc[[1]][,"Max_Gratiot"], lag.max=50, bty="n", las=1)
batchSE(mcmc, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmc)$statistics[,"Time-series SE"]
plot(result_Gratiot_mcmc, parameters=3, las=1, xlim=c(-10, 300))

## End(Not run)

```

plot.ECFOCF

Plot a result of clutch frequency fit.

Description

This function plots the result of fitCF().
 The result data plots the observed ECF-OCF table.
 The result dataOCF plots the observed OCF table.
 The result dataECF plots the observed ECF table.
 The result CF plots the true clutch frequency.
 The result OCF plots the observed clutch frequency.
 The result ECF plots the estimated clutch frequency.
 The result ECFOCF plots the bivariate observed vs. estimated clutch frequency.
 The result ECFOCF0 plots the bivariate observed vs. estimated clutch frequency without the 0 OCF.
 The result prob plots the probabilities of capture.
 The result period plots the probabilities of nesting according to period.
 If category is left to NA, the compound value for all the population is plotted.
 When result="data" is used, this is a parser for plot.TableECFOCF().
 See this function for the parameters.
 The parameter y.axis is the shift of the x legends for result="prob".

Usage

```

## S3 method for class 'ECFOCF'
plot(x, ..., result = "CF", category = NA, period = 1)

```

Arguments

x	A result for fitCF().
...	Graphic parameters, see plot.TableECFOCF() or par.
result	What result will be plotted: data, dataOCF, dataECF, ECF, OCF, ECFOCF, ECFOCF0, CF, Prob, period
category	What category will be plotted, numeric or NA for all.
period	The period that will be plotted.

Details

plot.ECFOCF plots a result of clutch frequency fit.

Value

Nothing

Author(s)

Marc Girondot

See Also

Other Model of Clutch Frequency: [ECFOCF_f](#), [TableECFOCF](#), [fitCF](#), [lnLCF](#), [logLik.ECFOCF](#), [plot.TableECFOCF](#)

Examples

```
## Not run:
library(phenology)
# Example
data(MarineTurtles_2002)
ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002)
o_mu1p2_NB <- fitCF(x = c(mu = 4.6426989650675701,
                        sd = 75.828239144717074,
                        p1 = 0.62036295627161053,
                        p2 = -2.3923021862881511,
                        OTN = 0.33107456308054345),
                  data=ECFOCF_2002)

par(mar=c(4, 4, 1, 1)+0.4)
plot(o_mu1p2_NB, result="data", category=NA,
     bty="n", las=1, cex.points=3, cex.axis = 0.8)
plot(o_mu1p2_NB, result="data", category=NA,
     bty="n", las=1, cex.points=3, pch=NA,
     col.labels = "red", show.labels=TRUE, cex.0=0.2,
     show.0 = TRUE, col.0="blue", pch.0=4)
plot(o_mu1p2_NB, result="dataOCF", category=NA,
     bty="n", las=1)
plot(o_mu1p2_NB, result="dataECF", category=NA,
     bty="n", las=1)
```

```

plot(o_mu1p2_NB, result="CF", bty="n", las=1)

plot(o_mu1p2_NB, result="OCF", category=1, bty="n", las=1)
plot(o_mu1p2_NB, result="OCF", category=2, bty="n", las=1)

plot(o_mu1p2_NB, result="ECFOCF", bty="n", las=1)

plot(o_mu1p2_NB, result="ECFOCF0", bty="n", las=1)
plot(o_mu1p2_NB, result="ECFOCF0", category=1, bty="n", las=1)
plot(o_mu1p2_NB, result="ECFOCF0", category=2, bty="n", las=1)

plot(o_mu1p2_NB, result="Prob", category=c(1, 2), bty="n", las=1)
plot(o_mu1p2_NB, result="Prob", category=c(2, 1), bty="n", las=1)

## End(Not run)

```

plot.fitRMU

Plot the synthesis of RMU fit.

Description

The function plot.fitRMU plots the results of fitRMU().

Usage

```

## S3 method for class 'fitRMU'
plot(x, ..., what = "proportions", order = NULL,
     control.legend = list(), show.legend = TRUE)

```

Arguments

x	A result file generated by fitRMU
...	Parameters used by plot
what	Can be proportions, numbers or total
order	Give the order of series in plot, from bottom to top. Can be used to not show series.
control.legend	Parameters send to legend
show.legend	If FALSE, does not show legend

Details

plot.fitRMU plots the results of a fit RMU.

Value

Return Nothing

Author(s)

Marc Girondot

See AlsoOther Fill gaps in RMU: [fitRMU_MHmcmc_p](#), [fitRMU_MHmcmc](#), [fitRMU](#), [logLik.fitRMU](#)**Examples**

```
## Not run:
library("phenology")
RMU.names.AtlanticW <- data.frame(mean=c("Yalimapo.French.Guiana",
                                       "Galibi.Suriname",
                                       "Irakumpapy.French.Guiana"),
                                 se=c("se_Yalimapo.French.Guiana",
                                       "se_Galibi.Suriname",
                                       "se_Irakumpapy.French.Guiana"))

data.AtlanticW <- data.frame(Year=c(1990:2000),
                             Yalimapo.French.Guiana=c(2076, 2765, 2890, 2678, NA,
                                                         6542, 5678, 1243, NA, 1566, 1566),
                             se_Yalimapo.French.Guiana=c(123.2, 27.7, 62.5, 126, NA,
                                                         230, 129, 167, NA, 145, 20),
                             Galibi.Suriname=c(276, 275, 290, NA, 267,
                                                  542, 678, NA, 243, 156, 123),
                             se_Galibi.Suriname=c(22.3, 34.2, 23.2, NA, 23.2,
                                                    4.3, 2.3, NA, 10.3, 10.1, 8.9),
                             Irakumpapy.French.Guiana=c(1076, 1765, 1390, 1678, NA,
                                                         3542, 2678, 243, NA, 566, 566),
                             se_Irakumpapy.French.Guiana=c(23.2, 29.7, 22.5, 226, NA,
                                                            130, 29, 67, NA, 15, 20))

cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
             colname.year="Year", model.trend="Constant",
             model.SD="Zero")
expo <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
             colname.year="Year", model.trend="Exponential",
             model.SD="Zero")
YS <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
            colname.year="Year", model.trend="Year-specific",
            model.SD="Zero")
YS1 <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
            colname.year="Year", model.trend="Year-specific",
            model.SD="Zero", model.rookeries="First-order")
YS1_cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
                colname.year="Year", model.trend="Year-specific",
                model.SD="Constant", model.rookeries="First-order",
                parameters=YS1$par)
YS2 <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
            colname.year="Year", model.trend="Year-specific",
            model.SD="Zero", model.rookeries="Second-order",
            parameters=YS1$par)
YS2_cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
```

```

colname.year="Year", model.trend="Year-specific",
model.SD="Constant", model.rookeries="Second-order",
parameters=YS1_cst$par)

compare_AIC(Constant=cst, Exponential=expo,
YearSpecific=YS)

compare_AIC(YearSpecific_ProportionsFirstOrder_Zero=YS1,
YearSpecific_ProportionsFirstOrder_Constant=YS1_cst)

compare_AIC(YearSpecific_ProportionsConstant=YS,
YearSpecific_ProportionsFirstOrder=YS1,
YearSpecific_ProportionsSecondOrder=YS2)

compare_AIC(YearSpecific_ProportionsFirstOrder=YS1_cst,
YearSpecific_ProportionsSecondOrder=YS2_cst)

barplot_errbar(YS1_cst$proportions[1, ], y.plus = YS1_cst$proportions.CI.0.95[1, ],
y.minus = YS1_cst$proportions.CI.0.05[1, ], las=1, ylim=c(0, 0.7),
main="Proportion of the different rookeries in the region")

plot(cst, main="Use of different beaches along the time", what="total")
plot(expo, main="Use of different beaches along the time", what="total")
plot(YS2_cst, main="Use of different beaches along the time", what="total")

plot(YS1, main="Use of different beaches along the time")
plot(YS1_cst, main="Use of different beaches along the time")
plot(YS1_cst, main="Use of different beaches along the time", what="numbers")

parpre <- par(mar=c(4, 4, 2, 5)+0.4)
par(xpd=TRUE)
plot(YS, main="Use of different beaches along the time",
control.legend=list(x=2000, y=0.4, legend=c("Yalimapo", "Galibi", "Irakumpapy")))
par(mar=parpre)

# Example to modify order of series
plot(cst, order=c("Galibi.Suriname", "Irakumpapy.French.Guiana"))
plot(cst, order=c("Galibi.Suriname", "Irakumpapy.French.Guiana", "Yalimapo.French.Guiana"))

## End(Not run)

```

plot.phenology

Plot the phenology from a result.

Description

The function plot.phenology plots the phenology graph from a result object. If cofactors have been added, the plot does not show their effects. plot.objects can be "observations", "ML" for maximum likelihood, "ML.SD" for dispersion of observations, "ML.quantiles" or "MCMC.quantiles" if a mcmc object is given

Usage

```
## S3 method for class 'phenology'
plot(x, ..., series = "all", moon = FALSE,
     replicate.CI = 10000, resultmcmc = NULL, chain = 1,
     replicate.CI.mcmc = "all", level = 0.95,
     plot.objects = c("observations", "ML", "ML.SD", "ML.quantiles",
                      "MCMC.quantiles"), col.ML = "black", col.SD = "red",
     col.MCMC.quantiles = "purple", col.ML.quantiles = "black",
     col.observations = "black", col.grouped.observations = "green")
```

Arguments

x	A result file generated by fit_phenology
...	Parameters used by plot
series	Name or number of series to be plotted or 'all'
moon	If TRUE, the moon phase is plotted. Default is FALSE
replicate.CI	Number of replicates for estimation of confidence interval
resultmcmc	A mcmc object
chain	The number of chain to be used in resultmcmc
replicate.CI.mcmc	Number of iterations to be used or "all"
level	Level to estimate confidence interval or credibility interval
plot.objects	What to plot?
col.ML	Color of the ML mean curve
col.SD	Color of the SD curve (distribution of observations)
col.MCMC.quantiles	Color of the quantiles curve based on mcmc
col.ML.quantiles	Color of the SE curve based on ML
col.observations	Color of the points
col.grouped.observations	Color of the lines indicating grouped observations

Details

plot.phenology plots the phenology.

Value

A list with four objects: synthesis is a data.frame with global estimate of nesting. details_MCMC, details_ML and details_mean are lists with day by day information for each series.

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
# Read a file with data
Gratiot <- read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name = "Complete",
reference = as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Plot the phenology and get some stats
output <- plot(result_Gratiot)
# Plot only part of the nesting season
ptoutput <- plot(result_Gratiot, xlim=c(as.Date("2001-03-01"),as.Date("2001-08-31")))
# Use month names in English
Sys.setlocale(category = "LC_TIME", locale = "en_GB.UTF-8")
output <- plot(result_Gratiot)
# set back the month name in local R language
Sys.setlocale(category = "LC_TIME", locale = "")
# plot based on quantiles of mcmc object
plot(result_Gratiot, resultmcmc=result_Gratiot_mcmc,
      plot.objects=c("observations", "MCMC.quantiles"))
plot(result_Gratiot, resultmcmc=result_Gratiot_mcmc,
      plot.objects=c("observations", "ML.SD", "ML.quantiles"))
plot(result_Gratiot, resultmcmc=result_Gratiot_mcmc,
      plot.objects=c("observations", "ML.SD", "MCMC.quantiles"))
plot(result_Gratiot, resultmcmc=result_Gratiot_mcmc,
      plot.objects=c("observations", "ML.quantiles", "MCMC.quantiles"))

## End(Not run)
```

plot.phenologymap

Plot a likelihood map with Delta and Phi varying.

Description

This function plots a likelihood map obtained after map_phenology.

Usage

```
## S3 method for class 'phenologymap'
plot(x, ..., col = heat.colors(128), xlab = "Phi",
      ylab = "Delta")
```


Arguments

x	A map generated with map_phenology.
...	not used
col	Colors could be heat.colors(128) or rainbow(64) or col=gray(c(seq(0, 1, length.out=128)))
xlab	Label for x axis
ylab	Label for y axis

Details

plot.phenologymap plots a likelihood map with Delta and Phi varying.

Value

Return None

Author(s)

Marc Girondot

Examples

```
## Not run:
library("phenology")
# Read a file with data
Gratiot<-read.delim("http://max2.esse.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot)
# Add constant Alpha and Tau values
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
pfixed<-c(parg1, Alpha=0, Tau=1)
pfixed<-pfixed[-which(names(pfixed)=="Theta")]
# The only fitted parameter will be Beta
parg2<-c(Beta=0.5, parg1["Theta"])
# Generate a likelihood map
# [default Phi=seq(from=0.1, to=20, length.out=100) but it is very long]
# Take care, it takes 20 hours ! The data map_Gratiot has the result
map_Gratiot<-map_phenology(data=data_Gratiot,
Phi=seq(from=0.1, to=20, length.out=100),
fitted.parameters=parg2, fixed.parameters=pfixed)
data(map_Gratiot)
```

```
# Plot the map
plot(map_Gratiot, col=heat.colors(128))

## End(Not run)
```

```
plot.TableECFOCF      Plot a TableECFOCF dataset.
```

Description

This function plots a CMR file summarized using TableECFOCF().

Usage

```
## S3 method for class 'TableECFOCF'
plot(x, ..., result = "ecfocf", period = 1,
     cex.points = 4, pch = 19, col = "black", cex.axis = 0.8,
     cex.labels = 0.5, col.labels = "red", show.labels = FALSE,
     show.0 = FALSE, pch.0 = 4, cex.0 = 0.5, col.0 = "blue")
```

Arguments

x	A CMR file summarized using TableECFOCF()
...	Graphic parameters
result	What should be plotted: ECFOCF, ECF, OCF.
period	The period that will be plotted.
cex.points	The maximum magnification to be used for points relative to the current setting of cex.
pch	Character to be used for points.
col	Color to be used for points.
cex.axis	The magnification to be used for axis annotation relative to the current setting of cex.
cex.labels	The magnification to be used for figures.
col.labels	Color of figures.
show.labels	Logical to be used to show figures.
show.0	Logical to show 0 counts.
pch.0	Character used for 0 counts.
cex.0	The magnification to be used for character for 0 counts.
col.0	Color of characters for 0 counts.

Details

plot.TableECFOCF plots a TableECFOCF dataset.

Value

Nothing

Author(s)

Marc Girondot

See AlsoOther Model of Clutch Frequency: [ECFOCF_f](#), [TableECFOCF](#), [fitCF](#), [lnLCF](#), [logLik.ECFOCF](#), [plot.ECFOCF](#)**Examples**

```
## Not run:
library(phenology)
# Example
data(MarineTurtles_2002)
ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002)
par(mar=c(4, 4, 1, 1)+0.4)
plot(ECFOCF_2002, bty="n", las=1, cex.points=3,
      cex.axis = 0.8, main="Year 2002")
plot(ECFOCF_2002, bty="n", las=1, cex.points=5, cex.0=0.2,
      col="red", show.0 = TRUE, col.0="blue")
plot(ECFOCF_2002, bty="n", las=1, cex.points=3, col="lightgrey",
      col.labels = "red", show.labels=TRUE)
plot(ECFOCF_2002, bty="n", las=1, cex.points=3, pch=NA,
      col.labels = "red", show.labels=TRUE)
plot(ECFOCF_2002, bty="n", las=1, cex.points=3, pch=NA,
      col.labels = "red", show.labels=TRUE, cex.0=0.2,
      show.0 = TRUE, col.0="blue", pch.0=4)
plot(ECFOCF_2002, bty="n", las=1, result="OCF")
plot(ECFOCF_2002, bty="n", las=1, result="ECF")
plot(ECFOCF_2002, bty="n", las=1, result="ECF", type="l", main="2002 season",
      xlab="Clutch frequency")
par(new=TRUE)
plot(ECFOCF_2002, bty="n", las=1, result="OCF", type="l", main="",
      ylim=ScalePreviousPlot()$ylim[c("begin", "end")],
      xlab="", ylab="",
      col="red",
      xaxt="n", yaxt="n", axes=FALSE)
legend("topright", legend=c("OCF", "ECF"), lty=1, col=c("red", "black"))

ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))

plot(ECFOCF_2002, period=13)

## End(Not run)
```

plot.Tagloss *Plot the daily rate of tag loss.*

Description

Plot the daily rate of tag loss.

To use this function without a result of Tagloss_fit(), see the hack in examples.

It does not work still with cumul and LR model.

Usage

```
## S3 method for class 'Tagloss'
plot(x, t = NULL, fitted.parameters = NULL,
     fixed.parameters = NULL, scale = 1, model_before = NULL,
     model_after = NULL, model = c("1", "2", "R1", "R2", "L1", "L2", "cumul",
     "cumul1"), col = grey.colors(4), text.col = rev(grey.colors(4)),
     add = FALSE, hessian = NULL, replicates = 1000, probs = c(0.025,
     0.975), progressbar = FALSE, decoration = FALSE, ...)
```

Arguments

x	Object obtained from Tagloss_fit()
t	Time for which values of model must be plotted
fitted.parameters	Set of parameters
fixed.parameters	Another set of parameters without standard error associated
scale	Scale value. When Cumul is used, scale is always 1.
model_before	Transformation of parameters before to use Tagloss_model()
model_after	Transformation of parameters after to use Tagloss_model()
model	Can be 1, 2, R1, R2, L1, L2 or Cumul (2 tags) or Cumul1 (1 tag)
col	The colors of shading areas of cumul or the color of line
text.col	The text color for cumul model
add	Should the data be added to a previous plot?
hessian	Should confidence interval be shown
replicates	Number of replicates for confidence interval
probs	Quantiles to show for confidence interval
progressbar	Is shown a progressbar?
decoration	Try to add name of parameters on the graph
...	Parameters transmitted to plot

Details

plot.tagloss plots the daily rate of tag loss.

Value

A dataframe with values used for plotting.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_L](#), [Tagloss_daymax](#), [Tagloss_fit](#), [Tagloss_format](#), [Tagloss_model](#), [Tagloss_simulate](#), [logLik.Tagloss](#)

Examples

```
## Not run:
library(phenology)
# Example
t <- 1:1000

par <- c(D1_1=200, D2D1_1=100, D3D2_1=200,
        A_1=-logit(0.02), B_1=-logit(0.05), C_1=-logit(0.07))
phenology::plot.Tagloss(x=list(), t=t, fitted.parameters=par, model="1")
phenology::plot.Tagloss(x=NULL, t=t, fitted.parameters=par, model="1",
                        scale=1000, decoration = TRUE)

par <- c(D1_2=200, D2D1_2=100, D3D2_2=200,
        A_2=-logit(0.05), B_2=-logit(0.03), C_2=-logit(0.03))
phenology::plot.Tagloss(x=list(), t=t, fitted.parameters=par, ylim=c(0, 1),
                        scale = 10, model="2")

par <- c(D1_L2=200, D2D1_L2=100, D3D2_L2=200,
        A_L2=-logit(0.05), B_L2=-logit(0.07), C_L2=-logit(0.07))
phenology::plot.Tagloss(x=list(), t=t, fitted.parameters=par, model="L2")

par <- c(D1_R2=200, D2D1_R2=0, D3D2_R2=700,
        A_R2=-logit(0.02), B_R2=-logit(0.05), C_R2=-logit(0.07))
phenology::plot.Tagloss(x=list(), t=t, fitted.parameters=par, model="R2",
                        col="red", add=TRUE)

par <- c(D1_L1=200, D2D1_L1=2000, D3D2_L1=2000,
        A_L1=-logit(0.05), B_L1=-logit(0.02), C_L1=-logit(0.1))
phenology::plot.Tagloss(x=list(), t=t, fitted.parameters=par, model="L1")

# To plot the history of individuals
par <- c(D1_1=200, D2D1_1=100, D3D2_1=200,
        A_1=-logit(5E-4), B_1=-logit(4E-4), C_1=-logit(5E-4),
        D1_2=200, D2D1_2=100, D3D2_2=200,
        A_2=-logit(6E-4), B_2=-logit(5E-4), C_2=-logit(6E-4))
```

```

phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par, model="Cumul",
                        decoration = TRUE)
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par, model="Cumul",
                        decoration = TRUE, col=c("red", "green", "blue"))

# To plot the history of individuals
par <- c(D1_R1=200, D2D1_R1=100, D3D2_R1=200,
        A_R1=-logit(5E-4), B_R1=-logit(4E-4), C_R1=-logit(5E-4),
        D1_R2=200, D2D1_R2=100, D3D2_R2=200,
        A_R2=-logit(6E-4), B_R2=-logit(5E-4), C_R2=-logit(6E-4),
        D1_L1=200, D2D1_L1=100, D3D2_L1=200,
        A_L1=-logit(5E-4), B_L1=-logit(4E-4), C_L1=-logit(5E-4),
        D1_L2=200, D2D1_L2=100, D3D2_L2=200,
        A_L2=-logit(6E-4), B_L2=-logit(5E-4), C_L2=-logit(6E-4))
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par, model="Cumul",
                        decoration = TRUE)

## End(Not run)

```

plot_delta

Plot a likelihood lineplot obtained after map_phenology.

Description

This function plots a likelihood lineplot obtained after map_phenology.

Usage

```
plot_delta(map = NULL, Phi = NULL, ...)
```

Arguments

map	A map generated with map_phenology
Phi	Phi value or NULL
...	Parameters for plot

Details

plot_delta plots the likelihood delta for fixed Phi value.

Value

Return None

Author(s)

Marc Girondot

Examples

```

## Not run:
library("phenology")
# Read a file with data
Gratiot<-read.delim("http://max2.es.e.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot)
# Add constant Alpha and Tau values
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
pfixed<-c(parg1, Alpha=0, Tau=1)
pfixed<-pfixed[-which(names(pfixed)=="Theta")]
# The only fitted parameter will be Beta
parg2<-c(Beta=0.5, parg1["Theta"])
# Generate a likelihood map
# [default Phi=seq(from=0.1, to=20, length.out=100) but it is very long]
# Take care, it takes 20 hours ! The data map_Gratiot has the result
map_Gratiot<-map_phenology(data=data_Gratiot,
Phi=seq(from=0.1, to=20, length.out=100),
fitted.parameters=parg2, fixed.parameters=pfixed)
data(map_Gratiot)
# Plot the min(-Ln L) for Delta varying with Phi equal to the value for maximum likelihood
plot_delta(map=map_Gratiot)
# Plot the min(-Ln L) for Delta varying with Phi the nearest to 15
plot_delta(map=map_Gratiot, Phi=15)

## End(Not run)

```

plot_phi

Plot the best likelihood for fixed Phi value.

Description

The function "plot_phi" plots the best likelihood for each Phi value.

Usage

```
plot_phi(map = NULL, ...)
```

Arguments

map A map generated with map_phenology
 ... Parameters for plot

Details

plot_phi plots the best likelihood for fixed Phi value.

Value

Return None

Author(s)

Marc Girondot

Examples

```
library("phenology")
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
## Not run:
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)

## End(Not run)
data(result_Gratiot)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot)
# Add constant Alpha and Tau values
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
pfixed<-c(parg1, Alpha=0, Tau=1)
pfixed<-pfixed[-which(names(pfixed)=="Theta")]
# The only fitted parameter will be Beta
parg2<-c(Beta=0.5, parg1["Theta"])
# Generate a likelihood map [default Phi=seq(from=0.1, to=20, length.out=100) but it is very long]
# Take care, it takes 20 hours ! The data map_Gratiot has the result
## Not run:
map_Gratiot<-map_phenology(data=data_Gratiot,
Phi=seq(from=0.1, to=20, length.out=100),
fitted.parameters=parg2, fixed.parameters=pfixed)
```



```
## End(Not run)
data(map_Gratiot)
# Plot the min(-Ln L) for Phi varying at any delta value
plot_phi(map=map_Gratiot)
```

print.phenology	<i>Print the result information from a result x.</i>
-----------------	--

Description

The function print.phenology displays from a result.

Usage

```
## S3 method for class 'phenology'
print(x, ...)
```

Arguments

x	A result file generated by fit_phenology
...	Not used

Details

print.phenology prints the information from a result x.

Value

None

Author(s)

Marc Girondot

Examples

```
library(phenology)
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
```

```

parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
## Not run:
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)

## End(Not run)
data(result_Gratiot)
# Show the result
result_Gratiot

```

`print.phenologymap` *Print information on a phenologymap object.*

Description

`print.phenologymap` print information on a phenologymap object

Usage

```

## S3 method for class 'phenologymap'
print(x, ...)

```

Arguments

<code>x</code>	A map generated with <code>map_phenology</code> .
<code>...</code>	Not used

Value

Return None

Author(s)

Marc Girondot

Examples

```

library("phenology")
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation

```

```

parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
## Not run:
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)

## End(Not run)
data(result_Gratiot)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot)
# Add constant Alpha and Tau values
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
pfixed<-c(parg1, Alpha=0, Tau=1)
pfixed<-pfixed[-which(names(pfixed)=="Theta")]
# The only fitted parameter will be Beta
parg2<-c(Beta=0.5, parg1["Theta"])
# Generate a likelihood map
# [default Phi=seq(from=0.1, to=20, length.out=100) but it is very long]
# Take care, it takes 20 hours ! The data map_Gratiot has the result
## Not run:
map_Gratiot<-map_phenology(data=data_Gratiot,
Phi=seq(from=0.1, to=20, length.out=100), fitted.parameters=parg2,
fixed.parameters=pfixed)

## End(Not run)
data(map_Gratiot)
# Print the information on a map
map_Gratiot

```

```
print.phenologyout      Print the information from a ouput x.
```

Description

The function `print.phenologyout` displays the output from a plot.

Usage

```
## S3 method for class 'phenologyout'
print(x, ...)
```

Arguments

<code>x</code>	An output generated by <code>plot_phenology</code>
<code>...</code>	Not used

Details

`print.phenologyout` prints the information from a result `x`.

Value

None

Author(s)

Marc Girondot

Examples

```
library(phenology)
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.esse.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Plot the phenology and get some stats
output <- plot(result_Gratiot)
# Show the output
output

## End(Not run)
```

remove_site

Removes site information from a set of parameters.

Description

This function is used to remove the information of the site from a set of parameters. It can be used to other timeseries after.

Usage

```
remove_site(parameters = NULL, help = FALSE)
```

Arguments

parameters	Set of parameters
help	If TRUE, an help is displayed

Details

remove_site removes beach information from a set of parameters.

Value

Return a set of modified parameters

Author(s)

Marc Girondot

Examples

```
library(phenology)
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.esse.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
## Not run:
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)

## End(Not run)
data(result_Gratiot)
# Extract parameters from result
parg<-extract_result(result_Gratiot)
# Remove site information
parg1<-remove_site(parg)
```

result_Gratiot

Result of the fit of Leatherback nest counts

Description

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1 The phenology has been fitted with MinE, MinB, Max, Flat, LengthB, LengthE, Peak, Theta.

Usage

result_Gratiot

Format

A list with Gratiot data and the result of the fit.

Details

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Gratiot, N., Gratiot, J., de Thoisy, B. & Kelle, L. 2006. Estimation of marine turtles nesting season from incomplete data ; statistical adjustment of a sinusoidal function. *Animal Conservation*, 9, 95-102.

Examples

```
## Not run:
library(phenology)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
# Read a file with result
data(result_Gratiot)

## End(Not run)
```

result_Gratiot1

Result of the fit of Leatherback nest counts

Description

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1 The phenology has been fitted with MinE, MinB, Max, Flat, LengthB, LengthE, Peak, Theta, Alpha, Beta, Tau, Phi, Delta

Usage

result_Gratiot1

Format

A list with Gratiot data and the result of the fit.

Details

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Gratiot, N., Gratiot, J., de Thoisy, B. & Kelle, L. 2006. Estimation of marine turtles nesting season from incomplete data ; statistical adjustment of a sinusoidal function. *Animal Conservation*, 9, 95-102.

Examples

```
library(phenology)
# Read a file with result
data(result_Gratiot1)
```

result_Gratiot2	<i>Result of the fit of Leatherback nest counts</i>
-----------------	---

Description

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1 The phenology has been fitted with MinE, MinB, Max, Flat, LengthB, LengthE, Peak, Theta, Alpha, Beta, Tau, Phi, Delta, Alpha1, Beta1, Tau1, Phi1, Delta1.

Usage

```
result_Gratiot2
```

Format

A list with Gratiot data and the result of the fit.

Details

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Gratiot, N., Gratiot, J., de Thoisy, B. & Kelle, L. 2006. Estimation of marine turtles nesting season from incomplete data ; statistical adjustment of a sinusoidal function. *Animal Conservation*, 9, 95-102.

Examples

```
library(phenology)
# Read a file with result
data(result_Gratiot2)
```

result_Gratiot_Flat *Result of the fit of Leatherback nest counts*

Description

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1. The phenology has been fitted with MinE, MinB, Max, LengthB, LengthE, Peak, Theta. The Flat parameter is set to 0 and is not fitted.

Usage

```
result_Gratiot_Flat
```

Format

A list with Gratiot data and the result of the fit.

Details

Result of the fit of Leatherback nest counts from Gratiot et al. (2006) Figure 1

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Gratiot, N., Gratiot, J., de Thoisy, B. & Kelle, L. 2006. Estimation of marine turtles nesting season from incomplete data ; statistical adjustment of a sinusoidal function. *Animal Conservation*, 9, 95-102.

Examples

```
library(phenology)
# Read a file with result
data(result_Gratiot_Flat)
```

result_Gratiot_mcmc *Result of the mcmc for Leatherback nest counts*

Description

Result of the mcmc for Leatherback nest counts from Gratiot et al. (2006) Figure 1 The phenology has been fitted with MinE, MinB, Max, Flat, LengthB, LengthE, Peak, Theta.

Usage

```
result_Gratiot_mcmc
```

Format

A mcmcComposite object with mcmc result.

Details

Result of the mcmc for Leatherback nest counts from Gratiot et al. (2006) Figure 1

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

References

Gratiot, N., Gratiot, J., de Thoisy, B. & Kelle, L. 2006. Estimation of marine turtles nesting season from incomplete data ; statistical adjustment of a sinusoidal function. *Animal Conservation*, 9, 95-102.

Examples

```
## Not run:
library(phenology)
data(result_Gratiot)
# Read a file with data
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg <- par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
# generate data for mcmc run
pmcmc <- phenology_MHmcmc_p(result_Gratiot, accept = TRUE)
result_Gratiot_mcmc <- phenology_MHmcmc(result = result_Gratiot,
n.iter = 10000,
```

```

      adaptive=TRUE,
      parametersMCMC = pmcmc,
      n.chains = 1, n.adapt = 0, thin = 1, trace = FALSE)
# Read a file with result
data(result_Gratiot_mcmc)
1-rejectionRate(as.mcmc(result_Gratiot_mcmc))

summary(result_Gratiot, resultmcmc=result_Gratiot_mcmc)

## End(Not run)

```

shift_sinusoid *Shift sinusoid information.*

Description

This function is used to shift sinusoid parameters from ", '1' or '2'.

Usage

```
shift_sinusoid(parameters = NULL, from = "", to = "1")
```

Arguments

parameters	set of parameters
from	The number of series to change
to	The number of series to change

Details

shift_sinusoid shift sinusoid information.

Value

Return a set of modified parameters

Author(s)

Marc Girondot

Examples

```

# Read a file with data
library("phenology")
## Not run:
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)

```

```

# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Fix parameter Flat to 0
pfixed=c(Flat=0)
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=pfixed)
# Fit is done
## Not run:
result_Gratiot_Flat<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=pfixed)

## End(Not run)
data(result_Gratiot_Flat)
parg<-extract_result(result_Gratiot_Flat)
# Add data for one sinusoid superimposed
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
parg<-c(parg, Alpha=0.5, Beta=0.8, Delta=3, Phi=15)
# Tau is fixed to 1
pfixed=c(Flat=0, Tau=1)
# Run the optimisation
## Not run:
result_Gratiot1<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=pfixed)
# Plot the phenology
output1<-plot(result_Gratiot1, moon=TRUE)
#'
## End(Not run)
data(result_Gratiot1)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot1)
# Shift sinusoid information to the '1'
parg2<-shift_sinusoid(parameters=parg1, from="", to="1")
# Tau is fixed to 1
pfixed=c(Flat=0, Tau1=1, Tau=1)
# Add data for another sinusoid superimposed
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
parg<-c(parg2, Alpha=0.5, Beta=0.8, Delta=3, Phi=10)
# Run the optimisation
## Not run:
result_Gratiot2<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=pfixed)
# Plot the phenology
output2<-plot(result_Gratiot2, moon=TRUE)

## End(Not run)
data(result_Gratiot2)

```

Description

The function `summary.phenology` shows result and estimates confidence interval.

Usage

```
## S3 method for class 'phenology'
summary(object, resultmcmc = NULL, chain = 1,
        series = "all", replicate.CI.mcmc = "all", replicate.CI = 10000,
        level = 0.95, print = TRUE, ...)
```

Arguments

<code>object</code>	A result file generated by <code>fit_phenology</code>
<code>resultmcmc</code>	A mcmc object
<code>chain</code>	The number of chain to be used in <code>resultmcmc</code>
<code>series</code>	Names of the series to be analyzed or "all"
<code>replicate.CI.mcmc</code>	Number of iterations to be used or "all"
<code>replicate.CI</code>	Number of replicates for ML resampling
<code>level</code>	Level to estimate confidence interval or credibility interval
<code>print</code>	Should information be shown
<code>...</code>	Not used

Details

`summary.phenology` prints the information from a result object.

Value

A list with four objects: `synthesis` is a data.frame with global estimate of nesting. `details_MCMC`, `details_ML` and `details_mean` are lists with day by day information for each series.

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
# Read a file with data
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
```

```

# Run the optimisation
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Display information from the result
summary(result_Gratiot)
# Using mcmc
summary(result_Gratiot, resultmcmc=result_Gratiot_mcmc)

## End(Not run)

```

summary.phenologymap *Print information on a phenologymap object.*

Description

summary.phenologymap print information on a phenologymap object

Usage

```

## S3 method for class 'phenologymap'
summary(object, ...)

```

Arguments

object	A map generated with map_phenology.
...	Not used

Value

Return None

Author(s)

Marc Girondot

Examples

```

library("phenology")
# Read a file with data
## Not run:
Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)

## End(Not run)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot<-add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation

```

```

parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
## Not run:
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)

## End(Not run)
data(result_Gratiot)
# Extract the fitted parameters
parg1<-extract_result(result_Gratiot)
# Add constant Alpha and Tau values
# [day d amplitude=(Alpha+Nd*Beta)^Tau with Nd being the number of counts for day d]
pfixed<-c(parg1, Alpha=0, Tau=1)
pfixed<-pfixed[-which(names(pfixed)=="Theta")]
# The only fitted parameter will be Beta
parg2<-c(Beta=0.5, parg1["Theta"])
# Generate a likelihood map
# [default Phi=seq(from=0.1, to=20, length.out=100) but it is very long]
# Take care, it takes 20 hours ! The data map_Gratiot has the result
## Not run:
map_Gratiot<-map_phenology(data=data_Gratiot,
Phi=seq(from=0.1, to=20, length.out=100),
fitted.parameters=parg2, fixed.parameters=pfixed)

## End(Not run)
data(map_Gratiot)
# Print the information on a map
summary(map_Gratiot)

```

summary.phenologyout *Print the summary information from a ouput object.*

Description

The function summary.phenologyout displays the output from a plot.

Usage

```

## S3 method for class 'phenologyout'
summary(object, ...)

```

Arguments

object	An output generated by plot.phenology() ou summary.phenology()
...	Not used

Details

summary.phenologyout prints the information from a result object.

Value

None

Author(s)

Marc Girondot

Examples

```
## Not run:
library(phenology)
# Read a file with data
Gratiot<-read.delim("http://max2.esse.u-psud.fr/epc/conservation/BI/Complete.txt", header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
data_Gratiot <- add_phenology(Gratiot, name="Complete",
reference=as.Date("2001-01-01"), format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot, fixed.parameters=NULL)
# Run the optimisation
result_Gratiot <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)
data(result_Gratiot)
# Plot the phenology and get some stats
output <- plot(result_Gratiot)
# Show the output
summary(output)

## End(Not run)
```

TableECFOCF

Format a CMR dataset into a file that fitCF can use.

Description

This function formats a CMR dataset to a file that fitCF can use.

If date0 is not null, a 3D TableECFOCF is generated.

3D table (ECF, OCF, period) has two attributes:

- table with 4 elements:

begin, end are the first and last elements with counts

min and max are the first and last period where a nest could have been laid based on MaxNests value

- characteristics with 5 elements:

MinimumDaysBetween2Nest, MeanDaysBetween2Nest MaxNests, date0, length_season

p parameter can be setup to +Inf until begin and after end

Usage

```
TableECFOCF(data = stop("A dataframe with a column 'ID' and a column 'Date'"),
  columnID = "ID", columnDate = "Date", MinimumDaysBetween2Nest = 7,
  MeanDaysBetween2Nest = 9.8, MaxNests = 15, date0 = NULL,
  length_season = floor(365/MeanDaysBetween2Nest) + 1)
```

Arguments

data	CMR file.
columnID	Name of the column in data for unique identifier of females.
columnDate	Name of the column in data for morning date when female has been seen on the beach.
MinimumDaysBetween2Nest	Number of minimum days between two nests.
MeanDaysBetween2Nest	Average number of days between two nests.
MaxNests	Maximum number of nests by a female.
date0	Date for the ordinal day 0.
length_season	The total length of season based on groups of interclutch intervals.

Details

TableECFOCF formats a CMR dataset into a file that fitCF can use.

Value

Return a matrix with counts for all OCF and ECF combinations.

Author(s)

Marc Girondot

See Also

Other Model of Clutch Frequency: [ECFOCF_f](#), [fitCF](#), [lnLCF](#), [logLik.ECFOCF](#), [plot.ECFOCF](#), [plot.TableECFOCF](#)

Examples

```
## Not run:
library(phenology)
# Example
data(MarineTurtles_2002)
ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002)
plot(ECFOCF_2002)
ECFOCF_2002 <- TableECFOCF(MarineTurtles_2002, date0=as.Date("2002-01-01"))
plot(ECFOCF_2002, period=11)

## End(Not run)
```

Tagloss_daymax	<i>Return the maximum number of days an individual has been observed in a dataset.</i>
----------------	--

Description

This function must be used to get the value of mx in Tagloss_L.

Usage

```
Tagloss_daymax(individuals)
```

Arguments

individuals Set of individuals

Details

Tagloss_daymax returns the maximum number of days an individual has been observed in a dataset.

Value

Return the maximum number of days an individual has been observed in a dataset.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_L](#), [Tagloss_fit](#), [Tagloss_format](#), [Tagloss_model](#), [Tagloss_simulate](#), [logLik.Tagloss](#), [plot.Tagloss](#)

Examples

```
## Not run:  
library(phenology)  
# Example  
data_f_21 <- Tagloss_format(outLR, model="21")  
daymax(data_f_21)  
  
## End(Not run)
```

Tagloss_fit *fit a model of tag loss using a CMR database.*

Description

This function fits a model of tag loss using a CMR database.

The names of parameters can be:

Left tag lost when 2 are present: D1_L2, D2D1_L2, D3D2_L2, A_L2, B_L2, C_L2, delta_L2

Right tag lost when 2 are present: D1_R2, D2D1_R2, D3D2_R2, A_R2, B_R2, C_R2, delta_R2

Left tag lost when 1 is present: D1_L1, D2D1_L1, D3D2_L1, A_L1, B_L1, C_L1, delta_L1

Right tag lost when 1 is present: D1_R1, D2D1_R1, D3D2_R1, A_R1, B_R1, C_R1, delta_R1

One tag lost when 2 are present: D1_2, D2D1_2, D3D2_2, A_2, B_2, C_2, delta_2

One tag lost when 1 is present: D1_1, D2D1_1, D3D2_1, A_1, B_1, C_1, delta_1

A, B and C are $-\logit(pA)$, $-\logit(pB)$ and $-\logit(pC)$ of the corresponding daily probabilities (p) of tag loss.

delta is used as: $p = p * \text{invlogit}(-\text{delta})$

The use of delta parameter is complicated.

Tag loss rate is pA at day 1

Tag loss rate changes gradually from pA to pB that is reached at day D1

Tag loss rate is pB from day D1 to day D2=D1+D2D1

Tag loss rate changes gradually from pB to pC that is reached at day D2+D3D2

If only one parameter is fitted, method must be "Brent" and upper and lower parameters must be set up with finite values.

Usage

```
Tagloss_fit(data = stop("A database formatted using Tagloss_format() must be used"),
  fitted.parameters = NULL, fixed.parameters = NULL, model_before = NULL,
  model_after = NULL, control = list(trace = 1, maxit = 10000),
  method = "Nelder-Mead", lower = -Inf, upper = Inf, hessian = FALSE,
  cores = detectCores(all.tests = FALSE, logical = TRUE), groups = NULL)
```

Arguments

data	An object formatted using Tagloss_format
fitted.parameters	Set of parameters to be fitted
fixed.parameters	Set of fixed parameters
model_before	Transformation of parameters before to use Tagloss_model()
model_after	Transformation of parameters after to use Tagloss_model()
control	Control parameters to be send to optim()
method	optim() method
lower	Lower value for parameter when Brent method is used

upper	Upper value for parameter when Brent method is used
hessian	Does the hessian matrix should be estimated
cores	Number of cores to use for parallel computing
groups	Number of groups for parallel computing

Details

Tagloss_fit fits a model of tag loss using a CMR database.

Value

Return a list object with the model describing tag loss.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_L](#), [Tagloss_daymax](#), [Tagloss_format](#), [Tagloss_model](#), [Tagloss_simulate](#), [logLik.Tagloss](#), [plot.Tagloss](#)

Examples

```
## Not run:
library(phenology)
# Example
data_f_21 <- Tagloss_format(outLR, model="21")
# Without the N20 the computing is much faster
data_f_21_fast <- subset(data_f_21, subset=(is.na(data_f_21$N20)))
par <- structure(c(48.8292784204825, 1039.02842229274, -89.3162940697861,
5.21817463244988, 8.00575451188548, 8.32971268127933, 161.265553603601,
602.935748681661, 2643.57415102633, 16.752815732218, 10.181616195839,
7.14279063312016), .Names = c("D1_2", "D2D1_2", "D3D2_2", "A_2",
"B_2", "C_2", "D1_1", "D2D1_1", "D3D2_1", "A_1", "B_1", "C_1"))
o <- Tagloss_fit(data=data_f_21_fast, fitted.parameters=par)
plot(o, model="1", col="red")
plot(o, model="2", col="blue", add=TRUE)
legend("topright", legend=c("2->1", "1->0"), lty=1, col=c("blue", "red"))

## End(Not run)
```

Tagloss_format	<i>Format a CMR dataset into a file that Tagloss_L can use.</i>
----------------	---

Description

This function formats a CMR dataset to a file that Tagloss_L can use.

The format of data is a data.frame with 4 columns:

ID is the column with the permanent identification code

L is the column with the non-permanent code located at left

R is the column with the non-permanent code located at right

Date is the column with the date of observation

Note that R and L columns can be exchanged if 21 model is used.

Usage

```
Tagloss_format(data, model = "21", progressbar = TRUE)
```

Arguments

data	CMR file
model	Can be "21" or "LR"
progressbar	Is a progressbar been shown?

Details

Tagloss_format formats a CMR dataset into a file that Tagloss_L can use.

Value

Return the maximum number of days an individual has been observed in a dataset.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_L](#), [Tagloss_daymax](#), [Tagloss_fit](#), [Tagloss_model](#), [Tagloss_simulate](#), [logLik.Tagloss](#), [plot.Tagloss](#)

Examples

```
## Not run:  
library(phenology)  
# Example  
data_f_21 <- Tagloss_format(outLR, model="21")  
  
## End(Not run)
```

Tagloss_L	<i>Return the -log likelihood of a set of individuals under a model of tagloss.</i>
-----------	---

Description

This function must be used within `optim()`.
`model_before` is applied to the `par` parameter.
`model_after` is applied after `par` is separated in `p1`, `p2`, `pL1`, `pL2`, `pR1` and `pR2` parameters.
`progressbar` is set to `FALSE` if `cores` is different from 1.

Usage

```
Tagloss_L(individuals, par, days.maximum = NULL, fixed.parameters = NULL,
          model_before = NULL, model_after = NULL, names.par = NULL,
          groups = NULL, cores = detectCores(all.tests = FALSE, logical = TRUE),
          progressbar = FALSE)
```

Arguments

<code>individuals</code>	Set of individuals
<code>par</code>	Set of parameters
<code>days.maximum</code>	Maximum number of days. Can be determined using <code>Tagloss_daymax()</code>
<code>fixed.parameters</code>	Set of fixed parameters
<code>model_before</code>	Transformation of parameters before to use <code>Tagloss_model()</code>
<code>model_after</code>	Transformation of parameters after to use <code>Tagloss_model()</code>
<code>names.par</code>	Name of parameters. Normally unused.
<code>groups</code>	Number of groups for parallel computing
<code>cores</code>	Number of cores to use for parallel computing
<code>progressbar</code>	Is shown a progressbar?

Details

`Tagloss_L` returns the -log likelihood of a set of individuals under a model of tagloss.

Value

Return the -log likelihood of a set of individuals

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_daymax](#), [Tagloss_fit](#), [Tagloss_format](#), [Tagloss_model](#), [Tagloss_simulate](#), [logLik.Tagloss](#), [plot.Tagloss](#)

Examples

```
## Not run:
library(phenology)

# Example with 21 format of data

data_f_21 <- Tagloss_format(outLR, model="21")
par <- structure(c(49.5658922243074, 808.136085362158, 106.283783786853,
5.22150592456511, 8.00608716525864, 8.32718202233396, 150.612916258503,
715.865805125223, 2242.06574225966, 119.212383120678, 10.1860735529433,
7.14231725937626), .Names = c("D1_2", "D2D1_2", "D3D2_2", "A_2",
"B_2", "C_2", "D1_1", "D2D1_1", "D3D2_1", "A_1", "B_1", "C_1"))
pfixed <- NULL
# All the data are analyzed; the N20 are very long to compute
Tagloss_L(individuals=data_f_21, par=par, days.maximum=Tagloss_daymax(data_f_21),
fixed.parameters=pfixed, cores=1, progressbar=TRUE)
# Without the N20 the computing is much faster
data_f_21_fast <- subset(data_f_21, subset=(is.na(data_f_21$N20)))
Tagloss_L(individuals=data_f_21_fast, par=par, days.maximum=Tagloss_daymax(data_f_21_fast),
fixed.par=pfixed, cores=1, progressbar=TRUE)
o <- Tagloss_fit(data=data_f_21_fast, fitted.parameters=par)
# Here it is the result of the previous function
o <- structure(list(par = structure(c(49.5658922243074, 808.136085362158,
106.283783786853, 5.22150592456511, 8.00608716525864, 8.32718202233396,
150.612916258503, 715.865805125223, 2242.06574225966, 119.212383120678,
10.1860735529433, 7.14231725937626), .Names = c("D1_2", "D2D1_2",
"D3D2_2", "A_2", "B_2", "C_2", "D1_1", "D2D1_1", "D3D2_1", "A_1",
"B_1", "C_1")), value = 5841.93084262461, counts = structure(c(1093L,
NA), .Names = c("function", "gradient")), convergence = 0L, message = NULL,
hessian = structure(c(0.0469808583147824, 0.000133240973809734,
6.68478605803102e-05, -2.53581288234273, -1.25931342154217,
-0.124650568977813, -2.46700437855907e-05, -1.11413100967184e-05,
-3.18323145620525e-06, 0, -0.0182945996130002, -0.00510601694259094,
0.000133240973809734, 1.45519152283669e-05, 7.50333128962666e-06,
-0.00452587300969753, -0.0191316757991444, -0.0255117811320815,
-1.13686837721616e-06, -1.36424205265939e-06, -2.27373675443232e-07,
0, 0.000335830918629654, -0.000448608261649497, 6.68478605803102e-05,
7.50333128962666e-06, 4.32009983342141e-06, -0.00226373231271282,
-0.00954059942159802, -0.0127809016703395, -4.54747350886464e-07,
-4.54747350886464e-07, -2.27373675443232e-07, 0, 0.000176896719494835,
-0.000224190443987027, -2.53581288234273, -0.00452587300969753,
-0.00226373231271282, 223.422489398217, 41.4073996353181,
3.77875949197914, 0.000986460690910462, 0.000398813426727429,
0.000117665877041873, 0, 0.727547330825473, 0.194675862985605,
-1.25931342154217, -0.0191316757991444, -0.00954059942159802,
41.4073996353181, 189.534394394286, 28.3386068531399, 0.00216437001654413,
0.00241834641201422, 0.000652562448522076, 0, 0.841939595375152,
```

```

1.0472297162778, -0.124650568977813, -0.0255117811320815,
-0.0127809016703395, 3.77875949197914, 28.3386068531399,
70.250493081403, -0.00022441781766247, -0.000161662683240138,
0.000257614374277182, 0, -0.578908839088399, 1.08917492980254,
-2.46700437855907e-05, -1.13686837721616e-06, -4.54747350886464e-07,
0.000986460690910462, 0.00216437001654413, -0.00022441781766247,
0.000148247636388987, 0.000145519152283669, 3.97903932025656e-05,
0, 0.0156976511789253, 0.0678746800986119, -1.11413100967184e-05,
-1.36424205265939e-06, -4.54747350886464e-07, 0.000398813426727429,
0.00241834641201422, -0.000161662683240138, 0.000145519152283669,
0.000145519152283669, 3.9676706364844e-05, 0, 0.0138438736030366,
0.0678776359563926, -3.18323145620525e-06, -2.27373675443232e-07,
-2.27373675443232e-07, 0.000117665877041873, 0.000652562448522076,
0.000257614374277182, 3.97903932025656e-05, 3.9676706364844e-05,
1.77351466845721e-05, 0, 0.00317095327773131, 0.0316927071253303,
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, -0.0182945996130002,
0.000335830918629654, 0.000176896719494835, 0.727547330825473,
0.841939595375152, -0.578908839088399, 0.0156976511789253,
0.0138438736030366, 0.00317095327773131, 0, 8.85630879565724,
4.44044781033881, -0.00510601694259094, -0.000448608261649497,
-0.000224190443987027, 0.194675862985605, 1.0472297162778,
1.08917492980254, 0.0678746800986119, 0.0678776359563926,
0.0316927071253303, 0, 4.44044781033881, 88.8524673428037
), .Dim = c(12L, 12L), .Dimnames = list(c("D1_2", "D2D1_2",
"D3D2_2", "A_2", "B_2", "C_2", "D1_1", "D2D1_1", "D3D2_1",
"A_1", "B_1", "C_1"), c("D1_2", "D2D1_2", "D3D2_2", "A_2",
"B_2", "C_2", "D1_1", "D2D1_1", "D3D2_1", "A_1", "B_1", "C_1"
))), .Names = c("par", "value", "counts", "convergence",
"message", "hessian"), class = "Tagloss")
par(mar=c(4, 4, 1, 1))
plot(o, t=1:3000, model="2", scale=1000, ylim=c(0, 3),
     col="red")
plot(o, t=1500:3000, model="1", scale=1000,
     add=TRUE)
legend("topright", legend=c("2 -> 1", "1 -> 0"), col=c("red", "black"), lty=1)

plot(o, t=1:300, model="2", scale=1000, ylim=c(0, 3),
     col="red", hessian=o$hessian)
plot(o, t=1:300, model="1", scale=1000,
     add=TRUE, hessian=o$hessian)
legend("topright", legend=c("2 -> 1", "1 -> 0"), col=c("red", "black"), lty=1)

##### Example with fixed.parameters

data_f_21 <- Tagloss_format(outLR, model="21")
# Without the N20 the computing is much faster
data_f_21_fast <- subset(data_f_21, subset=(is.na(data_f_21$N20)))
par <- structure(c(49.5658922243074, 5.22150592456511, 8.00608716525864,
                  50.612916258503, 6, 9),
                .Names = c("D1_2", "A_2", "B_2",
                          "D1_1", "A_1", "B_1"))
pfixed <- c(D2D1_2=10000, D3D2_2=10000, C_2=0, D2D1_1=10000, D3D2_1=10000, C_1=0)
o <- Tagloss_fit(data=data_f_21_fast, fitted.parameters=par, fixed.parameters=pfixed)

```

```

# Here it is the result of the previous function
o <- structure(list(par = structure(c(55.2184044121564, 5.2630294044259,
8.13359029885985, 14269.9757684677, 21.8702023948044, 6.46586480967269
), .Names = c("D1_2", "A_2", "B_2", "D1_1", "A_1", "B_1")), value = 5853.64634357369,
counts = structure(c(757L, NA), .Names = c("function", "gradient"
)), convergence = 0L, message = NULL, hessian = structure(c(0.036636720324168,
-2.26385645873961, -1.2330608569755, -2.95585778076202e-06,
-2.27373675443232e-07, -0.0399197688238928, -2.26385645873961,
232.345637869003, 47.1904784262733, 0.000118689058581367,
7.50333128962666e-06, 1.69928603099834, -1.2330608569755,
47.1904784262733, 304.432723851278, 0.000196678229258396,
1.36424205265939e-06, 2.8553522497532, -2.95585778076202e-06,
0.000118689058581367, 0.000196678229258396, 4.54747350886464e-07,
0, 0.00741636085876962, -2.27373675443232e-07, 7.50333128962666e-06,
1.36424205265939e-06, 0, 4.00177668780088e-05, 8.79936123965308e-05,
-0.0399197688238928, 1.69928603099834, 2.8553522497532, 0.00741636085876962,
8.79936123965308e-05, 107.941018768543), .Dim = c(6L, 6L), .Dimnames = list(
c("D1_2", "A_2", "B_2", "D1_1", "A_1", "B_1"), c("D1_2",
"A_2", "B_2", "D1_1", "A_1", "B_1"))), .Names = c("par",
"value", "counts", "convergence", "message", "hessian"), class = "Tagloss")
par(mar=c(4, 4, 1, 1))
plot(o, t=1:3000, model="2", scale=1000, ylim=c(0, 3),
col="red")
plot(o, t=1500:3000, model="1", scale=1000,
add=TRUE)
legend("topright", legend=c("2 -> 1", "1 -> 0"), col=c("red", "black"), lty=1)

plot(o, t=1:300, model="2", scale=1000, ylim=c(0, 3),
col="red", hessian=o$hessian)
plot(o, t=1:300, model="1", scale=1000,
add=TRUE, hessian=o$hessian)
legend("topright", legend=c("2 -> 1", "1 -> 0"), col=c("red", "black"), lty=1)

##### Example with delta

data_f_21 <- Tagloss_format(outLR, model="21")
# Without the N20 the computing is much faster
data_f_21_fast <- subset(data_f_21, subset=(is.na(data_f_21$N20)))
par <- structure(c(45.8764973711504, 5.22489974562498, 8.07602162728874,
-0.865444694177429), .Names = c("D1_2", "A_2", "B_2", "delta"
))
pfixed <- c(D2D1_2=10000, D3D2_2=10000, C_2=0)
o <- Tagloss_fit(data=data_f_21_fast, fitted.parameters=par, fixed.parameters=pfixed)
# Here it is the result of the previous function
o <- structure(list(par = structure(c(45.9035484983855, 5.22576211343279,
8.07585745169786, -0.865706100004634), .Names = c("D1_2", "A_2",
"B_2", "delta")), value = 5913.716964613, counts = structure(c(91L,
NA), .Names = c("function", "gradient")), convergence = 0L, message = NULL,
hessian = structure(c(0.0644593001197791, -2.88983483187621,
-1.49161280660337, -0.0875163550517755, -2.88983483187621,
221.02317802819, 45.3729608125286, 3.73816044429987, -1.49161280660337,
45.3729608125286, 440.129730122862, 30.4781699469459, -0.0875163550517755,
3.73816044429987, 30.4781699469459, 9.47964940678503), .Dim = c(4L,

```



```

    4L), .Dimnames = list(c("D1_2", "A_2", "B_2", "delta"), c("D1_2",
      "A_2", "B_2", "delta"))), .Names = c("par", "value", "counts",
      "convergence", "message", "hessian"), class = "Tagloss")
par(mar=c(4, 4, 1, 1))
plot(o, t=1:3000, model="2", scale=1000, ylim=c(0, 3),
      col="red")
plot(o, t=1:3000, model="1", scale=1000, col="blue",
      add=TRUE, hessian=o$hessian)
legend("topright", legend=c("2 -> 1", "1 -> 0"), col=c("red", "black"), lty=1)

##### Example with model_after
data_f_LR <- Tagloss_format(outLR, model="LR")
par <- structure(c(72.0399239978454, 58.1034231071992, 645.068735669251,
  5.10791337470247, 3538.47220045768, 7.83358940767931),
  .Names = c("D1_L2", "D2D1_L2", "D3D2_L2", "A_L2", "B_L2", "C_L2"))
pfixed <- NULL
# A progress bar can be shown when one core is used
system.time(
print(Tagloss_L(individuals=data_f_LR, par=par, days.maximum=Tagloss_daymax(data_f_LR),
  fixed.parameters=pfixed, cores=1, model_after="pR2=pL2;pR1=pL2;pL1=pL2",
  progressbar = TRUE))
)
# When parallel computing is done, no progress bar can be shown
system.time(
print(Tagloss_L(individuals=data_f_LR, par=par, days.maximum=Tagloss_daymax(data_f_LR),
  fixed.parameters=pfixed, model_after="pR2=pL2;pR1=pL2;pL1=pL2"))
)
# The NLR_00 are very long to calculate
data_f_LR_fast <- subset(data_f_LR, subset=(is.na(data_f_LR$NLR_00)))
system.time(
print(Tagloss_L(individuals=data_f_LR_fast, par=par, days.maximum=Tagloss_daymax(data_f_LR_fast),
  fixed.parameters=pfixed, model_after="pR2=pL2;pR1=pL2;pL1=pL2"))
)
o <- Tagloss_fit(data=data_f_LR_fast,
  fitted.parameters=par, fixed.parameters=pfixed,
  model_after="pR2=pL2;pR1=pL2;pL1=pL2")

par(mar=c(4, 4, 1, 1))
plot(o, t=1:3000, model="2", scale=1000, ylim=c(0, 3),
      col="red")

## End(Not run)

```

Tagloss_LengthObs	<i>Return a list with the number of days different kinds of individuals are seen.</i>
-------------------	---

Description

Usefull to summarize data

Usage

```
Tagloss_LengthObs(data, progressbar = TRUE)
```

Arguments

data	Set of individuals
progressbar	Is shown a progressbar?

Details

Tagloss_LengthObs returns a list with the number of days different kinds of individuals are seen.

Value

Return a list with the number of days different kinds of individuals are seen.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_L](#), [Tagloss_daymax](#), [Tagloss_fit](#), [Tagloss_format](#), [Tagloss_model](#), [Tagloss_simulate](#), [logLik.Tagloss](#), [plot.Tagloss](#)

Examples

```
## Not run:  
library(phenology)  
# Example  
data_f_21 <- Tagloss_format(outLR, model="21")  
Tagloss_LengthObs(data_f_21)  
  
## End(Not run)
```

Tagloss_model	<i>Return the daily rate of tag loss.</i>
---------------	---

Description

This function compute a model of daily tag loss rate for days t based on a set of parameters, par.

Usage

```
Tagloss_model(t, par)
```

Arguments

t Time for which values of model must be estimated
 par Parameter

Details

Tagloss_model returns the daily rate of tag loss.

Value

Return the daily rate of tag loss.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_L](#), [Tagloss_daymax](#), [Tagloss_fit](#), [Tagloss_format](#), [Tagloss_simulate](#), [logLik.Tagloss](#), [plot.Tagloss](#)

Examples

```
library(phenology)
## Not run:
# Example
t <- 1:1000
par <- c(D1=200, D2D1=100, D3D2=200,
        A=-logit(0.02), B=-logit(0.05), C=-logit(0.07))
y <- Tagloss_model(t, par)
plot(x=t, y, type="l")

## End(Not run)
```

Tagloss_simulate	<i>Return a list with the number of days different kinds of individuals are seen.</i>
------------------	---

Description

Generate data with known features.

model_before is applied to par parameter.

model_after is applied after par is separated in p1, p2, pL1, pL2, pR1 and pR2 parameters.

pobservation can be a vector of daily probabilities to be captured. The last value is repeated if necessary.

The maximum number of days of observation is exp(LengthObservation["max"]).

If model="12" then par must have _1 and _2 parameters.

if model="LR" then par must have _L2, _L1, _R2, R1 parameters.

Usage

```
Tagloss_simulate(n = 500, par, pobobservation = c(rep(0.05, 70), 0.01),
  LengthObservation = c(min = 0, max = 9), dailysurvival = 0.999,
  model = "12", model_before = NULL, model_after = NULL,
  progressbar = TRUE)
```

Arguments

n	Number of individuals to simulate
par	Set of parameters
pobobservation	Probability of daily observation
LengthObservation	The log of number of days of observations is a random number between min and max
dailysurvival	Daily probability of survival
model	Must be "12" or "LR"
model_before	Transformation of parameters before to use Tagloss_model()
model_after	Transformation of parameters after to use Tagloss_model()
progressbar	Is a progressbar should be shown?

Details

Tagloss_simulate returns a list with the number of days different kinds of individuals are seen.

Value

Return a list with the number of days different kinds of individuals are seen.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs](#), [Tagloss_L](#), [Tagloss_daymax](#), [Tagloss_fit](#), [Tagloss_format](#), [Tagloss_model](#), [logLik.Tagloss](#), [plot.Tagloss](#)

Examples

```
library(phenology)
## Not run:
# Example
par <- structure(c(49.5658922243074, 808.136085362158, 106.283783786853,
5.22150592456511, 8.00608716525864, 8.32718202233396, 150.612916258503,
715.865805125223, 2242.06574225966, 119.212383120678, 10.1860735529433,
7.14231725937626), .Names = c("D1_2", "D2D1_2", "D3D2_2", "A_2",
"B_2", "C_2", "D1_1", "D2D1_1", "D3D2_1", "A_1", "B_1", "C_1"))
cmr <- Tagloss_simulate(n=500,
```

```

                                par=par, model="12")
cmr_f <- Tagloss_format(cmr, model="12")

## End(Not run)

```

toggle_Min_PMin	<i>Transform a set of parameters from Min, MinB or MinE to PMin, PminB or PminE, or reverse</i>
-----------------	---

Description

This function is used to transform a set of parameters that uses Min, MinB or MinE to a set of parameters that uses PMin, PminB or PminE, or reverse.

Usage

```
toggle_Min_PMin(parameters = stop("A set of parameters must be indicated"))
```

Arguments

parameters Set of current parameters

Details

toggle_Min_PMin transforms a set of parameters from Min, MinB or MinE to PMin, PminB or PminE, or reverse

Value

Return a set of modified parameters

Author(s)

Marc Girondot

Examples

```

# Read a file with data
# Gratiot<-read.delim("http://max2.ese.u-psud.fr/epc/conservation/BI/Complete.txt", , header=FALSE)
data(Gratiot)
# Generate a formatted list named data_Gratiot
refdate <- as.Date("2001-01-01")
data_Gratiot<-add_phenology(Gratiot, name="Complete", reference=refdate, format="%d/%m/%Y")
# Generate initial points for the optimisation
parg<-par_init(data_Gratiot)
# Change the parameters to PMinB and PMinE
parg1<-toggle_Min_PMin(parameters=parg)
# And change back to MinB and MinE
parg2<-toggle_Min_PMin(parameters=parg1)

```

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