

Package ‘phenology’

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

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phenology-package	<i>Tools to Manage a Parametric Function that Describes Phenology and More</i>
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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.

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

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

```
install.packages("http://www.ese.u-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:	7.6 build 1168
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License: GPL (>= 2)
 LazyLoad: yes

Author(s)

Marc Girondot <marc.girondot@universite-paris-saclay.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.
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- 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

- Girondot, M., Rivalan, P., Wongsopawiro, R., Briane, J.-P., Hulin, V., Caut, S., Guirlet, E. & Godfrey, M. H. 2006. Phenology of marine turtle nesting revealed by a statistical model of the nesting season. *BMC Ecology*, 6, 11.
- Delcroix, E., Bédél, S., Santelli, G., Girondot, M., 2013. Monitoring design for quantification of marine turtle nesting with limited human effort: a test case in the Guadeloupe Archipelago. *Oryx* 48, 95-105.
- 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

See Also

Other Phenology model: `AutoFitPhenology()`, `BE_to_LBLE()`, `Gratiot`, `LBLE_to_BE()`, `LBLE_to_L()`, `L_to_LBLE()`, `MarineTurtles_2002`, `MinBMinE_to_Min()`, `add_SE()`, `add_phenology()`, `extract_result()`, `fit_phenology()`, `likelihood_phenology()`, `logLik.phenology()`, `map_Gratiot`, `map_phenology()`, `par_init()`, `phenology2fitRMU()`, `phenology_MHmcmc_p()`, `phenology_MHmcmc()`, `phenology()`, `plot.phenologymap()`, `plot.phenology()`, `plot_delta()`, `plot_phi()`, `print.phenologymap()`, `print.phenologyout()`, `print.phenology()`, `remove_site()`, `result_Gratiot1`, `result_Gratiot2`, `result_Gratiot_Flat`, `result_Gratiot_mcmc`, `result_Gratiot`, `summary.phenologymap()`, `summary.phenologyout()`, `summary.phenology()`

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")
```

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

The `colname.Date` included the dates in the format specified by the parameter `format`. If the number of nests is known for an exact date, 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 `sep.dates` character.

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

Note that date in the `colname.Date` column can be already formatted and in this case the parameter `format` is ignored.

The colname.Number includes the number of nests observed for this date or this range of dates. The colname.Rookery is optional and includes the name of the rookeries.

If only two columns are indicated, the name can be indicated as a parameter of the function with the parameter 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 colname.Rookery column.

#' The model cannot be fitted if a timeseries has no observation because the trivial solution is of course with max=0. The solution is to include a fake false observation at the closest position of the peak, and then the estimated number of nests/tracks will be the estimated number - 1.

If include0 is TRUE, then the series with no observation are included and one observation is added at the monitored date the closest of datepeakfor0.

The normal way to manage such a situation is as followed:

- 1- Format data with include0 being FALSE
- 2- Fit parameters using `fdf <- fit_phenology()`
- 3- Format data with include0 being TRUE and `datepeakfor0=fdf$par["Peak"]`
- 4- Fix previously fitted parameters using `pfixed <- fdf$par`
- 5- Generate new set of parameters with `par_init(data, fixed.parameters=pfixed)`
- 6- Run again `fit_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 parameter, the third column has priority.

Two different timeseries MUST have different name and characters _ and space are forbidden in timeseries names. They are automatically changed if they are present.

Usage

```
add_phenology(
  add = NULL,
  name = "Site",
  reference = NULL,
  month_ref = NULL,
  sep.dates = "-",
  colname.Date = 1,
  colname.Number = 2,
  colname.Rookery = 3,
  format = "%d/%m/%Y",
  previous = NULL,
  include0 = FALSE,
  datepeakfor0 = NULL,
  expandRange0Observation = TRUE,
  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
colname.Date	Name or number of column with dates
colname.Number	Name or number of column with numbers
colname.Rookery	Name or number of column with rookery names
format	The format of the dates
previous	Previous data formatted with add_phenology or NULL [default] if no previous data exist
include0	Does timeseries with only 0 should be included?
datepeakfor0	If series with no observation are included, where add a 1 value in ordinal date (see description)
expandRange0Observation	If TRUE, the range of date with 0 observations are expanded into individual dates
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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
## Not run:
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)
# 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)

#####
# Example of use of include0 and datepeakfor0
#####
# Let create a times series with only 0
data0 <- data.frame(Date=c("11/3/2015", "12/3/2015", "13/3/2015-18/3/2015", "25/3/2015"),
Number=c(0, 0, 0, 0),
Beach=rep("Site", 4), stringsAsFactors=FALSE)
# Here I don't include beach with no observation: error message
try1 <- add_phenology(data0, format="%d/%m/%Y", month_ref=1, include0=FALSE)
# Here I include timeseries with no observation
try1 <- add_phenology(data0, format="%d/%m/%Y", month_ref=1, include0=TRUE, datepeakfor0=100)
try1 <- add_phenology(data0, format="%d/%m/%Y", month_ref=1, include0=TRUE, datepeakfor0=73)
try1 <- add_phenology(data0, format="%d/%m/%Y", month_ref=1, include0=TRUE, datepeakfor0=70)
# It can be done in two steps
try1 <- add_phenology(data0, format="%d/%m/%Y", month_ref=1, include0=TRUE)
try2 <- add_phenology(previous=try1, include0=TRUE, datepeakfor0=100)
# Here I include the series without observation
try1 <- add_phenology(add=data0, format="%d/%m/%Y", month_ref=1,
include0=TRUE, expandRange0observation=TRUE)

## End(Not run)
```

add_SE

Add standard error for a fixed parameter.

Description

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

Usage

```
add_SE(fixed.parameters = NULL, parameters = NULL, SE = NULL)
```

Arguments

<code>fixed.parameters</code>	Set of fixed parameters
<code>parameters</code>	Set of current parameters
<code>SE</code>	Standard error value to be added

Details

`add_SE` adds standard error for a fixed parameter.

Value

The parameters set with the new SE value

Author(s)

Marc Girondot

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library(phenology)
# Generate a set of fixed parameter: Flat and Min
pfixed<-c(Flat=0, Min=0)
# Add SE for the Flat parameter
pfixed<-add_SE(fixed.parameters=pfixed, parameters="Flat", SE=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 <code>add_phenology()</code>
progressbar	If FALSE, do not show the progress bar
...	Parameters for <code>fit_phenology()</code>

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

See Also

Other Phenology model: [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

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

```
Bayesian.remigration Return a posterior remigration interval.
```

Description

Model of remigration interval

Usage

```
Bayesian.remigration(
  parameters = stop("Priors must be supplied"),
  data = stop("data must be supplied"),
  kl = NULL,
  n.iter = 1e+05,
  n.chains = 1,
  n.adapt = 10000,
  thin = 1,
  trace = 10,
  adaptive = TRUE,
  adaptive.lag = 500,
  adaptive.fun = function(x) { ifelse(x > 0.234, 1.3, 0.7) },
  intermediate = NULL,
  filename = "intermediate.Rdata",
  previous = NULL
)
```

Arguments

parameters	Priors for Bayesian MCMC
data	Data to be fitted
kl	Maximum number of years for remigration intervals.
n.iter	Number of iterations for MCMC
n.chains	Number of replicates
n.adapt	Number of iterations before to store outputs
thin	Number of iterations between each stored output
trace	Or FALSE or period to show progress
adaptive	Should an adaptive process for SDProp be used
adaptive.lag	Lag to analyze the SDProp value in an adaptive context
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

Bayesian.remigration fits a remigration interval using Bayesian MCMC

Value

Return a posterior remigration interval.

Author(s)

Marc Girondot

See Also

Other Model of Remigration Interval: [LnRI_norm\(\)](#), [RI\(\)](#), [plot.Remigration\(\)](#)

Examples

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

# Each year a fraction of 0.9 is surviving
s <- c(s=0.9)
# Probability of tag retention; 0.8
t <- c(t=0.8)
# Time-conditional return probability - This is the true remigration rate
r <- c(r1=0.1, r2=0.8, r3=0.7, r4=0.7, r5=1)
# Capture probability
p <- c(p1=0.6, p2=0.6, p3=0.6, p4=0.6, p5=0.6)
# Number of observations for 400 tagged females after 1, 2, 3, 4, and 5 years
OBS <- c(400, 10, 120, 40, 20, 10)

kl_s <- length(s)
kl_t <- length(t)
kl_r <- length(r)
kl_p <- length(p)

pMCMC <- data.frame(Density=c("newdbeta", "newdbeta", rep("dunif", kl_r),
                           rep("newdbeta", kl_p), "dunif"),
                   Prior1=c(s, t, rep(0, kl_r), rep(0.2, kl_p), 0),
                   Prior2=c(0.02, 0.02, rep(1, kl_r), rep(0.08, kl_p), 10),
                   SDProp=c(0.05, 0.05, rep(0.05, kl_r), rep(0.05, kl_p), 0.05),
                   Min=c(0, 0, rep(0, kl_r), rep(0, kl_p), 0),
                   Max=c(1, 1, rep(1, kl_r), rep(1, kl_p), 10),
                   Init=c(s, t, r, p, 1), stringsAsFactors = FALSE,
                   row.names=c("s",
                               "t",
                               names(r),
                               names(p), "sd")
                   )
rMCMC <- Bayesian.remigration(parameters = pMCMC,
```

```

n.iter = 1000000,
n.adapt = 300000,
trace=10000,
data=OBS)

plot(rMCMC)

## 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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
## Not run:
# 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)
# 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)
```

CI.RMU

Calculate the confidence interval of the results of fitRMU()

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 correspondence between mean, se and density for each rookery are given in the RMU.names data.frame.

This data.frame must have a column named mean, another named se and a third named density. If no sd column exists, no sd will be considered for the series and if no density column exists, it will be considered as being "dnorm".

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.

Variance for each value is additive based on both the observed SE (in the RMU.data object) and a constant value dependent on the rookery when model.SD is equal to "Rookery-constant". The value is a global constant when model.SD is "global-constant". The value is proportional to the observed number of nests when model.SD is "global-proportional" with aSD_*observed+SD_ with aSD_ and SD_ being fitted values. This value is fixed to zero when model.SD is "Zero".

If replicate.CI is 0, no CI is estimated, and only point estimation is returned.

Usage

```
CI.RMU(
  result = stop("A result obtained from fitRMU is necessary"),
  resultMCMC = NULL,
  chain = 1,
  replicate.CI = 10000,
  silent = FALSE
)
```

Arguments

result	A result of fitRMu()
resultMCMC	A results of fitRMU_MHmcmc()
chain	Number of MCMC chain to be used
replicate.CI	Number of replicates
silent	If TRUE does not display anything

Details

CI.RMU calculates the confidence interval of the results of fitRMU()

Value

Return a list with Total, Proportions, and Numbers

Author(s)

Marc Girondot

See Also

Other Fill gaps in RMU: [fitRMU_MHmcmc_p\(\)](#), [fitRMU_MHmcmc\(\)](#), [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"),
                                  density=c("density_Yalimapo.French.Guiana",
                                             "density_Galibi.Suriname",
                                             "density_Irakumpapy.French.Guiana"),
                                  stringsAsFactors = FALSE)

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),
density_Yalimapo.French.Guiana=rep("dnorm", 11),
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),
density_Galibi.Suriname=rep("dnorm", 11),
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),
density_Irakumpapy.French.Guiana=rep("dnorm", 11), stringsAsFactors = FALSE
)

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)))

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

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")

# Gamma distribution should be used for MCMC outputs

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"),
density=c("density_Yalimapo.French.Guiana",
"density_Galibi.Suriname",
"density_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),
density_Yalimapo.French.Guiana=rep("dgamma", 11),
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),
density_Galibi.Suriname=rep("dgamma", 11),
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),
density_Irakumpapy.French.Guiana=rep("dgamma", 11)
)
cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
colname.year="Year", model.trend="Constant",

```

```

                                model.SD="Zero")

## 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 μ_{season} and sd_{season} are equal to NA , the model is not temporalized.
 If μ_{season} and sd_{season} are not NA , the model is temporalized.

Usage

```

ECFOCF_f(
  mu,
  sd = NA,
  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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library(phenology)
## Not run:
# 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)
# 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 mu and sd 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 mu1, sd1 and mu2, sd2 indicates that two categories of females with different clutch frequencies distribution are present. Similarly p1 and p2 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 $ONT1/(ONT1+1)$ and for category 2 is $1/(ONT1+1)$. 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,
  verbose = FALSE
)
```

Arguments

x Initial parameters to be fitted

<code>fixed.parameters</code>	Parameters that are fixed.
<code>data</code>	CMR data formatted using <code>TableECFOCF()</code>
<code>method</code>	Method to be used by <code>optimx()</code>
<code>control</code>	List of controls for <code>optimx()</code>
<code>itnmax</code>	A vector with maximum iterations for each method.
<code>hessian</code>	Logical to estimate SE of parameters
<code>parallel</code>	If TRUE, will use parallel computing for <code>ECFOCF_f()</code>
<code>verbose</code>	If TRUE, print the parameters at each step

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)

# Paraetric model for clutch frequency
o_mu1p1_Cfp <- fitCF(x = c(mu = 2.1653229641404539,
  sd = 1.1465246643327098,
  p = 0.25785366120357966),
  fixed.parameters=NULL,
  data=ECFOCF_2002, hessian = TRUE)

# Non parametric model for clutch frequency
o_mu1p1_Cfnp <- fitCF(x = c(mu.1 = 18.246619595610383,
  mu.2 = 4.2702163522832892,
  mu.3 = 2.6289986859556458,
  mu.4 = 3.2496360919228611,
  mu.5 = 2.1602522716550943,
  mu.6 = 0.68617023351032846,
  mu.7 = 4.2623607001877026,
  mu.8 = 1.1805600042630455,
  mu.9 = 2.2786176350939731,
  mu.10 = 0.47676265496204945,
  mu.11 = 5.8988238539197062e-08,
  mu.12 = 1.4003187851424953e-07,
  mu.13 = 2.4128444894899776e-07,
  mu.14 = 2.4223748020049825e-07,
  p = 0.32094401970037578),
  fixed.parameters=c(mu.15 = 1E-10),
  data=ECFOCF_2002, hessian = TRUE)

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_CFp,
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("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)
par <- c(par, fp[attributes(ECFOCF_2002)$table["begin"]]:
        attributes(ECFOCF_2002)$table["end"]])
# The value of p (logit -capture probability) out of the period
# of monitoring is set to +Inf (capture probability=1)
# to indicate that no turtle is nesting in the period out of
# monitoring time
# p is set to -Inf (capture probability=0) to indicate that no
# monitoring has been done but some turtles could have been present.
fixed.parameters <- c(p=+Inf)
# The fitted values are:
par <- c(mu = 2.4911638591178051,
        sd = 0.96855483039640977,
        mu_season = 13.836059118657793,
        sd_season = 0.17440085345943984,
        p.10 = 1.3348233607728222,
        p.11 = 1.1960387774393837,
        p.12 = 0.63025680979544774,
        p.13 = 0.38648155002707452,

```


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 correspondence between mean, se and density for each rookery are given in the RMU.names data.frame.

This data.frame must have a column named mean, another named se and a third named density. If no sd column exists, no sd will be considered for the series and if no density column exists, it will be considered as being "dnorm".

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.

Variance for each value is additive based on both the observed SE (in the RMU.data object) and a value.

The value is a global constant when model.SD is "global-constant". The value is proportional to the observed number of nests when model.SD is "global-proportional" with $aSD_ * observed + SD_$ with aSD_ and SD_ being fitted values. This value is fixed to zero when model.SD is "Zero".

The value is dependent on the rookery when model.SD is equal to "Rookery-constant" or "Rookery-proportional" with a similar formula as previously described for "global".

Usage

```
fitRMU(
  RMU.data = stop("data parameter must be provided"),
  years.byrow = TRUE,
  RMU.names = NULL,
  model.trend = "Constant",
  model.rookeries = "Constant",
  model.SD = "Global-constant",
  parameters = NULL,
  fixed.parameters = NULL,
  SE = NULL,
  method = c("Nelder-Mead", "BFGS"),
  control = list(trace = 1),
  itnmax = c(1500, 1500),
  cptmax.optim = 100,
```

```

    limit.cpt.optim = 1e-05,
    hessian = TRUE,
    replicate.CI = 1000,
    colname.year = "Year",
    maxL = 1e+09
  )

```

Arguments

RMU.data	A data.frame with a column Year (the name is defined in colname.year) and one to three columns per rookery defined in RMU.names
years.byrow	If TRUE, the RMU.data data.frame is organized with years in rows
RMU.names	A dataframe with one to three columns indicating name of columns for mean, standard deviation, and distribution for roockeris
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, Global-constant, Global-proportional or Rookery-constant. See description.
parameters	Parameters to fit
fixed.parameters	Parameters that are fixed
SE	Parameters SE for example from fitRMU_MHmcmc()
method	Methods to be used by optimx()
control	List of controls for optimx()
itnmax	A vector with maximum iterations for each method.
cptmax.optim	How many times optim can be ran when likelihood is better.
limit.cpt.optim	Limit to consider that likelihood is better.
hessian	If TRUE, the hessian matrix is calculated and then the standard error of parameters.
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
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


```

density=c("density_Yalimapo.French.Guiana",
          "density_Galibi.Suriname",
          "density_Irakumpapy.French.Guiana"),
stringsAsFactors = FALSE)

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),
  density_Yalimapo.French.Guiana=rep("dgamma", 11),
  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),
  density_Galibi.Suriname=rep("dgamma", 11),
  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),
  density_Irakumpapy.French.Guiana=rep("dgamma", 11), stringsAsFactors = FALSE
)
cst <- fitRMU(RMU.data=data.AtlanticW, RMU.names=RMU.names.AtlanticW,
  colname.year="Year", model.trend="Constant",
  model.SD="Zero")

## 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() must be provided"),

```



```

n.iter = 10000,
parametersMCMC = stop("A parameter set from fitRMU_MHmcmc_p() must be provided"),
n.chains = 1,
n.adapt = 0,
thin = 1,
adaptive = FALSE,
adaptive.lag = 500,
adaptive.fun = function(x) { ifelse(x > 0.234, 1.3, 0.7) },
trace = FALSE,
traceML = 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
adaptive	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
trace	TRUE or FALSE or period, shows progress
traceML	TRUE or FALSE to show ML
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: `CI.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"),
  density = "dunif",
```

```

    accept = FALSE
  )

```

Arguments

result	An object obtained after a fitRMU() fit
density	Preset of density; can be dnorm or dunif
accept	If TRUE, does not wait for use 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: [CI.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 syntax is :

```
Result <- fit_phenology(data=dataset, fitted.parameters=par, fixed.parameters=pfixed, trace=1, 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. Default is TRUE for all.

hessian = FALSE does not estimate Hessian matrix and SE of parameters.

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

Special section about cofactors:

cofactors must be a data.frame with a column Date and a column for each cofactor

add.cofactors are the names of the column of parameter cofactors to use as a cofactor;

The model is then: parameter[add.cofactors] * cofactor[, add.cofactors]

If the name of the parameter is paste0(add.cofactors, "multi"), then the model is:

parameter[paste0(add.cofactors, "multi")] * cofactor[, add.cofactors] * (number of nests without cofactor)

Usage

```

fit_phenology(
  data = file.choose(),
  fitted.parameters = NULL,
  fixed.parameters = NULL,
  tol = 1e-06,
  zero_counts = TRUE,
  store.intermediate = FALSE,
  file.intermediate = "Intermediate.rda",
  parallel = TRUE,
  hessian = TRUE,
  silent = FALSE,
  growlnotify = TRUE,
  cofactors = NULL,
  add.cofactors = NULL,

```

```

    zero = 1e-09,
    lower = 0,
    upper = Inf,
    control = list(trace = 1, REPORT = 1, maxit = 1000),
    method = c("Nelder-Mead", "L-BFGS-B")
)

```

Arguments

data	A dataset generated by add_format
fitted.parameters	Set of parameters to be fitted
fixed.parameters	Set of fixed parameters
tol	Tolerance of recurrence for dSnbinom() used for convolution 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.
store.intermediate	TRUE or FALSE to save the intermediates
file.intermediate	Name of the file where to save the intermediates as a list
parallel	If FALSE, no parallel computing is done to evaluate likelihood
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
lower	Lower bound for each parameter
upper	Upper bound for each parameter
control	List for control parameters for optim
method	Method used by optim. Several can be setup.

Details

fit_phenology fits parameters to timeseries.

Value

Return a list of with data and result

Author(s)

Marc Girondot

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
## Not run:
library(phenology)
# 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)
# or
output <- summary(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")
# I keep only High tide level
td2 <- td[td$Tide=="High Tide", ]
# I get the date
td3 <- cbind(td2, Date=as.Date(td2$Date.Time))
td4 <- td3[(as.POSIXlt(td3$Date.Time)$hou<10) | (as.POSIXlt(td3$Date.Time)$hou>15), ]
td5 <- aggregate(x=td4[, c("Date", "Date.Time", "Level")],
by=list(Date=td4[, "Date"]), FUN=max)[, 2:4]
with(td5, plot(Date.Time, Level, type="l"))
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)

parg <- par_init(data_Gratiot, fixed.parameters=NULL, add.cofactors="Levelmulti")
```

```

result_Gratiot_CF2 <- fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL, cofactors=td6,
add.cofactors="Level")
compare_AIC(WithoutCF=result_Gratiot, WithCF2=result_Gratiot_CF2)
plot(result_Gratiot_CF2)

# 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="Complete1",
                             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_Complete1=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)

# An example with bimodality

g <- Gratiot
g[30:60, 2] <- sample(10:20, 31, replace = TRUE)
data_g <- add_phenology(g, name="Complete", reference=as.Date("2001-01-01"),
                        format="%d/%m/%Y")
parg <- c('Max.1_Complete' = 5.6344636692341856,
          'MinB.1_Complete' = 0.15488810581002324,
          'MinE.1_Complete' = 0.2,
          'LengthB.1' = 22.366647176407636,
          'Peak.1' = 47.902473939250036,
          'LengthE.1' = 17.828495918533015,
          'Max.2_Complete' = 33.053364083447434,
          'MinE.2_Complete' = 0.42438173496989717,
          'LengthB.2' = 96.651564706802702,
          'Peak.2' = 175.3451874571835,
          'LengthE.2' = 62.481968743789835,
          'Theta' = 3.6423908093342572)
pfixed <- c('MinB.2_Complete' = 0,
           'Flat.1' = 0,
           'Flat.2' = 0)
result_g <- fit_phenology(data=data_g, fitted.parameters=p0, fixed.parameters=pfixed)
plot(result_g)

## End(Not run)

```

fixed.parameters0 *Generate a set of fixed parameters for series with only 0 counts*

Description

This function generates a set of fixed parameters for series with only 0 counts. The parameter series must be a result from add_phenology().

Usage

```
fixed.parameters0(  
  series = stop("A result from add_phenology() must be provided.")  
)
```

Arguments

series Set of series generated with add_phenology()

Details

fixed.parameters0 generates a set of fixed parameters for series with only 0 counts

Value

Return a set of parameters

Author(s)

Marc Girondot

Examples

```
## Not run:  
refdate <- as.Date("2001-01-01")  
data_Gratiot <- add_phenology(Gratiot, name="Complete",  
reference=refdate, format="%d/%m/%Y")  
pfixed <- fixed.parameters0(data_Gratiot)  
  
## 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.

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library(phenology)
# Read a file with data
data(Gratiot)
```

 IPFit

Fit a model of Interesting Period for marine turtles.

Description

This function fits a model of interesting period using maximum likelihood or using Metropolis-Hastings algorithm with Bayesian model.

The fit using maximum likelihood is not the best strategy because the objective function is based on a stochastic model (and then a single set of parameters does not produce exactly the same output each time). The use of Metropolis-Hastings algorithm (a Markov chain Monte Carlo method) should be preferred.

Usage

```
IPFit(
  x = NULL,
  fixed.parameters = NULL,
  data = stop("Formatted data must be provided"),
  method = c("Nelder-Mead", "BFGS"),
  control = list(trace = 1, REPORT = 100, maxit = 500),
  itnmax = c(500, 100),
  hessian = TRUE,
  verbose = TRUE,
  parallel = TRUE,
  model = c("MH", "ML"),
  parametersMH,
  n.iter = 10000,
  n.chains = 1,
  n.adapt = 100,
  thin = 30,
  trace = TRUE,
  adaptive = TRUE,
  adaptive.lag = 500,
  adaptive.fun = function(x) { ifelse(x > 0.234, 1.3, 0.7) },
  intermediate = NULL,
  filename = "intermediate.Rdata"
)
```

Arguments

x	Initial parameters to be fitted
fixed.parameters	Parameters that are fixed.
data	Data as a vector
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
verbose	If TRUE, show the parameters for each tested model
parallel	If TRUE, will use parallel computing
model	Can be ML for Maximum likelihood or MH for Metropolis Hastings
parametersMH	The priors. See MHalgoGen
n.iter	See MHalgoGen
n.chains	See MHalgoGen
n.adapt	See MHalgoGen
thin	See MHalgoGen
trace	See MHalgoGen
adaptive	See MHalgoGen
adaptive.lag	See MHalgoGen
adaptive.fun	See MHalgoGen
intermediate	See MHalgoGen
filename	See MHalgoGen

Details

IPFit fit a model of Interesting Period for marine turtles.

Value

Return a list of class IP with the fit informations and the fitted model.

Author(s)

Marc Girondot

See Also

Other Model of Interesting Period: [IPModel\(\)](#), [IPPredict\(\)](#), [plot.IP\(\)](#), [summary.IP\(\)](#)

Examples

```
## Not run:
library(phenology)
# Example
data <- structure(c(`0` = 0, `1` = 47, `2` = 15, `3` = 6, `4` = 5, `5` = 4,
  `6` = 2, `7` = 5, `8` = 57, `9` = 203, `10` = 205, `11` = 103,
  `12` = 35, `13` = 24, `14` = 12, `15` = 10, `16` = 13, `17` = 49,
  `18` = 86, `19` = 107, `20` = 111, `21` = 73, `22` = 47, `23` = 30,
  `24` = 19, `25` = 17, `26` = 33, `27` = 48, `28` = 77, `29` = 83,
  `30` = 65, `31` = 37, `32` = 27, `33` = 23, `34` = 24, `35` = 22,
  `36` = 41, `37` = 42, `38` = 44, `39` = 33, `40` = 39, `41` = 24,
```

```

`42` = 18, `43` = 18, `44` = 22, `45` = 22, `46` = 19, `47` = 24,
`48` = 28, `49` = 17, `50` = 18, `51` = 19, `52` = 17, `53` = 4,
`54` = 12, `55` = 9, `56` = 6, `57` = 11, `58` = 7, `59` = 11,
`60` = 12, `61` = 5, `62` = 4, `63` = 6, `64` = 11, `65` = 5,
`66` = 6, `67` = 7, `68` = 3, `69` = 2, `70` = 1, `71` = 3, `72` = 2,
`73` = 1, `74` = 2, `75` = 0, `76` = 0, `77` = 3, `78` = 1, `79` = 0,
`80` = 2, `81` = 0, `82` = 0, `83` = 1), Year = "1994",
Species = "Dermochelys coriacea",
location = "Yalimapo beach, French Guiana",
totalnumber = 2526L, class = "IP")
par(mar=c(4, 4, 1, 1)+0.4)
plot(data, xlim=c(0,100))
text(100, 190, labels=bquote(italic(.(attributes(data)$Species))), pos=2)
text(100, 150, labels=attributes(data)$location, pos=2, cex=0.8)
text(100, 110, labels=paste0(as.character(attributes(data)$totalnumber), " females"), pos=2)

##### Fit using Maximum-Likelihood

par <- c(meanIP = 9.8229005713237623,
sdIP = 0.079176011861863474,
minIP = 6.8128364577569309,
pAbort = 1.5441529841959203,
meanAbort = 2.7958742380756121,
sdAbort = 0.99370406770777175,
pCapture = -0.80294884905867658,
meanECF = 4.5253772889275758,
sdECF = 0.20334743335612529)

fML <- IPFit(x=par,
fixed.parameters=c(N=20000),
data=data,
verbose=FALSE,
model="ML")

# Plot the fitted ECF
plot(fML, result="ECF")

# Plot the Internesting Period distribution
plot(fML, result="IP")

# Plot the distribution of days between tentatives
plot(fML, result="Abort", xlim=c(0, 15))
#'
##### Fit using ML and non parametric ECF

par <- c(ECF.2 = 0.044151921569961131,
ECF.3 = 2.0020778325280748,
ECF.4 = 2.6128345101617083,
ECF.5 = 2.6450582416622375,
ECF.6 = 2.715198206774927,
ECF.7 = 2.0288031327239904,
ECF.8 = 1.0028041546528881,
ECF.9 = 0.70977432157689235,

```

```
ECF.10 = 0.086052204035003091,
ECF.11 = 0.011400419961702518,
ECF.12 = 0.001825219438794076,
ECF.13 = 0.00029398731859899116,
ECF.14 = 0.002784886479846703,
meanIP = 9.9887100433529721,
sdIP = 0.10580250625108811,
minIP = 6.5159124624132048,
pAbort = 2.5702251748938956,
meanAbort = 2.2721679285648841,
sdAbort = 0.52006431730489933,
pCapture = 0.079471782729506113)

fML_NP <- IPFit(x=par,
               fixed.parameters=c(N=20000),
               data=data,
               verbose=FALSE,
               model="ML")

par <- fML_NP$ML$par

fML_NP <- IPFit(x=par,
               fixed.parameters=c(N=100000),
               data=data,
               verbose=FALSE,
               model="ML")

par <- c(ECF.2 = 0.016195025683080871,
        ECF.3 = 2.0858089267994315,
        ECF.4 = 3.1307578727979348,
        ECF.5 = 2.7495760827322622,
        ECF.6 = 2.8770821670450939,
        ECF.7 = 2.1592708144943145,
        ECF.8 = 1.0016227335391867,
        ECF.9 = 0.80990178270345259,
        ECF.10 = 0.081051214954249967,
        ECF.11 = 0.039757901443389344,
        ECF.12 = 6.3324056808464527e-05,
        ECF.13 = 0.00037500864146146936,
        ECF.14 = 0.0010383506745475582,
        meanIP = 10.004121090603523,
        sdIP = 0.10229422354470977,
        minIP = 6.5051758088487883,
        pAbort = 2.5335985958484839,
        meanAbort = 2.3145895392189173,
        sdAbort = 0.51192514362374153,
        pCapture = 0.055440514236842105,
        DeltameanIP = -0.046478049165483697)

fML_NP_Delta <- IPFit(x=par,
                     fixed.parameters=c(N=20000),
                     data=data,
                     verbose=FALSE,
```

```

        model="ML")

par <- fML_NP_Delta$ML$par

fML_NP_Delta <- IPFit(x=par,
                    fixed.parameters=c(N=1000000),
                    data=data,
                    verbose=FALSE,
                    model="ML")

# Test for stability of -Ln L value according to N
grandL.mean <- NULL
grandL.sd <- NULL
N <- c(10000, 20000, 30000, 40000, 50000,
       60000, 70000, 80000, 90000,
       100000, 200000, 300000, 400000, 500000,
       600000, 700000, 800000, 900000,
       1000000)
for (Ni in N) {
  print(Ni)
  smallL <- NULL
  for (replicate in 1:100) {
    smallL <- c(smallL,
                getFromNamespace(".IPlnL", ns="phenology")
                (x=par, fixed.parameters=c(N=Ni), data=data))
  }
  grandL.mean <- c(grandL.mean, mean(smallL))
  grandL.sd <- c(grandL.sd, sd(smallL))
}

grandL.mean <- c(242.619750064524, 239.596145944548, 238.640010536147, 237.965573853263,
237.727506424543, 237.240740566494, 237.527948232993, 237.297225856515,
237.17073080938, 237.103397800143, 236.855939567838,
236.704861853456, 236.82264801458, 236.606065021519, 236.685930841831,
236.697562908131, 236.568003663293, 236.58097471402, 236.594282543024
)
grandL.sd <- c(6.54334049298099, 3.04916614991682, 2.57932397492509, 2.15990307710982,
1.59826856034413, 1.54505295915354, 1.59734964880484, 1.41845032728396,
1.43096821211286, 1.20048923027244, 0.912467350448495,
0.75814052890774, 0.668841336554019, 0.539505594152166, 0.554662419326559,
0.501551009304687, 0.415199780254872, 0.472274287714195, 0.386237047201706
)

plot_errbar(x=N, y=grandL.mean, errbar.y = 2*grandL.sd,
            xlab="N", ylab="-Ln L (2 SD)", bty="n", las=1)

# Plot the fitted ECF
plot(fML_NP_Delta, result="ECF")

# Plot the Internesting Period distribution
plot(fML_NP_Delta, result="IP")

# Plot the distribution of days between tentatives

```



```

      ECF.13 = 6.366805760909012e-05,
      ECF.14 = 6.366805760909012e-05,
      meanIP = 6.366805760909012e-05,
      sdIP = 6.366805760909012e-05,
      minIP = 6.366805760909012e-05,
      pAbort = 6.366805760909012e-05,
      meanAbort = 6.366805760909012e-05,
      sdAbort = 6.366805760909012e-05,
      pCapture = 6.366805760909012e-05)),
Min=c(rep(0, 13), 8, 0.001, 0, -8, 0, 0.001, -8),
Max=c(rep(10, 13), 12, 1, 10, 8, 2, 1, 8),
Init=par, stringsAsFactors = FALSE)
rownames(df)<- names(par)

fMH <- IPFit(parametersMH=df,
fixed.parameters=c(N=10000),
data=data,
verbose=FALSE,
n.iter = 10000,
n.chains = 1, n.adapt = 100, thin = 1, trace = TRUE,
adaptive = TRUE,
model="MH")

# Plot the fitted ECF
plot(fMH, result="ECF")

## End(Not run)

```

IPModel

Estimates the pattern of interesting intervals for a set of parameters.

Description

This function fits a model of interesting period.
The parameters are:

- meanIP : The average number of days between two nesting processes
- DeltameanIP : The shift in days for IP at each new clutch.
- sdIP : The standard deviation of number of days between two nesting processes
- minIP : The minimum number of days between two nesting processes
- pAbort : The -logit of the probability to abort a nesting process
- meanAbort : The average of the number of days after the abortion of a nesting process
- sdAbort : The standard deviation of the number of days after the abortion of a nesting process
- pCapture : The -logit of the probability to capture a female on the beach
- meanECF : The average number of clutch a female will try to do being represented as ECF

- `sdECF` : The standard deviation of number of clutch a female will try to do
- `N` : The number of replicates to generate the distribution (default is 10000 if not indicated)
- `ECF.x` : The relative proportion of females nesting with $ECF = x$ ($ECF.1$ being fixed to 1)

Usage

```
IPModel(
  par,
  parallel = TRUE,
  limits = list(meanIP = 40, meanECF = 4, minIP = 15, sdAbort = 1, sdIP = 1, sdECF = 1,
    DeltameanIP = 0.5, maxDays = 365)
)
```

Arguments

<code>par</code>	Set of parameters
<code>parallel</code>	If TRUE, will use parallel computing
<code>limits</code>	A list of limits for various parameters

Details

IPModel estimates the pattern of interesting intervals for a set of parameters.

Value

Return a list with two elements.

Author(s)

Marc Girondot

See Also

Other Model of Interesting Period: [IPFit\(\)](#), [IPPredict\(\)](#), [plot.IP\(\)](#), [summary.IP\(\)](#)

Examples

```
## Not run:
library(phenology)
# Example
par <- c(meanIP = 9.8,
sdIP = 0.1,
minIP = 7,

pAbort = -logit(0.1),
meanAbort = 2,
sdAbort = 0.05,

pCapture = -logit(0.8),
```

```
meanECF = 4,  
sdECF = 0.1)  
  
model <- IPModel(c(par, N=10000))  
  
plot(model)  
  
## End(Not run)
```

IPPredict	<i>Predict the possible clutch number based on observed Interesting Period.</i>
-----------	---

Description

This function predicts the possible clutch number based on observed Interesting Period.

Usage

```
IPPredict(x = NULL, par = NULL, N = NULL, IP = 0:100)
```

Arguments

x	A result of IPFit().
par	A set of parameters.
N	Number of replicates
IP	A vector of Interesting Period

Details

IPPredict calculates the possible clutch number based on observed Interesting Period.

Value

A data.frame

Author(s)

Marc Girondot

See Also

Other Model of Interesting Period: [IPFit\(\)](#), [IPModel\(\)](#), [plot.IP\(\)](#), [summary.IP\(\)](#)

Examples

```
## Not run:
library(phenology)
# Example
##### Fit using Maximum-Likelihood

par <- c(meanIP = 9.9959691992722917,
         sdIP = 0.10066664270893474,
         minIP = 7.5684588178888754,
         pAbort = 2.2510012544630911,
         meanAbort = 2.8969185085603386,
         sdAbort = 0.92688983853803242,
         pCapture = -1.0393803705929086,
         meanECF = 3.9551519427394255,
         sdECF = 0.31657679943365019)

IPPredict(par=par, IP=c(10, 80))

## End(Not run)
```

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

See Also

Other Phenology model: `AutoFitPhenology()`, `BE_to_LBLE()`, `Gratiot`, `LBLE_to_L()`, `L_to_LBLE()`, `MarineTurtles_2002`, `MinBMinE_to_Min()`, `adapt_parameters()`, `add_SE()`, `add_phenology()`, `extract_result()`, `fit_phenology()`, `likelihood_phenology()`, `logLik.phenology()`, `map_Gratiot`, `map_phenology()`, `par_init()`, `phenology2fitRMU()`, `phenology_MHmcmc_p()`, `phenology_MHmcmc()`, `phenology()`, `plot.phenologymap()`, `plot.phenology()`, `plot_delta()`, `plot_phi()`, `print.phenologymap()`, `print.phenologyout()`, `print.phenology()`, `remove_site()`, `result_Gratiot1`, `result_Gratiot2`, `result_Gratiot_Flat`, `result_Gratiot_mcmc`, `result_Gratiot`, `summary.phenologymap()`, `summary.phenologyout()`, `summary.phenology()`

Examples

```
# 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)
# 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

See Also

Other Phenology model: `AutoFitPhenology()`, `BE_to_LBLE()`, `Gratiot`, `LBLE_to_BE()`, `L_to_LBLE()`, `MarineTurtles_2002`, `MinBMinE_to_Min()`, `adapt_parameters()`, `add_SE()`, `add_phenology()`, `extract_result()`, `fit_phenology()`, `likelihood_phenology()`, `logLik.phenology()`, `map_Gratiot`, `map_phenology()`, `par_init()`, `phenology2fitRMU()`, `phenology_MHmcmc_p()`, `phenology_MHmcmc()`, `phenology()`, `plot.phenologymap()`, `plot.phenology()`, `plot_delta()`, `plot_phi()`, `print.phenologymap()`, `print.phenologyout()`, `print.phenology()`, `remove_site()`, `result_Gratiot1`, `result_Gratiot2`, `result_Gratiot_Flat`, `result_Gratiot_mcmc`, `result_Gratiot`, `summary.phenologymap()`, `summary.phenologyout()`, `summary.phenology()`

Examples

```
# 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)
# 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,
  parallel = TRUE,
  result = NULL,
  cofactors = NULL,
  add.cofactors = NULL,
  tol = 1e-06,
  zero = 1e-09,
```

```

    out = TRUE
  )

```

Arguments

<code>data</code>	Dataset generated with <code>add_format</code>
<code>fitted.parameters</code>	Set of parameters to be fitted
<code>fixed.parameters</code>	Set of fixed parameters
<code>zero_counts</code>	example <code>c(TRUE, TRUE, FALSE)</code> indicates whether the zeros have been recorder for each of these timeseries. Default is TRUE for all.
<code>parallel</code>	If TRUE, parallel computing is used.
<code>result</code>	An object obtained after <code>fit_phenology()</code>
<code>cofactors</code>	data.frame with a column Date and a column for each cofactor
<code>add.cofactors</code>	Names of the column of parameter cofactors to use as a cofactor
<code>tol</code>	Tolerance of recurrence for <code>dSnbinom()</code> used for convolution of negative binomial distribution
<code>zero</code>	If the theoretical nest number is under this value, this value will be used
<code>out</code>	If TRUE, return the global likelihood; if FALSE, the likelihood for each series

Details

`likelihood_phenology` estimate likelihood for a set of parameters.

Value

The likelihood of the data with the parameters

Author(s)

Marc Girondot

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
## Not run:
# 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)
# 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, verbose = FALSE)
```

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.
verbose	if TRUE, show the parameters.

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)
```

LnRI_norm

Return a remigration interval.

Description

Model of remigration interval

The vector of parameters must include:

sx, survival for year x

if s is included, all years have the same survival

tx, Tag retention for year x

rx, probability of return for year x

cx, probability of return for year x
 px, probability of observation for year x

Usage

```
LnRI_norm(data, x, k1 = NULL)
```

Arguments

data	Data with remigration intervals
x	Vector of parameters
k1	Maximum number of years for remigration intervals.

Details

lnRI_norm returns a ln L

Value

Return a remigration interval.

Author(s)

Marc Girondot

See Also

Other Model of Remigration Interval: [Bayesian.remigration\(\)](#), [RI\(\)](#), [plot.Remigration\(\)](#)

Examples

```
## Not run:
library(phenology)
# Example
# Each year a fraction of 0.9 is surviving
s <- c(s1=0.9, s2=0.9, s3=0.9, s4=0.9, s5=0.9)
# Probability of tag retention; 0.95 the first year then after no loss
t <- c(t1=0.95, t2=1, t3=1, t4=1, t5=1)
# Time-conditional return probability - This is the true remigration rate
r <- c(r1=0.1, r2=0.8, r3=0.7, r4=0.7, r5=1)
# Capture probability
p <- c(p1=0.6, p2=0.6, p3=0.6, p4=0.6, p5=0.6)
# Number of observations for 400 tagged females after 1, 2, 3, 4, and 5 years
OBS <- c(400, 10, 120, 40, 20, 10)
# Likelihood of the observed number based on the model
LnRI_norm(data=OBS, x = c(s, t, r, p, sd=2) )
LnRI_norm(data=OBS, x = c(s=0.97, t, r, p, sd=2) )
```

```
## 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

Return Log Likelihood of a fit generated by fitRMU

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: [CI.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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

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

## End(Not run)
```

logLik.Tagloss

Return Log Likelihood of a fit generated by Tagloss_fit

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_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
# 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)
# 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.

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

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


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,
  tol = 1e-06,
  zero_counts = TRUE,
  progressbar = any(installed.packages()[, "Package"] == "pbapply"),
  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
tol	Tolerance of recurrence for dSnbinom() used for convolution 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.


```

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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
# 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)
# 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)
```

o_4p_p1p2

*Model of tagloss based on Rivalan data***Description**

Model of tagloss based on Rivalan data

Usage

```
o_4p_p1p2
```

Details

Model of tagloss based on Rivalan data

Author(s)

Marc Girondot

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.

See Also

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

Examples

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

# Same data fitted with new model
par <- c(D1_1 = 100.15324837975547, A_1 = 5.9576927964120188,
        B_1 = 8.769924225871069, B_2 = 8.2353860179664125)
pfixed <- c(D2D1_1 = 2568, D3D2_1 = 2568, D2D1_2 = 2568, D3D2_2 = 2568)
o_4p_p1p2 <- Tagloss_fit(data=data_f_21, fitted.parameters = par,
                        fixed.parameters = pfixed,
                        model_before = "par['C_1']=par['B_1'];
                        par['A_2']=par['A_1'];
                        par['C_2']=par['B_2'];
                        par['D1_2']=par['D1_1']", hessian=TRUE)

data(o_4p_p1p2)
plot(o_4p_p1p2, model="1", col="red")
```

```

plot(o_4p_p1p2, model="2", col="blue", add=TRUE)
legend("topright", legend=c("2->1", "1->0"), lty=1, col=c("blue", "red"))
plot(o_4p_p1p2, model="Cumul")

## End(Not run)

```

Parameter_Global_Year *Transform a set of parameters from Year to global effect, or reverse*

Description

This function is used to transform a set of parameters that uses Peak, LengthB, LengthE, B, E, or Length to the same parameter with Year effect, or reverse.

The parameter series can be or a result from add_phenology() or from fit_phenology() or simply a vector of names.

Usage

```

Parameter_Global_Year(
  parameters = stop("A set of parameters must be indicated"),
  parname = c("Peak", "LengthB", "LengthE", "B", "E", "Length"),
  series = NULL,
  sep_year = "-",
  perYear = TRUE
)

```

Arguments

parameters	Set of current parameters
parname	Name of parameter to transform
series	Set of series (see description)
sep_year	Character used to separate the year
perYear	TRUE if year-specific values must be setup

Details

Parameter_Global_Year transforms a set of parameters from Year to global effect, or reverse

Value

Return a set of modified parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
Parameter_Global_Year(parameters=c("Peak_Beach1-2018"=151, "Peak_Beach1-2019"=161),
                      parname="Peak", perYear=FALSE)
Parameter_Global_Year(parameters=c("Peak"=151),
                      series = c("beach1", "beach2"),
                      parname="Peak", perYear=TRUE)

## End(Not run)
```

par_init

Calculate initial set of parameters.

Description

This function is used to generate an initial set of parameters for fitting that is expected to be not 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 part of the name of the rookery.

The model for scale effect of sinusoid is: $\text{Alpha} + \text{Beta} * n(t) ^ \text{Tau}$ where $n(t)$ is the expected number for the day t without the sinusoid effect.

Usage

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


Arguments

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

Details

par_init calculates initial set of parameters.

Value

The initial set of parameters

Author(s)

Marc Girondot

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```

## Not run:
library(phenology)
# 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)

## When a series has only 0, it should be used in two steps
## Let see an example

```

```
# Let create a times series with only 0
data0 <- data.frame(Date=c("11/3/2015", "12/3/2015", "13/3/2015-18/3/2015", "25/3/2015"),
                    Number=c(0, 0, 0, 0),
                    Beach=rep("Site0", 4), stringsAsFactors=FALSE)
data1 <- data.frame(Date=c("15/3/2015", "16/3/2015", "20/3/2015-22/3/2015", "25/3/2015"),
                    Number=c(1, 0, 3, 0),
                    Beach=rep("Site1", 4), stringsAsFactors=FALSE)
data <- rbind(data0, data1)

# Here I include timeseries with no observation
try1 <- add_phenology(data, format="%d/%m/%Y", month_ref=1, include0=TRUE)
pfixed <- c(Min=0, Flat=0)
parg <- par_init(try1, fixed.parameters=pfixed)
# The Max value for the series without observations should not be fitted. The ML is for Max being 0
pfixed <- c(pfixed, parg[(substr(names(parg), 1, 4)=="Max_") & (parg == 0)])
parg <- parg[!(names(parg) %in% names(pfixed))]
```

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

See Also

Other Phenology model: `AutoFitPhenology()`, `BE_to_LBLE()`, `Gratiot`, `LBLE_to_BE()`, `LBLE_to_L()`, `L_to_LBLE()`, `MarineTurtles_2002`, `MinBMinE_to_Min()`, `adapt_parameters()`, `add_SE()`, `add_phenology()`, `extract_result()`, `fit_phenology()`, `likelihood_phenology()`, `logLik.phenology()`, `map_Gratiot`, `map_phenology()`, `par_init()`, `phenology2fitRMU()`, `phenology_MHmcmc_p()`, `phenology_MHmcmc()`, `plot.phenologymap()`, `plot.phenology()`, `plot_delta()`, `plot_phi()`, `print.phenologymap()`, `print.phenologyout()`, `print.phenology()`, `remove_site()`, `result_Gratiot1`, `result_Gratiot2`, `result_Gratiot_Flat`, `result_Gratiot_mcmc`, `result_Gratiot`, `summary.phenologymap()`, `summary.phenologyout()`, `summary.phenology()`

Examples

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

## End(Not run)
```

phenology2fitRMU

Create the data to be used with fitRMU() for a summary(phenology).

Description

This function takes the result of `plot.phenology()` and generates the information to be used with `fitRMU()`.

The value of density can be `dnorm` or `dgamma`. `dnorm` is better if ML results are used and `dgamma` is for MCMC.

Here are some example of regular expressions (regex) in `grep`:

If format of timeseries is beachname-2005: `rookeries.names.grep="(.)-.-+", years.grep=".+-(.)$" gsub("(.)-.-+", "\1", "beachname-2005"); gsub(".+-(.)$", "\1", "beachname-2005")`

If format of timeseries is beachname-2005-2006: `rookeries.names.grep="(.)-.-+", years.grep=".+([0-9]4,)-.+$"`

`gsub("(.)-.-+", "\1", "beachname-2005-2006"); gsub(".+([0-9]4,)-.+$", "\1", "beachname-2005-2006")`

If format of timeseries is beachname-20052006: `rookeries.names.grep="(.)-.-+", years.grep=".+([0-9]4,)([0-9]4,)$"`

`gsub("(.)-.-+", "\1", "beachname-20052006"); gsub(".+([0-9]4,)([0-9]4,)$", "\1", "beachname-20052006")`

The return is a list with these elements:

`RMU.data`, `years.byrow`, `colname.year`, and `RMU.names`.

If density is a vector, the density used is linked to the rank of the timeseries in `phenologyout`.

Usage

```
phenology2fitRMU(
  phenologyout = stop("A result obtained from summary(phenology)"),
  col.mean = "with_obs_Mean_ML",
  col.var = "with_obs_Var_ML",
```

```

rookeries.names.grep = "(.+)-.+",
years.grep = ".+-(.+)$",
limit.cv = +Inf,
limit.sd = +Inf,
density = "dgamma"
)

```

Arguments

phenologyout	A result of plot.phenology() or summary()
col.mean	Name of the column to be used as mean value. Can be a vector.
col.var	Name of the column to be used as variance value. Can be a vector.
rookeries.names.grep	The pattern to return the rookery name from names of timeseries.
years.grep	The pattern to return the year from names of timeseries.
limit.cv	Remove data with higher coefficient of variation than the limit.
limit.sd	Remove data with higher standard deviation than the limit.
density	What density should be used. Can be dnorm or dgamma. Can be a vector.

Details

phenology2fitRMU is used to prepare output of phenology to be used by fitRMU()

Value

Return a list with elements ready to be used with fitRMU().

Author(s)

Marc Girondot

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```

## Not run:
library("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 = 1,
  n.adapt = 0,
  thin = 1,
  trace = FALSE,
  traceML = 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 or period, shows progress
<code>traceML</code>	TRUE or FALSE to show ML

adaptive	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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

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"),
  default.density = "dunif",
  accept = FALSE
)

```

Arguments

<code>result</code>	An object obtained after a <code>fit_phenology()</code> fit
<code>default.density</code>	The default density, "dnorm" or "dunif"
<code>accept</code>	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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

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	<i>Plot a result of clutch frequency fit.</i>
-------------	---

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)
```

Description

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

Usage

```
## S3 method for class 'fitRMU'
plot(
  x,
  ...,
  resultMCMC = NULL,
  chain = 1,
  replicate.CI = 10000,
  CI.RMU = NULL,
  what = "proportions",
  aggregate = "both",
  order = NULL,
  control.legend = list(),
  show.legend = TRUE
)
```

Arguments

x	A result file generated by fitRMU
...	Parameters used by plot
resultMCMC	MCMC result for fitRUM
chain	Chain to be plotted for MCMC
replicate.CI	Number of replicates to estimate CI
CI.RMU	A result of CI.RMU()
what	Can be proportions, numbers or total
aggregate	Can be model or both
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 A list with result of CI.RMU()

Author(s)

Marc Girondot

See Also

Other Fill gaps in RMU: [CI.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"), stringsAsFactors = FALSE)
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), stringsAsFactors = FALSE)

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.IP

Plot a result of Interesting Period fit or data.

Description

This function plots the result of IPFit() or IPModel().

Usage

```

## S3 method for class 'IP'
plot(x, ..., N = NULL, clutch = 1, result = "data")

```

Arguments

x	A result for IPFit() or IPModel().
...	Graphic parameters, see par().
N	Number of replicates for IPModel().
clutch	The rank of clutch when DeltameanIP is used.
result	What result will be plotted: data, model, data&model, IP, Abort, ECF, reverseECF

Details

plot.IP plots a result of Interesting Period fit or data

Value

Nothing

Author(s)

Marc Girondot

See Also

Other Model of Interesting Period: [IPFit\(\)](#), [IPModel\(\)](#), [IPPredict\(\)](#), [summary.IP\(\)](#)

Examples

```
## Not run:
library(phenology)
# Example
data <- c(0, 47, 15, 6, 5, 4, 2, 5, 57, 203, 205, 103, 35, 24, 12, 10,
  13, 49, 86, 107, 111, 73, 47, 30, 19, 17, 33, 48, 77, 83, 65,
  37, 27, 23, 24, 22, 41, 42, 44, 33, 39, 24, 18, 18, 22, 22, 19,
  24, 28, 17, 18, 19, 17, 4, 12, 9, 6, 11, 7, 11, 12, 5, 4, 6,
  11, 5, 6, 7, 3, 2, 1, 3, 2, 1, 2, 0, 0, 3, 1, 0, 2, 0, 0, 1)
class(data) <- "IP"
plot(data)

##### Fit parametric ECF using Maximum-Likelihood

par <- c(meanIP = 9.9959691992722917,
  sdIP = 0.10066664270893474,
  minIP = 7.5684588178888754,
  pAbort = 2.2510012544630911,
  meanAbort = 2.8969185085603386,
  sdAbort = 0.92688983853803242,
  pCapture = -1.0393803705929086,
  meanECF = 3.9551519427394255,
  sdECF = 0.31657679943365019)

fML <- IPFit(x=par,
```



```

ECF.4 = 6.366805760909012e-05,
ECF.5 = 6.366805760909012e-05,
ECF.6 = 6.366805760909012e-05,
ECF.7 = 6.366805760909012e-05,
ECF.8 = 6.366805760909012e-05,
ECF.9 = 6.366805760909012e-05,
ECF.10 = 6.366805760909012e-05,
ECF.11 = 6.366805760909012e-05,
ECF.12 = 6.366805760909012e-05,
ECF.13 = 6.366805760909012e-05,
ECF.14 = 6.366805760909012e-05,
meanIP = 6.366805760909012e-05,
sdIP = 6.366805760909012e-05,
minIP = 6.366805760909012e-05,
pAbort = 6.366805760909012e-05,
meanAbort = 6.366805760909012e-05,
sdAbort = 6.366805760909012e-05,
pCapture = 6.366805760909012e-05)),
Min=c(rep(0, 13), 8, 0.001, 0, -8, 0, 0.001, -8),
Max=c(rep(10, 13), 12, 1, 10, 8, 2, 1, 8),
Init=par, stringsAsFactors = FALSE)
rownames(df)<- names(par)

fMH <- IPFit(parametersMH=df,
fixed.parameters=c(N=10000),
data=data,
verbose=FALSE,
n.iter = 10000,
n.chains = 1, n.adapt = 100, thin = 1, trace = TRUE,
adaptive = TRUE,
model="MH")

# Plot the fitted ECF
plot(fMH, result="ECF")

# Plot the posteriors and priors
plot(fMH$MH, parameters="meanIP", xlim=c(6, 14))

plot(x=1:length(fMH$MH$resultLnL[[1]]), y=fMH$MH$resultLnL[[1]],
type="l", xlab="Iterations", ylab="Ln L", bty="n", las=1)

## 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.SD.polygon = rgb(red = 1, green = 0, blue = 0, alpha = 0.2),
  col.MCMC.quantiles = "purple",
  col.MCMC.quantiles.polygon = rgb(red = 160/255, green = 32/255, blue = 240/255, alpha
    = 0.2),
  col.ML.quantiles = "black",
  col.ML.quantiles.polygon = rgb(red = 0, green = 0, blue = 0, alpha = 0.2),
  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.SD.polygon	Color of the polygon of the SD curve. If FALSE not shown.

```

col.MCMC.quantiles
    Color of the quantiles curve based on mcmc
col.MCMC.quantiles.polygon
    Color of the credibility interval polygon based on MCMC. If FALSE not shown.
col.ML.quantiles
    Color of the SE curve based on ML
col.ML.quantiles.polygon
    Color of the confidence interval polygon based on ML. If FALSE not shown.
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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```

## Not run:
library(phenology)
# 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)
parg <- c('Max_Complete' = 33.076044848500167, 25,
'MinB_Complete' = 0.21758630798131923,

```

```

'MinE_Complete' = 0.42493953463205936,
'LengthB' = 96.158007568020523,
'Peak' = 174.62435300274245,
'LengthE' = 62.084876419654634,
'Flat' = 0,
'Theta' = 3.5864650991821954)
# 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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
## Not run:
library("phenology")
# 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)
# 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.Remigration *Plot the remigration intervals.*

Description

Plot the remigration intervals.

Usage

```
## S3 method for class 'Remigration'
plot(x, legend = TRUE, ...)
```

Arguments

x	Object obtained from Bayesian.remigration()
legend	TRUE or FALSE or c(x, y)
...	Parameters transmitted to plot

Details

plot.Remigration plots the remigration intervals.

Value

An invisible dataframe with values used for plotting.

Author(s)

Marc Girondot

See Also

Other Model of Remigration Interval: [Bayesian.remigration\(\)](#), [LnRI_norm\(\)](#), [RI\(\)](#)

Examples

```

## Not run:
library(phenology)
# Example

# Each year a fraction of 0.9 is surviving
s <- c(s=0.9)
# Probability of tag retention; 0.8
t <- c(t=0.8)
# Time-conditional return probability - This is the true remigration rate
r <- c(r1=0.1, r2=0.8, r3=0.7, r4=0.7, r5=1)
# Capture probability
p <- c(p1=0.6, p2=0.6, p3=0.6, p4=0.6, p5=0.6)
# Number of observations for 400 tagged females after 1, 2, 3, 4, and 5 years
OBS <- c(400, 10, 120, 40, 20, 10)

kl_s <- length(s)
kl_t <- length(t)
kl_r <- length(r)
kl_p <- length(p)

pMCMC <- data.frame(Density=c("newdbeta", "newdbeta", rep("dunif", kl_r),
                           rep("newdbeta", kl_p), "dunif"),
                   Prior1=c(s, t, rep(0, kl_r), rep(0.2, kl_p), 0),
                   Prior2=c(0.02, 0.02, rep(1, kl_r), rep(0.08, kl_p), 10),
                   SDProp=c(0.05, 0.05, rep(0.05, kl_r), rep(0.05, kl_p), 0.05),
                   Min=c(0, 0, rep(0, kl_r), rep(0, kl_p), 0),
                   Max=c(1, 1, rep(1, kl_r), rep(1, kl_p), 10),
                   Init=c(s, t, r, p, 1), stringsAsFactors = FALSE,
                   row.names=c("s",
                               "t",
                               names(r),
                               names(p), "sd")
                   )
rMCMC <- Bayesian.remigration(parameters = pMCMC,
                             n.iter = 1000000,
                             n.adapt = 300000,
                             trace=10000,
                             data=OBS)

plot(rMCMC)

## End(Not run)

```

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",
  show.scale = TRUE,
  max.scale = NULL
)
```

Arguments

x	A CMR file summarized using TableECFOCF()
...	Graphic parameters
result	What should be plotted: ECFOCF or data, 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.
show.scale	If TRUE, show the scale as a legend
max.scale	Maximum value for scale; if NULL it is maximum of observations.

Details

plot.TableECFOCF plots a TableECFOCF dataset.

Value

Nothing

Author(s)

Marc Girondot

See Also

Other 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.

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", "N2", "N1", "N0",
            "NLR", "N0R", "NL0", "N00"),
  col = rev(grey.colors(4, start = 0.9, end = 0.3)),
  text.col = grey.colors(4, start = 0.9, end = 0.3),
  label.col = "black",
  add = FALSE,
  hessian = NULL,
  replicates = NULL,
  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
label.col	The text color used for labels when decoration is true
add	Should the data be added to a previous plot?
hessian	Hessian matrix of parameters
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

An invisible dataframe with values used for plotting.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs\(\)](#), [Tagloss_L\(\)](#), [Tagloss_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#)

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=list(), 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", decoration = TRUE)

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=300, D3D2_R1=200,
        A_R1=-logit(5E-4), B_R1=-logit(4E-4), C_R1=-logit(5E-4),
        D1_R2=200, D2D1_R2=200, D3D2_R2=200,
        A_R2=-logit(6E-4), B_R2=-logit(5E-4), C_R2=-logit(6E-4),
        D1_L1=200, D2D1_L1=400, 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)
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par, model="R1",
                        decoration = TRUE)
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par, model="R2",
                        decoration = TRUE)

## End(Not run)

```

Description

This function plots the result of `Tagloss_format()`.
The default ramp of colors is a grey ramp.

Usage

```
## S3 method for class 'TaglossData'
plot(
  x,
  ...,
  categories = c("N22", "N21", "N11", "N10", "N20"),
  col = grey(seq(from = 0.9, to = 0, length.out = length(categories))),
  title.legend = "Tag history",
  categories.legend = categories,
  show.legend = TRUE
)
```

Arguments

<code>x</code>	A result for <code>Tagloss_format</code> .
<code>...</code>	Graphic parameters, see <code>par()</code> .
<code>categories</code>	Categories to display.
<code>col</code>	The ramp of colors used for the categories.
<code>title.legend</code>	Title for legend box.
<code>categories.legend</code>	Name of categories to show in legend box.
<code>show.legend</code>	Should the legend box be shown ?

Details

`plot.TaglossData` plots formatted data used for tagloss analysis

Value

Nothing

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs\(\)](#), [Tagloss_L\(\)](#), [Tagloss_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.Tagloss\(\)](#)

Examples

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

## End(Not run)
```

plot_delta	<i>Plot a likelihood lineplot obtained after map_phenology.</i>
------------	---

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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library("phenology")
# 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
## 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      Print the result information from a result x.
```

Description

The function print displays a phenology 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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library(phenology)
# 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
## 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

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

Value

Return None

Author(s)

Marc Girondot

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library("phenology")
# 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
## 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 output x.*

Description

The function print.phenologyout displays the output of a summary(phenology).

Usage

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

Arguments

x	An output generated by plot_phenology
...	Not used

Details

print.phenologyout prints the information from a result x.

Value

None

Author(s)

Marc Girondot

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library(phenology)
# 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
## Not run:
result_Gratiot<-fit_phenology(data=data_Gratiot,
fitted.parameters=parg, fixed.parameters=NULL)

## End(Not run)
data(result_Gratiot)
# Extract parameters form 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.

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

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.

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

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

```
result_Gratiot2
```

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, 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.

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

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.

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

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.

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

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)
```

RI *Return an expected remigration interval.*

Description

Model of remigration interval

Note that r, s and t are conditional probabilities. If c is null, then return probabilities are estimated from r. r can be named vector. For example:

r <- c(r1=0.5, r2=0.60, r3=1) is equivalent to c <- c(c1=0.5, c2=0.3, c3=0.2)

The vector of r described the probability that a female returned after 1, 2, 3 years among those who have not nested before. The vector of r is the same but defining the return probability for an initial female.

Usage

```
RI(s, t, r = NULL, c = NULL, p)
```

Arguments

s	Time-conditional probability of survival
t	Time-conditional probability of tag retention
r	Time-conditional probability of return
c	Probability of return
p	Annual probability of observation

Details

RI returns an expected remigration interval

Value

Return a remigration interval.

Author(s)

Marc Girondot

See Also

Other Model of Remigration Interval: [Bayesian.remigration\(\)](#), [LnRI_norm\(\)](#), [plot.Remigration\(\)](#)

Examples

```
## Not run:
library(phenology)
# Example
s <- c(s1=1, s2=1, s3=1, s4=1, s5=1)
t <- c(t1=0.95, t2=1, t3=1, t4=1, t5=1)
r <- c(r1=0.1, r2=0.8, r3=0.7, r4=0.7, r5=1)
p <- c(p1=0.6, p2=0.6, p3=0.6, p4=0.6, p5=0.6)

# r is equivalent to
c <- c(c1=0.1, c2=0.72, c3=0.126, c4=0.0378, c5=0.0162)
# Then the true remigration interval is:
ri_true <- sum(1:5*c[1:5])

s_ri <- NULL
for (sx in seq(from=0.01, to=1, by=0.01)) {
  s[] <- sx
  ri1 <- RI(s=s, t=t, r=r, p=p)
  s_ri <- c(s_ri, sum(1:5*ri1)/sum(ri1))
}

par(mar=c(4, 4, 1, 1)+0.4)

plot(x=seq(from=0.01, to=1, by=0.01), y=s_ri, type="l",
     las=1, bty="n", ylim=c(0, 4),
     xlab="Annual survival probabilities", ylab="Naive Remigration Interval",
     main="")
segments(x0=0.01, x1=1, y0=ri_true, y1=ri_true, lty=2, col="red")
legend("topright", legend="True remigration interval", lty=2, col="red")

## 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")
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)

```

summary.IP

Print the result information from a IP object.

Description

The function summary.IP shows result and estimates confidence interval.

Usage

```

## S3 method for class 'IP'
summary(object, ..., N = NULL, probs = c(0.025, 0.975))

```

Arguments

object	A file of class IP
...	Not used
N	Number of replicates
probs	Probability of confidence interval

Details

summary.IP prints the information from a IP object.

Value

Nothing

Author(s)

Marc Girondot

See Also

Other Model of Interesting Period: [IPFit\(\)](#), [IPModel\(\)](#), [IPPredict\(\)](#), [plot.IP\(\)](#)

Examples

```
## Not run:
library(phenology)
# Read a file with data

## End(Not run)
```

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

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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenologyout\(\)](#)

Examples

```
## Not run:
library(phenology)
# 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)
# Display information from the result
summary(result_Gratiot)
# Using mcmc
summary(object=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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologyout\(\)](#), [summary.phenology\(\)](#)

Examples

```
library("phenology")
# 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
## 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

See Also

Other Phenology model: [AutoFitPhenology\(\)](#), [BE_to_LBLE\(\)](#), [Gratiot](#), [LBLE_to_BE\(\)](#), [LBLE_to_L\(\)](#), [L_to_LBLE\(\)](#), [MarineTurtles_2002](#), [MinBMinE_to_Min\(\)](#), [adapt_parameters\(\)](#), [add_SE\(\)](#), [add_phenology\(\)](#), [extract_result\(\)](#), [fit_phenology\(\)](#), [likelihood_phenology\(\)](#), [logLik.phenology\(\)](#), [map_Gratiot](#), [map_phenology\(\)](#), [par_init\(\)](#), [phenology2fitRMU\(\)](#), [phenology_MHmcmc_p\(\)](#), [phenology_MHmcmc\(\)](#), [phenology\(\)](#), [plot.phenologymap\(\)](#), [plot.phenology\(\)](#), [plot_delta\(\)](#), [plot_phi\(\)](#), [print.phenologymap\(\)](#), [print.phenologyout\(\)](#), [print.phenology\(\)](#), [remove_site\(\)](#), [result_Gratiot1](#), [result_Gratiot2](#), [result_Gratiot_Flat](#), [result_Gratiot_mcmc](#), [result_Gratiot](#), [summary.phenologymap\(\)](#), [summary.phenology\(\)](#)

Examples

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

begin, end are the first and last elements with counts

final is the last period with information

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_cumul	<i>Return the cumulative rate of tag loss.</i>
---------------	--

Description

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

If `hessian` is not null, it will estimate standard error of the output using numerical delta method if `replicates` is null or using resampling if `replicates` is not null.

Parameters are described in [Tagloss_fit](#).

Usage

```
Tagloss_cumul(
  t,
  par = NULL,
  hessian = NULL,
  model_before = NULL,
  model_after = NULL,
  model = NULL,
  replicates = NULL,
  x = NULL
)
```

Arguments

<code>t</code>	Time for which values of model must be estimated
<code>par</code>	Parameters
<code>hessian</code>	hessian matrix of parameters
<code>model_before</code>	Function to be used before estimation of daily tagloss rate
<code>model_after</code>	Function to be used after estimation of daily tagloss rate
<code>model</code>	The model of parameter to use, can be N2, N1 or N0; or NLR, NL0, NOR, or N00 or NULL if <code>hessian</code> is NULL.
<code>replicates</code>	Number of replicates to estimate se of output for resampling method
<code>x</code>	A Tagloss fitted model

Details

Tagloss_cumul returns the cumulative rate of tag loss.

Value

Return the cumulative rate of tag loss if hessian is null or a data.frame with distribution of cumulative rate of tag loss if hessian is not null.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs\(\)](#), [Tagloss_L\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [plot.Tagloss\(\)](#)

Examples

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

# Data from Rivalan et al. 2005 - Table 2, line 1 - Fig 1D
par <- c(a0_2=-5.43E-2, a1_2=-103.52, a2_2=0, a3_2=0, a4_2=5.62E-4)
(y <- Tagloss_cumul(t=(1:6)*365, par=par))
plot(y[, "time"], y[, "N2"], type="l", bty="n",
      xlab="Days after tagging", ylab="N2 proportion")

# Data from Rivalan et al. 2005 - Table 2, line 2 - Fig 1E
par <- c(a0_2=-6.80E-2, a1_2=-81.15, a2_2=-2.20E-4, a3_2=6348.01, a4_2=1.65E-3)
(y <- Tagloss_cumul(t=(1:6)*365, par=par))
plot(y[, "time"], y[, "N2"], type="l",
      xlab="Days after tagging", ylab="N2 proportion")

# Data from Rivalan et al. 2005 - Table 2, line 3 - Fig 1F
par <- c(a0_2=-6.93E-2, a1_2=-78.92, a2_2=8.45E-4, a3_2=-16272.76, a4_2=2.87E-4)
(y <- Tagloss_cumul(t=(1:6)*365, par=par))
plot(y[, "time"], y[, "N2"], type="l",
      xlab="Days after tagging", ylab="N2 proportion")

# Data from Rivalan et al. 2005 - Table 2, line 4 - Fig 1C
par <- c(a0_2=-1.68E-3, a1_2=-4141.68, a2_2=0, a3_2=0, a4_2=0)
(y <- Tagloss_cumul(t=(1:6)*365, par=par))
plot(y[, "time"], y[, "N2"], type="l",
      xlab="Days after tagging", ylab="N2 proportion")

# Data from Rivalan et al. 2005 - Table 2, line 5 - Fig 1B
par <- c(a0_2=-3.77E-4, a1_2=-2000, a2_2=-0.001, a3_2=0, a4_2=5.00E-8)
(y <- Tagloss_cumul(t=(1:6)*365, par=par))
```

```

plot(y[, "time"], y[, "N2"], type="l",
      xlab="Days after tagging", ylab="N2 proportion")

# Data from Rivalan et al. 2005 - Table 2, line 6 - Fig 1A
par <- c(a0_2=-1E5, a1_2=-2000, a2_2=0, a3_2=4000, a4_2=8.34E-4)
(y <- Tagloss_cumul(t=(1:6)*365, par=par))
plot(y[, "time"], y[, "N2"], type="l",
      xlab="Days after tagging", ylab="N2 proportion")

# Data from Rivalan et al. 2005 - Table 2, line 1 - Fig 1D
# With tagloss rate dependency on tage number
par <- c(a0_2=-5.43E-2, a1_2=-103.52, a2_2=0, a3_2=0, a4_2=5.62E-4,
        a0_1=-5.43E-2, a1_1=-103.52, a2_1=0, a3_1=0, a4_1=5.62E-4, delta_1=3.2E-4)
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par,
                        model="Cumul",
                        decoration = TRUE)

p2 <- Tagloss_model(t=1:(6*365), par=par, model="2")
p1 <- Tagloss_model(t=1:(6*365), par=par, model="1")
par(mar=c(4, 5, 2, 1))
plot(x=1:(6*365), y=p2, bty="n", type="l", las=1, ylim=c(0,0.003), ylab="")
mtext("Daily tag loss", side=2, line=4)
lines(x=1:(6*365), y=p1, col="red")
legend("topright", legend=c(">1", ">0"), lty=1, col=c("black", "red"))

Tagloss_cumul(t=(1:6)*365, par=par)

# Without tagloss rate dependency on tag number
par <- c(a0_2=-5.43E-2, a1_2=-103.52, a2_2=0, a3_2=0, a4_2=5.62E-4,
        a0_1=-5.43E-2, a1_1=-103.52, a2_1=0, a3_1=0, a4_1=5.62E-4)
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par,
                        model="Cumul",
                        decoration = TRUE)
Tagloss_cumul(t=(1:6)*365, par=par)

#### Data from Casale et al. 2017
# Table 1 - Model II
par <- c(CasaleModelIIa0_2=-0.0511, CasaleModelIIa1_2=-100, CasaleModelIIa4_2=0.00014)
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par,
                        model="Cumul",
                        decoration = TRUE)
Tagloss_cumul(t=(1:6)*365, par=par)

# Table 1 - Model IV
par <- c(CasaleModelIVa0_2=-0.0132, CasaleModelIVa1_2=-100,
        CasaleModelIVa2_2=0.0327, CasaleModelIVa3_2=109.98,
        CasaleModelIVa4_2=0.00011)
phenology:::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par,
                        model="Cumul",
                        decoration = TRUE)
Tagloss_cumul(t=(1:6)*365, par=par)

# Table 1 - Model I

```

```

par <- c(CasaleModelIc_2=0.00027)
phenology::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par,
                        model="Cumul",
                        decoration = TRUE)
Tagloss_cumul(t=(1:6)*365, par=par)

# Table 1 - Model III
par <- c(CasaleModelIIIa0_2=1.14E-10, CasaleModelIIIa1_2=-110.04,
        CasaleModelIIIa4_2=0.00055)
phenology::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par,
                        model="Cumul",
                        decoration = TRUE)
Tagloss_cumul(t=(1:6)*365, par=par)

# Table 1 - Model V
par <- c(CasaleModelVa0_2=4.04E-10, CasaleModelVa1_2=-90,
        CasaleModelVa2_2=-0.0326, CasaleModelVa3_2=100.31,
        CasaleModelVa4_2=0.00006)
phenology::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par,
                        model="Cumul",
                        decoration = TRUE)
Tagloss_cumul(t=(1:6)*365, par=par)

## 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, what = "max")
```

Arguments

individuals	Set of individuals
what	By default is max, but can be min, mean or all

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_cumul\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [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:

Model Pfaller et al. (Submitted):

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

pA, pB and pC are the daily probabilities of tag loss with $p_A = -\text{logit}(A)$, $p_B = -\text{logit}(B)$ and $p_C = -\text{logit}(C)$

.

delta is used as: $p = p + \text{delta}$. Note that delta can be negative

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 p_B to p_C that is reached at day $D_3=D_2+D_3D_2$

When parameters from Rivalan et al. (2005) are used:

One tag lost when 2 are present $a_{0_2}, a_{1_2}, a_{2_2}, a_{3_2}, a_{4_2}, \text{delta_2}$

One tag lost when 1 is present $a_{0_1}, a_{1_1}, a_{2_1}, a_{3_1}, a_{4_1}, \text{delta_1}$

When parameters from Casale et al. (2017) are used:

Model I

One tag lost when 2 are present CasaleModelIc_2

One tag lost when 1 is present CasaleModelIc_1

Model II

One tag lost when 2 are present CasaleModelIIa0_2, CasaleModelIIa1_2, CasaleModelIIa4_2

One tag lost when 1 is present CasaleModelIIa0_1, CasaleModelIIa1_1, CasaleModelIIa4_1

Model III

One tag lost when 2 are present CasaleModelIIIa0_2, CasaleModelIIIa1_2, CasaleModelIIIa4_2

One tag lost when 1 is present CasaleModelIIIa0_1, CasaleModelIIIa1_1, CasaleModelIIIa4_1

Model IV

One tag lost when 2 are present CasaleModelIVa0_2, CasaleModelIVa1_2, CasaleModelIVa2_2,
CasaleModelIVa3_2, CasaleModelIVa4_2

One tag lost when 1 is present CasaleModelIVa0_1, CasaleModelIVa1_1, CasaleModelIVa2_1,
CasaleModelIVa3_1, CasaleModelIVa4_1

Model V

One tag lost when 2 are present CasaleModelVa0_2, CasaleModelVa1_2, CasaleModelVa2_2,
CasaleModelVa3_2, CasaleModelVa4_2

One tag lost when 1 is present CasaleModelVa0_1, CasaleModelVa1_1, CasaleModelVa2_1, CasaleModelVa3_1,
CasaleModelVa4_1

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

model_before can be ""par['a0_1']=par['a0_2'];par['a1_1']=par['a1_2']". model_after can be "p1=p2"

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

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.

Casale, P., Freggi, D., Salvemini, P., 2017. Tag loss is a minor limiting factor in sea turtle tagging programs relying on distant tag returns: the case of Mediterranean loggerhead sea turtles. *European Journal of Wildlife Research* 63.

Pfaller, J.B., Williams, K.L., Frick, M.G., Shamblin, B.M., Nairn, C.J., Girondot, M., Submitted. Genetic determination of tag loss dynamics in nesting loggerhead turtles: A new chapter in “the tag loss problem”.

See Also

Other Model of Tag-loss: [Tagloss_LengthObs\(\)](#), [Tagloss_L\(\)](#), [Tagloss_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [plot.Tagloss\(\)](#)

Examples

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

# model fitted by Rivalan et al. 2005
par <- c(a0_2=-5.43E-2, a1_2=-103.52, a4_2=5.62E-4,
        delta_1=3.2E-4)
pfixed <- c(a2_2=0, a3_2=0, a2_1=0, a3_1=0)
model_before <- "par['a0_1']=par['a0_2'];par['a1_1']=par['a1_2'];par['a4_1']=par['a4_2']"
o <- Tagloss_fit(data=data_f_21, fitted.parameters=par, fixed.parameters=pfixed,
                model_before=model_before)
plot(o, t=1:1000, model="cumul")
plot(o, t=1:1000, model="1")
plot(o, t=1:1000, model="2", add=TRUE, col="red")

# Same data fitted with new model
par <- c(D1_1 = 100.15324837975547, A_1 = 5.9576927964120188,
        B_1 = 8.769924225871069, B_2 = 8.2353860179664125)
pfixed <- c(D2D1_1 = 2568, D3D2_1 = 2568, D2D1_2 = 2568, D3D2_2 = 2568)
o_4p_p1p2 <- Tagloss_fit(data=data_f_21, fitted.parameters = par,
                        fixed.parameters = pfixed,
                        model_before = "par['C_1']=par['B_1'];
                        par['A_2']=par['A_1'];
                        par['C_2']=par['B_2'];
                        par['D1_2']=par['D1_1']", hessian=TRUE)

# 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

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

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_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [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 Giron dot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs\(\)](#), [Tagloss_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [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,
0.000241834641201422, -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,
3.13359029885985, 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 for different kinds of individuals are seen.</i>
-------------------	---

Description

Usefull to summarize data

Usage

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

Arguments

data	Set of indivuals
progressbar	Is shown a progressbar?

Details

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

Value

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

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_L\(\)](#), [Tagloss_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [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_mcmc

Bayesian model of tag loss using a CMR database.

Description

This function fits a model of tag loss using a CMR database using Bayesian mcmc. The parameters must be stored in a data.frame with named rows for each parameter with the following columns:

- Density. The density function name, example dnorm, dlnorm, dunif
- Prior1. The first parameter to send to the Density function
- Prior2. The second parameter to send to the Density function
- SDProp. The standard error from new proposition value of this parameter
- Min. The minimum value for this parameter
- Max. The maximum value for this parameter
- Init. The initial value for this parameter

Usage

```

Tagloss_mcmc(
  data = stop("A database formatted using Tagloss_format() must be used"),
  parameters = stop("Priors must be supplied"),
  fixed.parameters = NULL,
  model_before = NULL,
  model_after = NULL,
  cores = detectCores(all.tests = FALSE, logical = TRUE),
  groups = detectCores(all.tests = FALSE, logical = TRUE),
  n.iter = 10000,
  n.chains = 1,
  n.adapt = 100,
  thin = 30,
  trace = FALSE,
  traceML = 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

data An object formatted using Tagloss_format

parameters	A data.frame with priors; see description and examples
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()
cores	Number of cores to use for parallel computing
groups	Number of groups for parallel computing
n.iter	Number of iterations for each chain
n.chains	Number of chains
n.adapt	Number of iteration to stabilize likelihood
thin	Interval for thinning likelihoods
trace	Or FALSE or period to show progress
traceML	TRUE or FALSE to show ML
adaptive	Should an adaptive process for SDProp be used
adaptive.lag	Lag to analyze the SDProp value in an adaptive context
adaptive.fun	Function used to change the SDProp
intermediate	Or NULL of period to save intermediate result
filename	Name of file in which intermediate results are saved
previous	The content of the file in which intermediate results are saved

Details

Tagloss_mcmc Bayesian model of tag loss using a CMR database.

Value

Return a list object with the Bayesian model describing tag loss.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs\(\)](#), [Tagloss_L\(\)](#), [Tagloss_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_model\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [plot.Tagloss\(\)](#)

Examples

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

# model fitted by Rivalan et al. 2005
par <- c(a0_2=-5.43E-2, a1_2=-103.52, a4_2=5.62E-4,
        delta_1=3.2E-4)
pfixed <- c(a2_2=0, a3_2=0, a2_1=0, a3_1=0)
model_before <- "par['a0_1']=par['a0_2'];par['a1_1']=par['a1_2'];par['a4_1']=par['a4_2']"
pMCMC <- data.frame()
o <- Tagloss_mcmc(data=data_f_21, parameters=pMCMC, fixed.parameters=pfixed,
                 model_before=model_before)

## 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 . If hessian is not null, it will estimate standard error of the output using numerical delta method is replicates is null or using resampling if replicates is not null. Parameters are described in [Tagloss_fit](#).

Usage

```
Tagloss_model(
  t,
  par = NULL,
  hessian = NULL,
  model_before = NULL,
  model_after = NULL,
  model = NULL,
  replicates = NULL,
  x = NULL
)
```

Arguments

t	Time for which values of model must be estimated
par	Parameters
$hessian$	hessian matrix of parameters
$model_before$	Function to be used before estimation of daily tagloss rate
$model_after$	Function to be used after estimation of daily tagloss rate

model	The model of parameter to be used, can be 1, 2, L1, L2, R1 or R2
replicates	Number of replicates to estimate se of output
x	A Tagloss fitted model

Details

Tagloss_model returns the daily rate of tag loss.

Value

Return the daily rate of tag loss if hessian is null or a data.frame with distribution of daily rate of tag loss if hessian is not null.

Author(s)

Marc Girondot

See Also

Other Model of Tag-loss: [Tagloss_LengthObs\(\)](#), [Tagloss_L\(\)](#), [Tagloss_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_simulate\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [plot.Tagloss\(\)](#)

Examples

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

# 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")
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))
y <- Tagloss_model(t, par, model="1")
phenology::plot.Tagloss(x=list(), t=1:1000, fitted.parameters=par, model="1")

# Fig1A in Rivalan et al. 2005 (note an error for a0; a0 must be negative)
par <- c(a0=-1E5, a1=-2000, a2=0, a3=2*max(t), a4=0.1)
y <- Tagloss_model(t, par)
plot(x=t, y, type="l")

# Fig1B in Rivalan et al. 2005
par <- c(a0=-0.5, a1=-2000, a2=-0.001, a3=0, a4=0.1)
y <- Tagloss_model(t, par)
plot(x=t, y, type="l")

# Fig1C in Rivalan et al. 2005
par <- c(a0=-1, a1=-6, a2=0, a3=0, a4=0)
```

```

y <- Tagloss_model(t, par)
plot(x=t, y, type="l")

# Fig1D in Rivalan et al. 2005
par <- c(a0=-1, a1=-6, a2=0, a3=0, a4=0.1)
y <- Tagloss_model(t, par)
plot(x=t, y, type="l")

# Fig1E in Rivalan et al. 2005
par <- c(a0=-0.1, a1=-10, a2=-0.2, a3=60, a4=0.1)
y <- Tagloss_model(t, par)
plot(x=t, y, type="l")

# Fig1F in Rivalan et al. 2005
par <- c(a0=-0.1, a1=-10, a2=0.2, a3=60, a4=0.1)
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,
  pobservation = 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
pobservation	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_cumul\(\)](#), [Tagloss_daymax\(\)](#), [Tagloss_fit\(\)](#), [Tagloss_format\(\)](#), [Tagloss_mcmc\(\)](#), [Tagloss_model\(\)](#), [logLik.Tagloss\(\)](#), [o_4p_p1p2](#), [plot.TaglossData\(\)](#), [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
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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