

Package ‘embryogrowth’

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Type Package

Title Tools to Analyze the Thermal Reaction Norm of Embryo Growth

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Description Tools to analyze the embryo growth and the sexualisation thermal reaction norms.

Depends deSolve, optimx, numDeriv, parallel, HelpersMG (>= 4.0),R (>= 4.0)

Suggests entropy, shiny, coda, polynom, car, lmf, gam

License GPL-2

LazyData yes

LazyLoad yes

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NeedsCompilation no

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embryogrowth-package *The package embryogrowth*

Description

Tools to analyze the embryo growth and the sexualisation thermal reaction norms.

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

```
install.packages("http://max2.es.e.u-psud.fr/epc/conservation/CRAN/HelpersMG.tar.gz", repos=NULL,
type="source")
```

```
install.packages("http://max2.es.e.u-psud.fr/epc/conservation/CRAN/embryogrowth.tar.gz", repos=NULL,
type="source")
```

Details

Fit a parametric function that describes dependency of embryo growth to temperature

Package:	embryogrowth
Type:	Package
Version:	8.0 build 1133
Date:	2020-10-22
License:	GPL (>= 2)
LazyLoad:	yes

Author(s)

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

References

Girondot, M. & Kaska, Y. 2014. A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*. 45, 96-102.

Fuentes, M.M.P.B., Monsinjon, J., Lopez, M., Lara, P., Santos, A., dei Marcovaldi, M.A.G., Girondot, M., 2017. Sex ratio estimates for species with temperature-dependent sex determination differ according to the proxy used. *Ecological Modelling* 365, 55-67.

Girondot, M., Monsinjon, J., Guillon, J.-M., 2018. Delimitation of the embryonic thermosensitive period for sex determination using an embryo growth model reveals a potential bias for sex ratio prediction in turtles. *Journal of Thermal Biology* 73, 32-40.

Monsinjon, J., Jribi, I., Hamza, A., Ouerghi, A., Kaska, Y., Girondot, M., 2017. Embryonic growth rate thermal reaction norm of Mediterranean *Caretta caretta* embryos from two different thermal habitats, Turkey and Libya. *Chelonian Conservation and Biology* 16, 172-179.

See Also

Delmas, V., Prevot-Julliard, A.-C., Pieau, C. & Girondot, M. 2008. A mechanistic model of temperature-dependent sex determination in a Chelonian, the European pond turtle. *Functional Ecology*, 22, 84-93.

Girondot, M., Ben Hassine, S., Sellos, C., Godfrey, M. & Guillon, J.-M. 2010. Modeling thermal influence on animal growth and sex determination in Reptiles: being closer of the target gives new views. *Sexual Development*, 4, 29-38.

Girondot, M. 1999. Statistical description of temperature-dependent sex determination using maximum likelihood. *Evolutionary Ecology Research*, 1, 479-486.

Girondot, M., & Kaska, Y. (2014). Nest temperatures in a loggerhead- nesting beach in Turkey is more determined by sea surface temperature than air temperature. *Journal of Thermal Biology*, 47, 13-18.

Examples

```
## Not run:
library("embryogrowth")
packageVersion("embryogrowth")
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(115.758929130522, 428.649022170996, 503.687251738993,
12.2621455821612, 306.308841227278, 116.35048615105), .Names = c("DHA",
"DHH", "DHL", "DT", "T12L", "Rho25"))
# or
x <- structure(c(118.431040984352, 498.205702157603, 306.056280989839,
118.189669472381), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)

#####
#
# The values of rK=2.093313 and M0=1.7 were used in
# Girondot, M. & Kaska, Y. 2014. A model to predict the thermal
# reaction norm for the embryo growth rate from field data. Journal of
```

```

# Thermal Biology. 45, 96-102.
#
# Based on recent analysis on table of development for both Emys orbicularis and
# Caretta caretta, best value for pfixed should be 1.209 and M0 should be 0.34.
# Girondot, M., Monsinjon, J., Guillon, J.-M., Submitted. Delimitation of the
# embryonic thermosensitive period for sex determination using an embryo growth
# model reveals a potential bias for sex ratio prediction in turtles.
#
# See the example in the stages datasets
#
#####

resultNest_4p_SSM4p <- searchR(parameters=x, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_SSM4p)
par(mar=c(4, 4, 1, 1))
plot(resultNest_4p_SSM4p$data[[1]][, 1]/60/24,resultNest_4p_SSM4p$data[[1]][, 2], bty="n", las=1,
      xlab="Days of incubation", ylab="Temperatures in °C",
      type="l", xlim=c(0,70),ylim=c(20, 35))
for (i in 2:resultNest_4p_SSM4p$data$IndiceT[3]) {
  par(new=TRUE)
  plot(resultNest_4p_SSM4p$data[[i]][, 1]/60/24,resultNest_4p_SSM4p$data[[i]][, 2],
      bty="n", las=1, xlab="", ylab="", type="l", xlim=c(0,70),ylim=c(20, 35), axes = FALSE)
}
par(mar=c(4, 4, 1, 1))
pMCMC <- TRN_MHmcmc_p(resultNest_4p_SSM4p, accept=TRUE)
# Take care, it can be very long, sometimes several days
resultNest_mcmc_4p_SSM4p <- GRTRN_MHmcmc(result=resultNest_4p_SSM4p,
parametersMCMC=pMCMC, n.iter=10000, n.chains = 1, n.adapt = 0,
thin=1, trace=TRUE)
data(resultNest_mcmc_4p_SSM4p)
out <- as.mcmc(resultNest_mcmc_4p_SSM4p)
# This out obtained after as.mcmc can be used with coda package
# plot() can use the direct output of GRTRN_MHmcmc() function.
plot(resultNest_mcmc_4p_SSM4p, parameters=1, xlim=c(0,550))
plot(resultNest_mcmc_4p_SSM4p, parameters=3, xlim=c(290,320))
# But rather than to use the SD for each parameter independantly, it is
# more logical to estimate the distribution of the curves
new_result <- ChangeSSM(resultmcmc = resultNest_mcmc_4p_SSM4p, result = resultNest_4p_SSM4p,
      temperatures = seq(from = 20, to = 35, by = 0.1),
      initial.parameters = NULL)
par(mar=c(4, 4, 1, 5)+0.4)

plotR(result = resultNest_4p_SSM4p, parameters = new_result$par,
      ylabH = "Temperatures\ndensity", ylimH=c(0, 0.3), atH=c(0, 0.1, 0.2),
      ylim=c(0, 3), show.hist=TRUE)

# Beautiful density plots

plotR(result = resultNest_4p_SSM4p,
      resultmcmc=resultNest_mcmc_4p_SSM4p,
      curves = "MCMC quantiles", show.density=TRUE)

```

```

plotR(resultNest_6p_SSM6p, resultmcmc=resultNest_mcmc_6p_SSM6p,
      ylim=c(0, 4), show.density=TRUE, show.hist=TRUE,
      curves = "MCMC quantiles",
      ylimH=c(0,0.5), atH=c(0, 0.1, 0.2))

## End(Not run)

```

calibrate.datalogger *Calibrate data loggers and correct time series of temperatures*

Description

Calibrate a time series of temperatures. Use or gam or glm. If no temperatures.series is given, it will use the read.temperatures.

Usage

```

calibrate.datalogger(
  control.temperatures = stop("Control temperatures is missing"),
  read.temperatures = stop("Read temperatures must be indicated"),
  temperatures.series = NULL,
  gam = TRUE,
  se.fit = TRUE
)

```

Arguments

control.temperatures	The true temperatures during the calibration process
read.temperatures	The read temperatures during the calibration process
temperatures.series	The temperatures to be converted using calibration
gam	Does gam should be used (TRUE) or glm (FALSE).
se.fit	Do standard errors are to be returned

Details

calibrate.datalogger calibrates data loggers and correct time series of temperatures.

Value

The function will return a corrected time series of temperatures as a vector if se.fit is FALSE or a list if se.fit is TRUE.

Author(s)

Marc Girondot

See Also

Other Data loggers utilities: [movement\(\)](#), [uncertainty.datalogger\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
calibrate.datalogger(control.temperatures=20:30,
                    read.temperatures=(20:30)+rnorm(11))

## End(Not run)
```

ChangeSSM

Generate set of parameters for different forms of thermal norm of reaction

Description

Generate a set of parameters for thermal reaction norm model.

If `initial.parameters` is NULL and `resultmcmc` is not NULL, it will generate parameters and SE based on the average of the curves.

Usage

```
ChangeSSM(
  result = NULL,
  resultmcmc = NULL,
  temperatures = seq(from = 20, to = 35, by = 0.1),
  parameters = NULL,
  initial.parameters = NULL,
  fixed.parameters = NULL,
  outmcmc = "quantiles",
  progressbar = TRUE,
  ...
)
```

Arguments

<code>result</code>	A result obtained by <code>searchR()</code>
<code>resultmcmc</code>	A result obtained by <code>GRTRN_MHmcmc()</code>
<code>temperatures</code>	A vector with incubation temperatures in degrees Celsius
<code>parameters</code>	A vector of parameters for model to be converted. Not necessary if <code>result</code> is provided.

```

initial.parameters      NULL or a vector of parameters for initial model model to be fitted
fixed.parameters       NULL of a vector of parameters to be used but fixed
outmcmc                What statistic will be estimated if a mcmc is provided. Can be "mean-sd" or
                        "quantiles".
progressbar            If TRUE, a progressbar is shown
...                    A control list to be used with optim, see ?optim

```

Details

ChangeSSM convert different forms of thermal norm of reaction

Value

A vector with parameters or a result object formatted with new parameters is result is non null

Author(s)

Marc Girondot

Examples

```

## Not run:
data(resultNest_6p_SSM6p)
x1 <- resultNest_6p_SSM6p$par
data(resultNest_4p_SSM4p)
x2 <- resultNest_4p_SSM4p$par
temperaturesC <- (200:350)/10
s <- ChangeSSM(temperatures=temperaturesC, parameters=x1, initial.parameters=x2)
sY <- plotR(resultNest_6p_SSM6p, ylim=c(0,3), col="black", curves = "ML")
plotR(resultNest_4p_SSM4p, col="red", scaleY=sY, new=FALSE)
plotR(s$par, col="green", scaleY=sY, new=FALSE, curves = "ML")
legend("topleft", legend=c("r function to mimic", "Initial new r function",
"Fitted new r function"), lty=c(1, 1, 1), col=c("black", "red", "green"))
# Other example to fit anchored parameters
data(resultNest_4p_SSM4p)
x0 <- resultNest_4p_SSM4p$par
t <- hist(resultNest_4p_SSM4p, plot=FALSE)
x <- c(3.4, 3.6, 5.4, 5.6, 7.6, 7.5, 3.2)
names(x) <- seq(from=range(t$temperatures)[1], to=range(t$temperatures)[2],
length.out=7)
newx <- ChangeSSM(temperatures = (200:350)/10, parameters = x0,
initial.parameters = x,
control=list(maxit=5000))
# Example on how to generate a set of SSM parameters from anchored parameters
xanchor <- GenerateAnchor(nests=resultNest_4p_SSM4p)
x <- resultNest_4p_SSM4p$par
xanchor["294"] <- 0
xanchor["308"] <- 2.3291035
x <- ChangeSSM(parameters = xanchor,

```



```

        initial.parameters = x, control=list(maxit=5000))
sY <- plotR(resultNest_4p_SSM4p$par, ylim = c(0,3), curves="ML")
plotR(xprime$par, col="red", scaleY=sY, new=FALSE, curves="ML")
legend("topleft", legend=c("Fitted parameters", "Constrained parameters"), lty=1,
      col=c("black", "red"))
# Weibull model
x <- ChangeSSM(temperatures = (200:350)/10,
              parameters = resultNest_4p_SSM4p$par,
              initial.parameters = structure(c(73, 300, 26),
                                           .Names = c("k", "lambda", "scale")),
              control=list(maxit=1000))
# normal asymmetric model
x <- ChangeSSM(temperatures = (200:350)/10,
              parameters = resultNest_4p_SSM4p$par,
              initial.parameters = structure(c(3, 10, 8, 32),
                                           .Names = c("Scale", "sdL", "sdH", "Peak")),
              control=list(maxit=1000))
# trigonometric model
x <- ChangeSSM(temperatures = (200:350)/10,
              parameters = resultNest_4p_SSM4p$par,
              initial.parameters = structure(c(3, 20, 40, 32),
                                           .Names = c("Max", "LengthB", "LengthE", "Peak")),
              control=list(maxit=1000))

# example with a mcmc object, CI being 2.SD
# Note the symmetric CI
data(resultNest_mcmc_4p_SSM4p)
new_result <- ChangeSSM(resultmcmc = resultNest_mcmc_4p_SSM4p, result = resultNest_4p_SSM4p,
                      temperatures = seq(from = 20, to = 35, by = 0.1),
                      outmcmc = "mean-sd",
                      initial.parameters = NULL)

plotR(new_result, ylim=c(0, 3), curves="ML")
# example with a mcmc object, CI being defined by 2.5%-97.5% quantiles
# Note the asymmetric CI
data(resultNest_mcmc_4p_SSM4p)
new_result <- ChangeSSM(resultmcmc = resultNest_mcmc_4p_SSM4p, result = resultNest_4p_SSM4p,
                      temperatures = seq(from = 20, to = 35, by = 0.1),
                      outmcmc = "quantiles",
                      initial.parameters = NULL)

plotR(new_result, ylim=c(0, 3), curves="ML")
plotR(new_result, ylim=c(0, 3), curves="ML quantiles")

## End(Not run)

```

DatabaseNestingArea *Database of RMU for marine turtles*

Description

Database of RMU for marine turtles

Usage

DatabaseNestingArea

Format

A dataframe with raw data.

Details

Database of RMU for marine turtles

Author(s)

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

Maria Sousa Martins <maria.esmartins@gmail.com>

References

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., Duenas, R. B., Casale, P., Choudhury, B. C., Costa, A., Dutton, P. H., Fallabrino, A., Girard, A., Girondot, M., Godfrey, M. H., Hamann, M., Lopez-Mendilaharsu, M., Marcovaldi, M. A., Mortimer, J. A., Musick, J. A., Nel, R., Seminoff, J. A., Troeng, 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.

Examples

```
## Not run:
library(embryogrowth)
data(DatabaseNestingArea)

## End(Not run)
```

DatabaseTSD

Database of TSD information for reptiles

Description

Database of TSD information for reptiles

The columns are:

* Species: Name de the species in binominal nomenclature

* Country: From which country the eggs come from

* Area: Name of the beach or region the eggs come from

* RMU: For marine turtles, name of the RMU for this population; 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., Duenas, R.B., Casale, P.,

Choudhury, B.C., Costa, A., Dutton, P.H., Fallabrino, A., Girard, A., Girondot, M., Godfrey, M.H., Hamann, M., Lopez-Mendilaharsu, M., Marcovaldi, M.A., Mortimer, J.A., Musick, J.A., Nel, R., Seminoff, J.A., Troeng, 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.

- * Incubation.temperature: Nominal incubation temperature
 - * Incubation.temperature.Accuracy: What is the accuracy of the measure of temperature
 - * Incubation.temperature.SD: Experimental SD of incubation temperatures
 - * Incubation.temperature.Amplitude: How much the temperature could fluctuate around nominal temperature
 - * Correction.factor: Difference between the incubator temperature and the eggs temperature
 - * IP.min: Shorter incubation period
 - * IP.max: Longer incubation period
 - * IP.mean: Mean incubation periods
 - * IP.SD: Standard deviation for incubation periods
 - * Total: Total number of eggs incubated
 - * Hatched: Number of hatchlings
 - * NotHatched: Number of embryos with development visible but dead during incubation
 - * Undeveloped: Number of embryos showing no development
 - * Intersexes: Number of individuals intersexes or ambiguous for sex phenotype
 - * Males: Number of individuals identified as males
 - * Females: Number of individuals identified as females
 - * Sexed: Number of sexed individuals
 - * Clutch: Identity of clutch
 - * Reference: Bibliographic reference
 - * Note: Diverse information for this incubation
 - * Version: Date of the version of this database
- Initial version of this database has been built by Maria Sousa Martins.

Usage

DatabaseTSD

Format

A dataframe with raw data.

Details

Database of TSD information for marine turtles

Author(s)

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

References

Binckley C.A., Spotila J.R., Wilson K.S. and Paladino F.V. (1998) Sex determination and sex ratios of Pacific Leatherback Turtles, *Dermodochelys coriacea*. *Copeia*, 1998(2), 291-300.

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See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [P_TRT\(\)](#), [TSP.list](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
data(DatabaseTSD)
DatabaseTSD.version()
totalIncubation_Lo <- subset(DatabaseTSD,
                             Species=="Lepidochelys olivacea" & (!is.na(Sexed) & Sexed!=0),
```

```
      select=c("Males", "Females", "Incubation.temperature"))
tot_Lo <- with(totalIncubation_Lo, tsd(males=Males, females=Females,
  temperatures=Incubation.temperature), parameters.initial = c(P=30.5, S=-0.4))
predict(tot_Lo)

## End(Not run)
```

DatabaseTSD.version *Version of database of TSD information for reptiles*

Description

Return the date of the most recent update of the database.

Usage

```
DatabaseTSD.version()
```

Details

Database of TSD information for marine turtles

Value

The date of the lastest updated version

Author(s)

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

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD](#), [P_TRT\(\)](#), [TSP.list](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
DatabaseTSD.version()

## End(Not run)
```

dydt.exponential *Return the derivative of the exponential function*

Description

Return the derivative of the exponential function
 dydt.exponential(t, size, parms)

Usage

```
dydt.exponential(t, size, parms)
```

Arguments

t	The time in any unit
size	The current size
parms	A vector with alpha and K values being c(alpha=x1, K=x2). K is not used.

Details

dydt.exponential returns the derivative of the exponential function.

Value

A list with the derivative

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(306.174998729436, 333.708348843241,
299.856306141849, 149.046870203155),
.Names = c("DHA", "DHH", "T12H", "Rho25"))
# K or rK are not used for dydt.linear or dydt.exponential
resultNest_4p_exponential <- searchR(parameters=x, fixed.parameters=NULL,
temperatures=formatted, derivate=dydt.exponential, M0=1.7,
test=c(Mean=39.33, SD=1.92))

## End(Not run)
```

dydt.Gompertz *Return the derivative of the Gompertz function*

Description

Return the derivative of the Gompertz function
dydt.Gompertz(t, size, parms)

Usage

```
dydt.Gompertz(t, size, parms)
```

Arguments

t	The time in any unit
size	The current size
parms	A vector with alpha and K values being c(alpha=x1, K=x2)

Details

dydt.Gompertz returns the derivative of the Gompertz function.

Value

A list with the derivative

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(118.768297442004, 475.750095909406, 306.243694918151,
116.055824800264), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
# K or rK are not used for dydt.linear or dydt.exponential
resultNest_4p_SSM4p <- searchR(parameters=x, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_SSM4p)
```

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

```
dydt.linear          Return the derivative of the linear function
```

Description

Return the derivative of the linear function
 dydt.linear(t, size, parms)

Usage

```
dydt.linear(t, size, parms)
```

Arguments

t	The time in any unit
size	The current size
parms	A vector with alpha being c(alpha=x1, K=x2). Only alpha is used.

Details

dydt.Linear returns the derivative of the linear function.

Value

A list with the derivative

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(306.174998729436, 333.708348843241, 299.856306141849,
149.046870203155), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# K or rK are not used for dydt.linear or dydt.exponential
resultNest_4p_linear <- searchR(parameters=x, fixed.parameters=NULL,
temperatures=formatted, derivate=dydt.linear, M0=1.7,
test=c(Mean=39.33, SD=1.92))
```

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

 FormatNests

Create a dataset of class Nests to be used with searchR

Description

Will create a dataset of class Nests to be used with searchR
 FormatNests(nest, previous=x) with x being a previously formatted data.
 The raw data must be organized being:
 First column is the time in minutes since the beginning of incubation
 Each column next is the trace of temperatures, one column for each nest.
 For example, for two nests:
 Time Nest1 Nest2
 0 29.8 27.6
 90 30.2 28.8
 120 30.4 30.7
 180 31.2 32.6
 ...
 65800 30.8 32.6
 65890 30.2
 65950 30.4

The Nest1 ends incubation at 65800 minutes whereas Nest2 ends incubation at 65950 (last row with temperature for each).

The parameter Weight is a vector: weight=c(Nest1=1, Nest2=1.2)

It can be used to format database already formatted with old format; in this case, just use data=xxx with xxx being the old format database.

Usage

```
FormatNests(  
  data = stop("A dataset must be provided !"),  
  previous = NULL,  
  simplify = TRUE,  
  weight = NULL  
)
```

Arguments

data	Data to be newly formatted
previous	Data already formatted
simplify	If TRUE, simply the time series by removing identical time series of temperatures
weight	Named vector with weight for likelihood

Details

FormatNests creates a dataset of class "Nests" to be used with searchR

Value

A list with all the nests formatted to be used with searchR.

Author(s)

Marc Girondot

Examples

```
## Not run:  
library(embryogrowth)  
data(nest)  
formatted <- FormatNests(nest, previous=NULL)  
formatted <- FormatNests(nest)  
  
## End(Not run)
```

GenerateAnchor

Generate a set of anchored parameters

Description

Generate a set of anchored parameters.

It is important that the anchors (i.e. the temperatures used as anchors) encompass the highest and lowest temperatures that are present in nests.

The value for each anchor is $R * 1E5$. The $1E5$ factor allows to value to be close to unity.

Usage

```
GenerateAnchor(  
  temperatures = NULL,  
  nests = NULL,  
  parameters = NULL,  
  number.anchors = 7  
)
```

Arguments

temperatures	A vector with temperatures to serve as anchors
nests	Formatted nest data or result object obtained from searchR()
parameters	A set of parameters value
number.anchors	Number of anchors

Details

GenerateAnchor Generate a set of anchored parameters

Value

A vector with parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
# Example to generate anchored parameters
newp <- GenerateAnchor()
newp <- GenerateAnchor(temperatures=seq(from=20,
  to=35, length.out=7))
newp <- GenerateAnchor(number.anchors=7)
data(nest)
formatted <- FormatNests(nest, previous=NULL)
newp <- GenerateAnchor(nests=formatted)
newp <- GenerateAnchor(nests=formatted, number.anchors=10)
data(resultNest_4p_SSM4p)
newp <- GenerateAnchor(nests=resultNest_4p_SSM4p, number.anchors=7)
newp <- GenerateAnchor(nests=resultNest_4p_SSM4p, temperatures=seq(from=20,
  to=35, length.out=10))
newp <- GenerateAnchor(nests=resultNest_4p_SSM4p, number.anchors=7)
newp <- c(newp, Scale=1)

## End(Not run)
```

GenerateConstInc	<i>Generate a data.frame with constant incubation temperature and incubation duration</i>
------------------	---

Description

Generate a data.frame from constant incubation temperature and incubation duration

Usage

```
GenerateConstInc(
  durations = stop("At least one incubation length must be provided"),
  temperatures = stop("At least one incubation temperature must be provided"),
  names = NULL
)
```

Arguments

durations A vector with incubation durations
 temperatures A vector with incubation temperatures
 names A vector of column names

Details

GenerateConstInc generates a data.frame with constant incubation temperature and incubation duration

Value

A data.frame that can be used with FormatNests()

Author(s)

Marc Girondot

Examples

```
## Not run:
temp_cst <- GenerateConstInc(durations=c(150000, 100100, 100000),
  temperatures=c(28, 30.5, 30.6),
  names=c("T28", "T30.5", "T30.6"))

## End(Not run)
```

GenerateTest

Generate a data.frame that can be used as test value for searchR()

Description

Generate a data.frame that can be used as test value for searchR()

Usage

```
GenerateTest(
  series = stop("A result object or names of series must be provided"),
  size = NULL,
  previous = NULL
)
```

Arguments

series Name of series or object from searchR()
 size Size or mass at hatching. Will be recycled if necessary
 previous Previous formatted test data

Details

GenerateTest Generate a data.frame that can be used as test value for searchR()

Value

A data.frame with size or mass at hatching for each nest

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(resultNest_4p_SSM4p)
testsize1 <- GenerateTest(resultNest_4p_SSM4p)
testsize2 <- GenerateTest(series=resultNest_4p_SSM4p,
size=c(Mean=39.3, SD=1.92))

## End(Not run)
```

GRTRN_MHmcmc

Metropolis-Hastings algorithm for Embryo Growth Rate Thermal Reaction Norm

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

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

To get the SE of the point estimates from `result_mcmc <- GRTRN_MHmcmc(result=try)`, use:

```
result_mcmc$SD
```

coda package is necessary for this function.

The parameters `intermediate` and `filename` are used to save intermediate results every 'intermediate' iterations (for example 1000). Results are saved in a file named `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 processes with user limited time.

Usage

```
GRTRN_MHmcmc(
  result = NULL,
  n.iter = 10000,
  parametersMCMC = NULL,
  n.chains = 1,
  n.adapt = 0,
  thin = 1,
  trace = NULL,
  traceML = FALSE,
  parallel = TRUE,
  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
<code>parallel</code>	If true, try to use several cores using parallel computing
<code>adaptive</code>	Should an adaptive process for SDProp be used
<code>adaptive.lag</code>	Lag to analyze the SDProp value in an adaptive content
<code>adaptive.fun</code>	Function used to change the SDProp
<code>intermediate</code>	Period for saving intermediate result, NULL for no save
<code>filename</code>	If intermediate is not NULL, save intermediate result in this file
<code>previous</code>	Previous result to be continued. Can be the filename in which intermediate results are saved.

Details

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

Value

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

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "T12H", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(118.768297442004, 475.750095909406, 306.243694918151,
116.055824800264), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
resultNest_4p_SSM4p <- searchR(parameters=x, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_SSM4p)
pMCMC <- TRN_MHmcmc_p(resultNest_4p_SSM4p, accept=TRUE)
# Take care, it can be very long; several days
resultNest_mcmc_4p_SSM4p <- GRTRN_MHmcmc(result=resultNest_4p_SSM4p,
adaptive = TRUE,
parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,
n.adapt = 0, thin=1, trace=TRUE)
data(resultNest_mcmc_4p_SSM4p)
out <- as.mcmc(resultNest_mcmc_4p_SSM4p)
# This out can be used with coda package
# Test for stationarity and length of chain
require(coda)
heidel.diag(out)
raftery.diag(out)
# plot() can use the direct output of GRTRN_MHmcmc() function.
plot(resultNest_mcmc_4p_SSM4p, parameters=1, xlim=c(0,550))
plot(resultNest_mcmc_4p_SSM4p, parameters=3, xlim=c(290,320))
# summary() permits to get rapidly the standard errors for parameters
# They are store in the result also.
se <- result_mcmc_4p_SSM4p$SD
# the confidence interval is better estimated by:
apply(out[[1]], 2, quantile, probs=c(0.025, 0.975))
# The use of the intermediate method is as followed;
# Here the total mcmc iteration is 10000, but every 1000, intermediate
# results are saved in file intermediate1000.Rdata:
resultNest_mcmc_4p_SSM4p <- GRTRN_MHmcmc(result=resultNest_4p_SSM4p,
parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,
n.adapt = 0, thin=1, trace=TRUE,
intermediate=1000, filename="intermediate1000.Rdata")
# If run has been stopped for any reason, it can be resumed with:
resultNest_mcmc_4p_SSM4p <- GRTRN_MHmcmc(previous="intermediate1000.Rdata")
# Example to use of the epsilon parameter to get confidence level
```

```

resultNest_4p_epsilon <- resultNest_4p
resultNest_4p_epsilon$fixed.parameters <- c(resultNest_4p_epsilon$par,
      resultNest_4p_epsilon$fixed.parameters)
resultNest_4p_epsilon$par <- c(epsilon = 0)
pMCMC <- TRN_MHmcmc_p(resultNest_4p_epsilon, accept = TRUE)
resultNest_mcmc_4p_epsilon <- GRTRN_MHmcmc(result = resultNest_4p_epsilon,
      n.iter = 10000, parametersMCMC = pMCMC,
      n.chains = 1, n.adapt = 0, thin = 1, trace = TRUE, parallel = TRUE)
data(resultNest_mcmc_4p_epsilon)
plot(resultNest_mcmc_4p_epsilon, parameters="epsilon", xlim=c(-11, 11), las=1)
plotR(resultNest_4p_epsilon, SE=c(epsilon = unname(resultNest_mcmc_4p_epsilon$SD)),
      ylim=c(0, 3), las=1)

## End(Not run)

```

HatchingSuccess.fit *Fit a hatching success model to data using maximum likelihood*

Description

Set of functions to study the hatching success.

The first version of the model was published in:

Laloč, J.-O., Monsinjon, J., Gaspar, C., Touron, M., Genet, Q., Stubbs, J., Girondot, M. & Hays, G.C. (2020) Production of male hatchlings at a remote South Pacific green sea turtle rookery: conservation implications in a female-dominated world. *Marine Biology*, 167, 70.

The version available here is enhanced by using a double flexit model rather than a double logistic model. The flexit model is described here:

Abreu-Grobois, F.A., Morales-Mérida, B.A., Hart, C.E., Guillon, J.-M., Godfrey, M.H., Navarro, E. & Girondot, M. (2020) Recent advances on the estimation of the thermal reaction norm for sex ratios. *PeerJ*, 8, e8451.

Usage

```

HatchingSuccess.fit(
  par = NULL,
  data = stop("data must be provided"),
  fixed.parameters = NULL,
  column.Incubation.temperature = "Incubation.temperature",
  column.Hatched = "Hatched",
  column.NotHatched = "NotHatched",
  hessian = TRUE
)

```

Arguments

par A set of parameters.

data A dataset in a data.frame with a least three columns: Incubation.temperature, Hatched and NotHatched
fixed.parameters A set of parameters that must not be fitted.
column.Incubation.temperature Name of the column with incubation temperatures
column.Hatched Name of the column with hatched number
column.NotHatched Name of the column with not hatched number
hessian Should Hessian matrix be estimated?

Details

HatchingSuccess.fit fits a hatching success model to data

Value

Return a object of class HatchingSuccess

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc_p\(\)](#), [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.lnL\(\)](#), [HatchingSuccess.model\(\)](#), [logLik.HatchingSuccess\(\)](#), [nobs.HatchingSuccess\(\)](#), [plot.HatchingSuccess\(\)](#), [predict.HatchingSuccess\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=0.8)

g.logistic <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccess.lnL(par=g.logistic$par, data=totalIncubation_Cc)

plot(g.logistic)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10,
         K1.low=1, K2.low=-1, K1.high=1, K2.high=-1,
```

```

MaxHS=0.8)

g.flexit <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccess.InL(par=g.flexit$par, data=totalIncubation_Cc)

compare_AICc(logistic=g.logistic, flexit=g.flexit)
plot(x=g.logistic, what = c("observations", "ML", "CI"), replicates=10000)

pMCMC <- HatchingSuccess.MHmcmc_p(result = g.logistic, accept = TRUE)
MCMC <- HatchingSuccess.MHmcmc(result = g.logistic, parametersMCMC = pMCMC,
                               n.iter = 100000,
                               adaptive = TRUE)

plot(MCMC, parameters = "S.low")
plot(MCMC, parameters = "S.high")
plot(MCMC, parameters = "P.low")
plot(MCMC, parameters = "deltaP")
plot(MCMC, parameters = "MaxHS")

plot(x=g.logistic, what = c("observations", "ML", "CI"),
     replicates=10000, resultmcmc=MCMC)

## End(Not run)

```

HatchingSuccess.InL *Return -log likelihood of the data and the parameters*

Description

Set of functions to study the hatching success.

Usage

```

HatchingSuccess.InL(
  par,
  data,
  fixed.parameters = NULL,
  column.Incubation.temperature = "Incubation.temperature",
  column.Hatched = "Hatched",
  column.NotHatched = "NotHatched"
)

```

Arguments

par A set of parameters.

data A dataset in a data.frame with a least three columns: Incubation.temperature, Hatched and NotHatched
fixed.parameters A set of parameters that must not be fitted.
column.Incubation.temperature Name of the column with incubation temperatures
column.Hatched Name of the column with hatched number
column.NotHatched Name of the column with not hatched number

Details

HatchingSuccess.InL return -log likelihood of the data and the parameters

Value

Return -log likelihood of the data and the parameters

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc_p\(\)](#), [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.fit\(\)](#), [HatchingSuccess.model\(\)](#), [logLik.HatchingSuccess\(\)](#), [nobs.HatchingSuccess\(\)](#), [plot.HatchingSuccess\(\)](#), [predict.HatchingSuccess\(\)](#)

Examples

```

## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=0.8)

HatchingSuccess.InL(par=par, data=totalIncubation_Cc)

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccess.InL(par=g$par, data=totalIncubation_Cc)

t <- seq(from=20, to=40, by=0.1)
CIq <- predict(g, temperature=t)

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

```

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

```
HatchingSuccess.MHmcmc
```

```
Metropolis-Hastings algorithm for hatching success
```

Description

Run the Metropolis-Hastings algorithm for hatching success.

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

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

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

To get the SE from `result_mcmc <- HatchingSuccess.MHmcmc(result=try)`, use:

```
result_mcmc$BatchSE or result_mcmc$TimeSeriesSE
```

The batch standard error procedure is usually thought to be not as accurate as the time series methods.

Based on Jones, Haran, Caffo and Neath (2005), the batch size should be equal to $\sqrt{n.iter}$.

Jones, G.L., Haran, M., Caffo, B.S. and Neath, R. (2006) Fixed Width Output Analysis for Markov chain Monte Carlo, Journal of the American Statistical Association, 101:1537-1547.

coda package is necessary for this function.

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 processes at time limited.

Usage

```
HatchingSuccess.MHmcmc(
  result = stop("Give a result of HatchingSuccess.fit()"),
  n.iter = 10000,
  parametersMCMC = NULL,
  n.chains = 1,
  n.adapt = 0,
  thin = 1,
  trace = FALSE,
  traceML = FALSE,
  batchSize = sqrt(n.iter),
  adaptive = FALSE,
  adaptive.lag = 500,
  adaptive.fun = function(x) { ifelse(x > 0.234, 1.3, 0.7) },
  intermediate = NULL,
  filename = "intermediate.Rdata",
  previous = NULL
)
```



```

!is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
        P.low=25, deltaP=10, MaxHS=logit(0.8))

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)
pMCMC <- HatchingSuccess.MHmcmc_p(g, accept=TRUE)
mcmc <- HatchingSuccess.MHmcmc(result=g, parameters = pMCMC,
                              adaptive=TRUE, n.iter=100000, trace=1000)

## End(Not run)

```

HatchingSuccess.MHmcmc_p

Generates set of parameters to be used with HatchingSuccess.MHmcmc()

Description

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

Usage

```

HatchingSuccess.MHmcmc_p(
  result = NULL,
  parameters = NULL,
  fixed.parameters = NULL,
  accept = FALSE
)

```

Arguments

result	An object obtained after a HatchingSuccess.fit() fit
parameters	A set of parameters. Replace the one from result
fixed.parameters	A set of fixed parameters. Replace the one from result
accept	If TRUE, the script does not wait user information

Details

HatchingSuccess.MHmcmc_p generates set of parameters to be used with HatchingSuccess.MHmcmc()

Value

A matrix with the parameters

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.fit\(\)](#), [HatchingSuccess.lnL\(\)](#), [HatchingSuccess.model\(\)](#), [logLik.HatchingSuccess\(\)](#), [nobs.HatchingSuccess\(\)](#), [plot.HatchingSuccess\(\)](#), [predict.HatchingSuccess\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=0.8)

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)
pMCMC <- HatchingSuccess.MHmcmc_p(g, accept=TRUE)
mcmc <- HatchingSuccess.MHmcmc(result=g, parameters = pMCMC,
                              adaptive=TRUE, n.iter=100000, trace=1000)

## End(Not run)
```

`HatchingSuccess.model` *Return the hatching success according the set of parameters and temperatures*

Description

Set of functions to study the hatching success.

Usage

```
HatchingSuccess.model(par, temperature)
```

Arguments

`par` A set of parameters.
`temperature` A vector of temperatures.

Details

HatchingSuccess.model returns the hatching success according the set of parameters and temperatures

Value

Return the hatching success according the set of parameters and temperatures

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc_p\(\)](#), [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.fit\(\)](#), [HatchingSuccess.lnL\(\)](#), [logLik.HatchingSuccess\(\)](#), [nobs.HatchingSuccess\(\)](#), [plot.HatchingSuccess\(\)](#), [predict.HatchingSuccess\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=0.8)

HatchingSuccess.lnL(par=par, data=totalIncubation_Cc)

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccess.lnL(par=g$par, data=totalIncubation_Cc)

plot(g)

## End(Not run)
```

hist.Nests

Show the histogram of temperatures with set of nests

Description

Show the histogram of temperatures with set of nests hist(data)

Usage

```
## S3 method for class 'Nests'  
hist(x, series = "all", ...)
```

Arguments

x	Data formatted using formatdata.
series	Series to be used, logical (TRUE ou FALSE), numbers or names. If "all", all series are used.
...	Parameters used by hist function

Details

hist.Nests shows the histogram of temperatures with set of nests

Value

A list with an histogram object with information on histogram or NULL if no series was selected and the complete set of temperatures used.

Author(s)

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

Examples

```
## Not run:  
library(embryogrowth)  
data(nest)  
formatted <- FormatNests(nest)  
h <- hist(formatted, series="all")  
  
## End(Not run)
```

hist.NestsResult	<i>Show the histogram of temperatures with set of nests</i>
------------------	---

Description

Show the histogram of temperatures with set of nests hist(data)

Usage

```
## S3 method for class 'NestsResult'  
hist(x, series = "all", ...)
```

Arguments

x	Results obtained after searchR
series	Series to be used, logical (TRUE ou FALSE), numbers or names. If "all", all series are used.
...	Parameters used by hist function (example main="Title")

Details

hist.NestsResult shows the histogram of temperatures with set of nests

Value

A list with an histogram object with information on histogram or NULL if no series was selected and the complete set of temperatures used.

Author(s)

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

Examples

```
## Not run:
library(embryogrowth)
data(resultNest_4p_SSM4p)
h <- hist(resultNest_4p_SSM4p, series=c(1:5))

## End(Not run)
```

info.nests

Calculte statistics about nests

Description

This function calculates many statistics about nests.

The embryo.stages is a named vector with relative size as compared to final size at the beginning of the stage. Names are the stages.

For example for SCL in *Caretta caretta*:

```
embryo.stages=structure(c(8.4, 9.4, 13.6, 13.8, 18.9, 23.5, 32.2, 35.2, 35.5, 38.5)/39.33),
.Names = c("21", "22", "23", "24", "25", "26", "27", "28", "29", "30", "31"))
```

indicates that the stages 21 begins at the relative size of 8.4/39.33.

Series can be indicated as the name of the series, their numbers or series or sucession of TRUE or FALSE. "all" indicates that all series must be analyzed.

The likelihood object is just the total likelihood of the data in the model.

If one parameter is named "pipping_emergence" it is used as the number of days between pipping and emergence to calculate the 1/3 and 2/3 of incubation.

The summary object is a data.frame composed of these elements:

- Temperature.max Maximum temperature recorded during incubation

- TimeWeighted.temperature.mean Average temperature weighed by the time at each temperature for all incubation
- TimeWeighted.temperature.se Standard error for the average temperature weighed by the time at each temperature for all incubation
- GrowthWeighted.temperature.mean Average temperature weighed by the growth of embryo for all incubation
- GrowthWeighted.temperature.se Standard error for the average temperature weighed by the growth of embryo for all incubation
- GrowthRateWeighted.temperature.mean Average temperature weighed by the growth rate of embryo for all incubation
- GrowthRateWeighted.temperature.se Standard error for the average temperature weighed by the growth rate of embryo for all incubation
- TSP.TimeWeighted.temperature.mean Average temperature during the TSP weighed by the time at each temperature
- TSP.TimeWeighted.temperature.se Standard error for the average temperature during the TSP weighed by the time at each temperature
- TSP.GrowthWeighted.temperature.mean Average temperature during the TSP weighed by the growth of embryo at each temperature
- TSP.GrowthWeighted.temperature.se Standard error for the average temperature during the TSP weighed by the growth of embryo at each temperature
- TSP.GrowthRateWeighted.temperature.mean Average temperature during the TSP weighed by the growth rate of embryo at each temperature
- TSP.GrowthRateWeighted.temperature.se Standard error for the average temperature during the TSP weighed by the growth rate of embryo at each temperature
- TSP.STRNWeighted.temperature.mean Averaged temperature during the TSP weighed by sexualisation thermal reaction norm
- TSP.STRNWeighted.temperature.se Standard error for temperature during the TSP weighed by sexualisation thermal reaction norm
- TSP.GrowthWeighted.STRNWeighted.temperature.mean Averaged temperature during the TSP weighed by sexualisation thermal reaction norm and embryo growth
- TSP.GrowthWeighted.STRNWeighted.temperature.se Standard error for temperature during the TSP weighed by sexualisation thermal reaction norm and embryo growth
- TSP.GrowthRateWeighted.STRNWeighted.temperature.mean Averaged temperature during the TSP weighed by sexualisation thermal reaction norm and embryo growth rate
- TSP.GrowthRateWeighted.STRNWeighted.temperature.se Standard error for temperature during the TSP weighed by sexualisation thermal reaction norm and embryo growth rate
- TSP.length.mean Average length of the TSP
- TSP.length.se Standard error for length of the TSP
- TSP.begin.mean Average time of the beginning of the TSP
- TSP.begin.se Standard error for the beginning of the TSP
- TSP.end.mean Average time of the end of the TSP

- TSP.se Standard error for the end of the TSP
- PM.GrowthWeighted.mean Proportion of males based on Massey et al. 2019, weighted by growth of embryo
- PM.GrowthWeighted.se Standard error for the proportion of males based on Massey et al. 2019, weighted by growth of embryo
- PM.GrowthRateWeighted.mean Proportion of males based on Massey et al. 2019, weighted by growth rate of embryo
- PM.GrowthRateWeighted.se Standard error for the proportion of males based on Massey et al. 2019, weighted by growth rate of embryo
- PM.TimeWeighted.mean Proportion of males with time effect
- PM.TimeWeighted.se Standard error for the proportion of males with time effect
- Incubation.length.mean Average number of days for the incubation length
- Incubation.length.se Standard error for number of days for the incubation length
- Middlethird.begin.mean Average day at which the middle third incubation begins
- Middlethird.begin.se Standard error for day at which the middle third incubation begins
- Middlethird.end.mean Average day at which the middle third incubation ends
- Middlethird.end.se Standard error at which the middle third incubation ends
- Middlethird.length.mean Average days for second third of incubation
- Middlethird.length.se Standard error for second third of incubation
- MiddleThird.TimeWeighted.temperature.mean Average temperature during the middle third of incubation
- MiddleThird.TimeWeighted.temperature.se Standard error for the temperature during the middle third of incubation
- MiddleThird.GrowthWeighted.temperature.mean Average temperature during the middle third of incubation weighted by embryo growth
- MiddleThird.GrowthWeighted.temperature.se Standard error for temperature during the middle third of incubation weighted by embryo growth
- MiddleThird.GrowthRateWeighted.temperature.mean Average temperature during the middle third of incubation weighted by embryo growth rate
- MiddleThird.GrowthRateWeighted.temperature.se Standard error for temperature during the middle third of incubation weighted by embryo growth rate

The metric object is a list composed of data.frames which have the following attributes for each element of the list:

- time.begin.tsp Average time at the beginning of TSP
- time.end.tsp Average time at the end of TSP
- time.begin.middlethird Average time at the beginning of the middle third of incubation
- time.end.middlethird Average time at the end of the middle third of incubation
- time.begin.tsp.se Standard error for the time at the beginning of TSP
- time.end.tsp.se Standard error for the time at the end of TSP

- `time.begin.middlethird.se` Standard error for the time at the beginning of the middle third of incubation
- `time.end.middlethird.se` Standard error for the time at the end of the middle third of incubation
- `stopattest` NA if `stopattest` was false, TRUE if at least one incubation series was longer than hatchling size and FALSE at contrary

If you indicate new set of temperatures, you must probably also indicate new test values.

Note: four species have predefined embryo stages. `embryo.stages` parameter can take the values:

- `Caretta caretta.SCL`
- `Chelonia mydas.SCL`
- `Emys orbicularis.SCL`
- `Emys orbicularis.mass`
- `Podocnemis expansa.SCL`
- `Generic.ProportionDevelopment`

But remember that mass is not the best proxy to describe the growth of an embryo because it can decrease if the substrate becomes dry.

The progress bar is based on both replicates and timeseries progress.

If `replicate.CI` is null or 0, only maximum likelihood is used and no confidence interval is calculated.

If `replicate.CI` is 1, one random value for the parameters is used but no confidence interval is calculated.

In other cases, `replicate.CI` random samples are used to estimate confidence interval.

Usage

```
info.nests(
  x = NULL,
  parameters = NULL,
  NestsResult = NULL,
  resultmcmc = NULL,
  hessian = NULL,
  GTRN.CI = NULL,
  fixed.parameters = NULL,
  SE = NULL,
  temperatures = NULL,
  derivate = NULL,
  test = NULL,
  stopattest = FALSE,
  M0 = NULL,
  series = "all",
  TSP.borders = NULL,
  embryo.stages = "Generic.ProportionDevelopment",
  TSP.begin = 0,
  TSP.end = 0.5,
```

```

replicate.CI = 100,
weight = NULL,
out = "likelihood",
fill = NULL,
SexualisationTRN = NULL,
SexualisationTRN.mcmc = NULL,
SexualisationTRN.CI = NULL,
metric.end.incubation = NA,
metabolic.heating = 0,
temperature.heterogeneity = 0,
progress = FALSE,
warnings = TRUE,
parallel = TRUE,
tsd = NULL,
tsd.CI = NULL,
tsd.mcmc = NULL
)

```

Arguments

x	A set of parameters to model the embryo growth thermal reaction norm or a NestsResult object.
parameters	A set of parameters to model the embryo growth thermal reaction norm. It will replace the parameters included in NestsResult (same as x).
NestsResult	A NestsResult object generated by searchR to model the embryo growth thermal reaction
resultmcmc	A mcmc result for embryo growth thermal reaction norm
hessian	An hessian matrix for embryo growth thermal reaction norm. It will replace the hessian matrix included in NestResult object.
GTRN.CI	How to estimate CI for embryo growth thermal reaction norm; can be NULL, "SE", "MCMC", or "Hessian".
fixed.parameters	A set of fixed parameters to model the embryo growth thermal reaction norm. It will replace the fixed parameters included in NestsResult.
SE	Standard error for each parameter. It will replace the SE in NestsResult. Use SE=NA to remove SE from NestResult
temperatures	Timeseries of temperatures formatted using formatNests(). It will replace the one in NestsResult.
derivate	Function used to fit embryo growth: dydt.Gompertz, dydt.exponential or dydt.linear. It will replace the one in NestsResult.
test	Mean and SD of size of hatchlings. It will replace the one in NestsResult.
stopattest	TRUE or FALSE. If TRUE, the model stops when proxy of size reached the mean test size.
M0	Measure of hatchling size proxy at laying date. It will replace the one in NestsResult.

series	The name or number of the series to be estimated.
TSP.borders	The limits of TSP in stages. See embryo.stages parameter.
embryo.stages	The embryo stages. At least TSP.borders stages must be provided to estimate TSP borders. See note.
TSP.begin	Where TSP begin during the stage of beginning? In relative proportion of the stage.
TSP.end	Where TSP begin during the stage of ending? In relative proportion of the stage.
replicate.CI	Number of replicates to estimate CI. See description
weight	Weights of the different nests to estimate likelihood. It will replace the ones in NestsResult.
out	Can take the values of "likelihood" or "metric" or "summary". "metric" and "summary" can be combined: c("metric", "summary")
fill	Number of minutes between two records. Create new one if they do not exist. NULL does not change the time of temperature recordings.
SexualisationTRN	A set of parameters used to model sexualisation thermal reaction norm during TSP or a result of STRN()
SexualisationTRN.mcmc	A mcmc object obtained from STRN_MHmcmc() to generate variability for sexualisation thermal reaction norm during TSP
SexualisationTRN.CI	How to estimate CI of sexualisation thermal reaction norm. Can be NULL, "SE", "MCMC", or "Hessian".
metric.end.incubation	The expected metric at the end of incubation. Used to calibrate TSP size. If NULL, take the maximum Mean of the test parameter. If NA, use the actual final size. Can be a vector and is recycled if necessary.
metabolic.heating	Degrees Celsius to be added at the end of incubation due to metabolic heating.
temperature.heterogeneity	SD of heterogeneity of temperatures. Can be 2 values, sd_low and sd_high and then HelpersMG::r2norm() is used.
progress	If FALSE, the progress bar is not shown (useful for using with sweave or knitr)
warnings	If FALSE, does not show warnings
parallel	If TRUE use parallel version for nests estimation
tsd	A object from tsd() that describe the thermal react norm of sex ratio at constant temperatures
tsd.CI	How to estimate CI for sex ratio thermal reaction norm; Can be NULL, "SE", "MCMC", or "Hessian".
tsd.mcmc	A object from tsd_MHmcmc()

Details

Calculate statistics about nests

Value

Return of the total likelihood or a list with \$metric and \$summary depending on out parameter

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(resultNest_4p_SSM4p)
summary.nests <- info.nests(resultNest_4p_SSM4p, out="summary",
  embryo.stages="Caretta caretta.SCL",
  replicate.CI=100,
  resultmcmc=resultNest_mcmc_4p_SSM4p,
  GTRN.CI="MCMC",
  progress=TRUE)
# Result is in summary.nests$summary
infoall <- info.nests(resultNest_4p_SSM4p)
# Result is a value
infoall.df <- info.nests(resultNest_4p_SSM4p, out="metric",
  embryo.stages="Caretta caretta.SCL",
  replicate.CI=100,
  resultmcmc=resultNest_mcmc_4p_SSM4p,
  GTRN.CI="MCMC",
  progress=TRUE)
# Result is in infoall.df$metric
infoall.both <- info.nests(resultNest_4p_SSM4p,
  embryo.stages="Caretta caretta.SCL",
  out=c("metric", "summary"), replicate.CI=100,
  resultmcmc=resultNest_mcmc_4p_SSM4p,
  GTRN.CI="MCMC",
  progress=TRUE)
# Results are in infoall.both$summary and in infoall.both$metric
infoall.both <- info.nests(resultNest_4p_SSM4p,
  embryo.stages="Caretta caretta.SCL",
  out=c("metric", "summary"), replicate.CI=100,
  GTRN.CI="Hessian",
  progress=TRUE)
infoall.both <- info.nests(resultNest_4p_SSM4p,
  embryo.stages="Caretta caretta.SCL",
  out=c("metric", "summary"), replicate.CI=100,
  GTRN.CI="SE",
  progress=TRUE)
# Example of use of embryo.stages and TSP.borders:
summary.nests <- info.nests(resultNest_4p_SSM4p, out="summary",
  embryo.stages=c("10"=0.33, "11"=0.33, "12"=0.66, "13"=0.66),
  TSP.borders = c(10, 12),
  replicate.CI=100,
  progress=TRUE)
```

```
#####
# Sex ratio using Massey et al. method PM
#####

# Massey, M.D., Holt, S.M., Brooks, R.J., Rollinson, N., 2019. Measurement
# and modelling of primary sex ratios for species with temperature-dependent
# sex determination. J Exp Biol 222, 1-9.

CC_Mediterranean <- subset(DatabaseTSD, RMU=="Mediterranean" &
Species=="Caretta caretta" & (!is.na(Sexed) & Sexed!=0))
tsdL <- with (CC_Mediterranean, tsd(males=Males, females=Females,
                                temperatures=Incubation.temperature,
                                equation="logistic", replicate.CI=NULL))

PM <- info.nests(resultNest_4p_SSM4p,
embryo.stages="Caretta caretta.SCL", replicate.CI=100,
GTRN.CI="Hessian",
out="summary", progress=TRUE, tsd=tsdL)

sr_TSP_SCLW <- predict(tsdL, temperatures=PM$summary[, "TSP.GrowthWeighted.temperature.mean"],
                      temperature.se=PM$summary[, "TSP.GrowthWeighted.temperature.se"])

plot_errbar(x=sr_TSP_SCLW["50%", ], y=PM$summary[, "PM.GrowthWeighted.mean"],
            x.minus=sr_TSP_SCLW["2.5%", ],
            x.plus=sr_TSP_SCLW["97.5%", ],
            errbar.y=2*PM$summary[, "PM.GrowthWeighted.se"], xlab="CTE SCL growth",
            ylab="PM Massey et al. 2016", xlim=c(0, 1), ylim=c(0, 1), las=1)
segments(x0=0, y0=0, x1=1, y1=1, lty=2, col="red")

sr_TSP_TW <- predict(tsdL, temperatures=PM$summary[, "TSP.TimeWeighted.temperature.mean"],
                    temperature.se=PM$summary[, "TSP.TimeWeighted.temperature.se"])

plot_errbar(x=sr_TSP_TW["50%", ], y=PM$summary[, "PM.GrowthWeighted.mean"],
            x.minus=sr_TSP_TW["2.5%", ],
            x.plus=sr_TSP_TW["97.5%", ],
            errbar.y=2*PM$summary[, "PM.GrowthWeighted.se"], xlab="CTE Time",
            ylab="PM Massey et al. 2016", xlim=c(0, 1), ylim=c(0, 1), las=1)
segments(x0=0, y0=0, x1=1, y1=1, lty=2, col="red")

plot_errbar(x=sr_TSP_TW["50%", ], y=sr_TSP_SCLW["50%", ],
            x.minus=sr_TSP_TW["2.5%", ],
            x.plus=sr_TSP_TW["97.5%", ],
            y.minus=sr_TSP_SCLW["2.5%", ],
            y.plus=sr_TSP_SCLW["97.5%", ], xlab="CTE Time",
            ylab="CTE SCL", xlim=c(0, 1), ylim=c(0, 1), las=1)
segments(x0=0, y0=0, x1=1, y1=1, lty=2, col="red")

# Relationship between growth and growth rate

infoall.df <- info.nests(resultNest_4p_SSM4p, out="metric",
embryo.stages="Caretta caretta.SCL",
replicate.CI=100,
resultmcmc=resultNest_mcmc_4p_SSM4p,
```

```

GTRN.CI="MCMC",
progress=TRUE)
layout(1)
plot(x=infoall.df$metric[[1]][, "Time"][-nrow(infoall.df$metric[[1])],
      y=infoall.df$metric[[1]][, "R"][-nrow(infoall.df$metric[[1])],
      type="l", las=1, bty="n",
      xlab="Time in minute", ylab="Growth Rate", ylim=c(0, 3E-5), xlim=c(0, 100000))
plot(x=infoall.df$metric[[1]][, "Time"][-nrow(infoall.df$metric[[1])],
      y=diff(infoall.df$metric[[1]][, "SCL"]),
      type="l", las=1, bty="n",
      xlab="Time in minute", ylab="Growth", ylim=c(0, 5), xlim=c(0, 100000))
plot(x=infoall.df$metric[[1]][, "Time"][-nrow(infoall.df$metric[[1])],
      y=diff(infoall.df$metric[[1]][, "SCL"])/diff(infoall.df$metric[[1]][, "Time"]),
      type="l", las=1, bty="n",
      xlab="Time in minute", ylab="Growth per minute", ylim=c(0, 0.0008), xlim=c(0, 100000))
plot(x=infoall.df$metric[[1]][, "Time"][-nrow(infoall.df$metric[[1])],
      y=(diff(infoall.df$metric[[1]][, "SCL"])/diff(infoall.df$metric[[1]][, "Time"])) /
        (infoall.df$metric[[1]][, "R"][-nrow(infoall.df$metric[[1])]),
      type="l", las=1, bty="n",
      xlab="Time in minute", ylab="Ratio Actual Growth / Growth rate",
      ylim=c(0, 40), xlim=c(0, 100000))

## End(Not run)

```

likelihoodR

Estimate the likelihood of a set of parameters for nest incubation data

Description

Estimate the likelihood of a set of parameters for nest incubation data

Usage

```

likelihoodR(
  result = NULL,
  parameters = NULL,
  fixed.parameters = NULL,
  temperatures = NULL,
  derivate = NULL,
  test = NULL,
  M0 = NULL,
  hessian = FALSE,
  weight = NULL,
  parallel = TRUE,
  echo = TRUE
)

```

Arguments

result	A object obtained after searchR or likelihoodR
parameters	A set of parameters
fixed.parameters	A set of parameters that will not be changed
temperatures	Timeseries of temperatures
derivate	Function used to fit embryo growth: dydt.Gompertz, dydt.exponential or dydt.linear
test	Mean and SD of size of hatchlings
M0	Measure of hatchling size or mass proxi at laying date
hessian	If TRUE, the hessian matrix is estimated and the SE of parameters estimated.
weight	A named vector of the weight for each nest for likelihood estimation
parallel	If true, try to use several cores using parallel computing.
echo	If FALSE, does not display the result.

Details

likelihoodR estimates the likelihood of a set of parameters for nest incubation data

Value

A result object

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
# K for Gompertz must be set as fixed parameter or being a constant K
# or relative to the hatchling size rK
x <- structure(c(118.768297442004, 475.750095909406, 306.243694918151,
116.055824800264), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
# K or rK are not used for dydt.linear or dydt.exponential
lresultNest_4p <- likelihoodR(parameters=x, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_SSM4p)
```

```
LresultNest_4p <- likelihoodR(result=resultNest_4p_SSM4p)
## End(Not run)
```

```
logLik.HatchingSuccess
      Return -log L of a fit
```

Description

Set of functions to study the hatching success.

Usage

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

Arguments

object	The return of a fit done with fitHS.
...	Not used

Details

logLik.HatchingSuccess returns -log L of a fit

Value

Return -log L of a fit

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc_p\(\)](#), [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.fit\(\)](#), [HatchingSuccess.lnL\(\)](#), [HatchingSuccess.model\(\)](#), [nobs.HatchingSuccess\(\)](#), [plot.HatchingSuccess\(\)](#), [predict.HatchingSuccess\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=logit(0.8))

HatchingSuccesss.lnL(par=par, data=totalIncubation_Cc)

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccesss.lnL(par=g$par, data=totalIncubation_Cc)

t <- seq(from=20, to=40, by=0.1)
CIq <- predict(g, temperature=t)

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

## End(Not run)
```

logLik.NestsResult *Return Log Likelihood of a fit generated by searchR*

Description

Return Log Likelihood of a fit generated by searchR

Usage

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

Arguments

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

Details

logLik.NestsResult Return Log Likelihood of a fit

Value

The Log Likelihood value of the fitted model and data

Author(s)

Marc Girondot

Examples

```
## Not run:  
library(embryogrowth)  
data(resultNest_4p_SSM4p)  
logLik(resultNest_4p_SSM4p)  
AIC(resultNest_4p_SSM4p)  
  
## End(Not run)
```

logLik.STRN

Return Log Likelihood of a fit generated by STRN

Description

Return Log Likelihood of a fit generated by STRN

Usage

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

Arguments

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

Details

logLik.STRN Return Log Likelihood of a fit

Value

The Log Likelihood value of the fitted model and data

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(resultNest_4p_SSM4p)
logLik(resultNest_4p_SSM4p)
AIC(resultNest_4p_SSM4p)

## End(Not run)
```

`logLik.tsd`*Return Log Likelihood of a fit generated by tsd*

Description

Return Log Likelihood of a fit generated by tsd. The object has 3 attributes: `nall`, and `nobs` the number of observations, `df`, the number of fitted parameters.

Usage

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

Arguments

<code>object</code>	A result file generated by tsd
<code>...</code>	Not used

Details

`logLik.tsd` Return Log Likelihood of a fit

Value

The Log Likelihood value of the fitted model and data

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
m <- c(10, 14, 7, 4, 3, 0, 0)
f <- c(0, 1, 2, 4, 15, 10, 13)
t <- c(25, 26, 27, 28, 29, 30, 31)
result <- tsd(males=m, females=f, temperatures=t)
logLik(result)
```

```
AIC(result)
## End(Not run)
```

movement	<i>Analyze movement recorded within a nest with an accelerometer datalogger</i>
----------	---

Description

This function is used to evaluate significant movement within a nest.

Usage

```
movement(
  x = stop("data.frame must be provided"),
  col.time = "Time",
  col.x = "x",
  col.y = "y",
  col.z = "z",
  NumberRecordBeforeEmergence = 1900,
  k = 4,
  Windowsize = 15
)
```

Arguments

x	A data.frame with 4 columns, one for time and three for x, y, and z position
col.time	Name of the column with time
col.x	Name of the column with x positions
col.y	Name of the column with y positions
col.z	Name of the column with z positions
NumberRecordBeforeEmergence	Number of records in quiet period
k	Factor to multiply SD to prevent false positive detection
Windowsize	Number of records used for moving average

Details

movement is a function that permits to analyze movement datalogger

Value

The function will return a list

Author(s)

Marc Girondot

See AlsoOther Data loggers utilities: [calibrate.datalogger\(\)](#), [uncertainty.datalogger\(\)](#)**Examples**

```
## Not run:
library(embryogrowth)
mv <- movement(x=dataf,
               col.time="Time",
               col.x="x", col.y="y", col.z="z")

## End(Not run)
```

MovingIncubation

Simulate incubation of a nest with the beginning of incubation varying

Description

Simulate incubation of a nest with the beginning varying day by day
Temperatures must be in a data.frame with one column (Time) being the time and the second the temperatures (Temperature). A third column can indicate the temperature at the end of incubation (Temperature.end.incubation). Do not use FormatNests() for this dataframe.

Usage

```
MovingIncubation(
  NestsResult = NULL,
  resultmcmc = NULL,
  temperatures.df = stop("A data.frame must be provided"),
  metabolic.heating = 0,
  GTRN.CI = "Hessian",
  temperature.heterogeneity = 0,
  average.incubation.duration = 60 * 1440,
  skip = 1,
  parameters = NULL,
  fixed.parameters = NULL,
  SE = NULL,
  hessian = NULL,
  derivate = NULL,
  test = NULL,
  M0 = NULL,
  TSP.borders = c(21, 26),
  embryo.stages = "Caretta caretta.SCL",
```

```

SexualisationTRN = NULL,
SexualisationTRN.CI = "Hessian",
SexualisationTRN.mcmc = NULL,
replicate.CI = 1,
parallel = TRUE,
progressbar = TRUE
)

```

Arguments

NestsResult	A result file generated by searchR
resultmcmc	A mcmc result. Will be used rather than SE if provided.
temperatures.df	A data.frame with 2 or 3 columns: Times, Temperatures and Temperatures.end.incubation (facultative)
metabolic.heating	Degrees Celsius to be added at the end of incubation due to metabolic heating
GTRN.CI	How to estimate CI for embryo growth thermal reaction norm; can be NULL, "SE", "MCMC", or "Hessian".
temperature.heterogeneity	SD of heterogeneity of temperatures. Can be 2 values, sd_low and sd_high and then HelpersMG::r2norm() is used.
average.incubation.duration	The average time to complete incubation (not used if metabolic heating is setup)
skip	Number of data to skip between two runs
parameters	A set of parameters if result is not provided.
fixed.parameters	Another set of parameters if result is not provided.
SE	Standard error for each parameter if not present in result is not provided
hessian	A hessian matrix
derivate	Function used to fit embryo growth: dydt.Gompertz, dydt.exponential or dydt.linear
test	Mean and SD of size of hatchlings as a vector ie test=c(Mean=xx, SD=yy)
M0	Measure of hatchling size proxi at laying date
TSP.borders	The limits of TSP
embryo.stages	The embryo stages. At least TSP.borders stages must be provided to estimate TSP length
SexualisationTRN	A model for sexualisation thermal reaction norm during TSP obtained using STRN()
SexualisationTRN.CI	How to estimate CI of sexualisation thermal reaction norm. Can be NULL, "SE", "MCMC", or "Hessian".
SexualisationTRN.mcmc	MCMC object for STRN.

replicate.CI	Number of randomizations to estimate CI
parallel	Should parallel computing be used. TRUE or FALSE
progressbar	Should a progress bar be shown ? TRUE or FALSE

Details

MovingIncubation simulate incubation of a nest with the beginning varying day by day

Value

A dataframe with informations about thermosensitive period length and incubation length day by day of incubation

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(resultNest_4p_SSM4p)
ti <- seq(from=0, to=(60*24*100), by=60)
temperatures <- rnorm(length(ti), 29, 5)
temperatures <- temperatures+ti/(60*24*100)/2
layout(mat=1:3)
parpre <- par(mar=c(4, 4, 1, 1)+0.4)
plot(ti/(60*24), temperatures, type="l", xlab="Days",
      ylab=expression("Nest temperature in "*degree*"C"), bty="n", las=1)
# The sexualisation thermal reaction norm is calculated for South Pacific RMU
out <- MovingIncubation(NestsResult=resultNest_4p_SSM4p,
  temperatures.df=data.frame(Time=ti, Temperature=temperatures),
  metabolic.heating = 0,
  SexualisationTRN = structure(c(71.922411148397, 613.773055147801,
  318.059753164125, 120.327257089974),
  .Names = c("DHA", "DHH", "T12H", "Rho25"))
with(out, plot(Time/(60*24), Incubation.length.mean/(60*24),
  xlab="Days along the season",
  ylab="Incubation duration",
  type="l", bty="n", las=1, ylim=c(70, 80)))
with(out, plot(Time/(60*24), TSP.GrowthWeighted.STRNWeighted.temperature.mean,
  xlab="Days along the season",
  ylab=expression("CTE for sex ratio in "*degree*"C"),
  type="l", bty="n", las=1, ylim=c(30, 31)))
par(mar=parpre)
layout(mat=c(1))

## End(Not run)
```

nest *Timeseries of temperatures for nests*

Description

Timeseries of temperatures for nests

Usage

nest

Format

A dataframe with raw data

Details

Timeseries of temperatures for nests

Author(s)

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

References

Girondot, M. & Kaska, Y. 2014. A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*. 45, 96-102.

Examples

```
## Not run:  
library(embryogrowth)  
data(nest)  
  
## End(Not run)
```

nobs.HatchingSuccess *Return number of observations of a fit*

Description

Set of functions to study the hatching success.

Usage

```
## S3 method for class 'HatchingSuccess'  
nobs(object, ...)
```

Arguments

object	The return of a fit done with fitHS.
...	Not used

Details

nobs.NestsResult Return number of observations of a fit

Value

Return number of observations of a fit

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc_p\(\)](#), [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.fit\(\)](#), [HatchingSuccess.lnL\(\)](#), [HatchingSuccess.model\(\)](#), [logLik.HatchingSuccess\(\)](#), [plot.HatchingSuccess\(\)](#), [predict.HatchingSuccess\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=logit(0.8))

HatchingSuccess.lnL(par=par, data=totalIncubation_Cc)

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccess.lnL(par=g$par, data=totalIncubation_Cc)

plot(g)

## End(Not run)
```

nobs.NestsResult *Return number of observations of a fit*

Description

Return number of observations of a fit.
This function is used for `bbmle::ICtb()`.

Usage

```
## S3 method for class 'NestsResult'  
nobs(object, ...)
```

Arguments

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

Details

nobs.NestsResult Return number of observations of a fit

Value

Return number of observations of a fit

Author(s)

Marc Girondot

Examples

```
## Not run:  
library(embryogrowth)  
data(resultNest_4p_SSM4p)  
logLik(resultNest_4p_SSM4p)  
AIC(resultNest_4p_SSM4p)  
nobs(resultNest_4p_SSM4p)  
  
## End(Not run)
```

plot.HatchingSuccess *Plot results of HatchingSuccess.fit() that best describe hatching success*

Description

Plot the estimates that best describe hatching success.

If replicates is 0, it returns only the fitted model.

If replicates is null and resultmcmc is not null, it will use all the mcmc data.

if replicates is lower than the number of iterations in resultmcmc, it will use sequence of data regularly thined.

Usage

```
## S3 method for class 'HatchingSuccess'
plot(
  x,
  xlim = c(20, 40),
  ylim = c(0, 1),
  xlab = "Constant incubation temperatures",
  ylab = "Hatching success",
  bty = "n",
  las = 1,
  col.observations = "red",
  pch.observations = 19,
  cex.observations = 1,
  show.CI.observations = TRUE,
  col.ML = "black",
  lty.ML = 1,
  lwd.ML = 1,
  col.median = "black",
  lty.median = 2,
  lwd.median = 1,
  col.CI = "black",
  lty.CI = 3,
  lwd.CI = 1,
  replicates = NULL,
  resultmcmc = NULL,
  polygon = TRUE,
  color.polygon = rgb(red = 0.8, green = 0, blue = 0, alpha = 0.1),
  what = c("observations", "ML", "CI"),
  ...
)
```

Arguments

x A result file generated by HatchingSuccess.fit()

<code>xlim</code>	Range of temperatures
<code>ylim</code>	Hatching success range for y-axis
<code>xlab</code>	x label
<code>ylab</code>	y label
<code>bty</code>	bty graphical parameter
<code>las</code>	las graphical parameter
<code>col.observations</code>	Color of observations
<code>pch.observations</code>	Character used for observation (no observations if NULL)
<code>cex.observations</code>	Size of characters for observations
<code>show.CI.observations</code>	Should the confidence interval of the observations be shown ?
<code>col.ML</code>	Color of the maximum likelihood model
<code>lty.ML</code>	Line type of the maximum likelihood model (no line if NULL)
<code>lwd.ML</code>	Line width of the maximum likelihood model
<code>col.median</code>	Color of the median model
<code>lty.median</code>	Line type of the median model (no line if NULL)
<code>lwd.median</code>	Line width of the mean model
<code>col.CI</code>	Color of the 95% confidence interval lines
<code>lty.CI</code>	Line type of the 95% confidence interval lines (no line if NULL)
<code>lwd.CI</code>	Line width of the 95% confidence interval lines
<code>replicates</code>	Number of replicates to estimate confidence interval
<code>resultmcmc</code>	Results obtained using <code>HatchingSuccess.MHmcmc()</code>
<code>polygon</code>	If TRUE, confidence interval is shown as a polygon
<code>color.polygon</code>	The color used for polygon
<code>what</code>	Indicate what to plot: "observations", "ML", "CI"
<code>...</code>	Parameters for <code>plot()</code>

Details

`plot.HatchingSuccess` plot result of `HatchingSuccess.fit()` or `HatchingSuccess.MHmcmc()` that best describe hatching success

Value

Nothing

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc_p\(\)](#), [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.fit\(\)](#), [HatchingSuccess.lnL\(\)](#), [HatchingSuccess.model\(\)](#), [logLik.HatchingSuccess\(\)](#), [nobs.HatchingSuccess\(\)](#), [predict.HatchingSuccess\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=logit(0.8))

HatchingSuccess.lnL(par=par, data=totalIncubation_Cc)

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccess.lnL(par=g$par, data=totalIncubation_Cc)

plot(g, replicates=0)
plot(g, replicates=10000)

pMCMC <- HatchingSuccess.MHmcmc_p(g, accept=TRUE)
mcmc <- HatchingSuccess.MHmcmc(result=g, parameters = pMCMC,
                              adaptive=TRUE, n.iter=100000, trace=1000)

plot(g, resultmcmc=mcmc)
plot(g, resultmcmc=mcmc, pch.observations=NULL, lty.mean=NULL)

## End(Not run)
```

plot.NestsResult *Plot the embryo growth*

Description

Plot the embryo growth from one or several nests.

The `embryo.stages` is a named vector with relative size as compared to final size at the beginning of the stage. Names are the stages.

For example for SCL in *Caretta caretta*:

```
embryo.stages=structure(c(8.4, 9.4, 13.6, 13.8, 18.9, 23.5, 32.2, 35.2, 35.5, 38.5)/39.33),
```

```
.Names = c("21", "22", "23", "24", "25", "26", "27", "28", "29", "30", "31"))
```

indicates that the stages 21 begins at the relative size of 8.4/39.33.

Series can be indicated as the name of the series, its number or succession of TRUE or FALSE. "all" indicates that all series must be printed.

`show.fioritures` parameter does not affect `show.test` option.

Note: Four species have predefined embryo stages. `embryo.stages` parameter can take the values:

- `Caretta caretta.SCL`
- `Chelonia mydas.SCL`
- `Emys orbicularis.SCL`
- `Emys orbicularis.mass`
- `Podocnemis expansa.SCL`
- `Generic.ProportionDevelopment`

Usage

```
## S3 method for class 'NestsResult'
plot(
  x,
  ...,
  parameters = NULL,
  fixed.parameters = NULL,
  resultmcmc = NULL,
  hessian = NULL,
  SE = NULL,
  temperatures = NULL,
  derivate = NULL,
  test = NULL,
  stopattest = FALSE,
  M0 = NULL,
  weight = NULL,
  series = "all",
  TSP.borders = NULL,
  embryo.stages = NULL,
  TSP.begin = 0,
  TSP.end = 0.5,
  replicate.CI = 100,
  metric.end.incubation = NULL,
  col.stages = "blue",
  col.PT = "red",
  col.TSP = "gray",
  col.temperatures = "green",
  col.S = "black",
  lty.temperatures = 1,
  lwd.temperatures = 2,
  ylimT = NULL,
  ylimS = NULL,
  xlim = NULL,
  show.stages = TRUE,
  show.TSP = TRUE,
  show.third = TRUE,
  GTRN.CI = NULL,
```

```

show.metric = TRUE,
show.fioritures = TRUE,
show.temperatures = TRUE,
show.PT = TRUE,
PT = c(mean = NA, SE = NA),
show.test = TRUE,
add = FALSE,
lab.third = "2nd third of incubation",
at.lab.third = 10,
lab.PT = "PT",
lab.stages = "Stages",
at.lab.TSP = 8,
lab.TSP = "TSP",
mar = c(4, 5, 4, 5) + 0.3,
xlab = "Days of incubation",
ylabT = expression("Temperature in " * degree * "C"),
ylabS = "Embryo metric",
progress = TRUE,
parallel = TRUE
)

```

Arguments

x	A result file generated by searchR
...	Parameters for plot()
parameters	A set of parameters if result is not provided.
fixed.parameters	Another set of parameters if result is not provided.
resultmcmc	A mcmc result. Will be used rather than SE if provided.
hessian	An Hessian matrix.
SE	Standard error for each parameter if result is not provided, or replace the one in NestsResult. Use SE=NA to remove SE from NestResult
temperatures	Timeseries of temperatures formatted using formatNests(). Will replace the one in result.
derivate	Function used to fit embryo growth: dydt.Gompertz, dydt.exponential or dydt.linear
test	Mean and SD of size of hatchlings
stopattest	TRUE or FALSE. If TRUE, the model stops when proxy of size reached the mean test size.
M0	Measure of hatchling size proxi at laying date
weight	Weights of the different nests to estimate likelihood
series	The name or number of the series to be displayed. Only one series can be displayed at a time.
TSP.borders	The limits of TSP in stages. See embryo.stages parameter.
embryo.stages	The embryo stages. At least TSP.borders stages must be provided to estimate TSP borders. See note.

TSP.begin	Where TSP begin during the stage of beginning? In relative proportion of the stage.
TSP.end	Where TSP begin during the stage of ending? In relative proportion of the stage.
replicate.CI	Number of replicates to estimate CI. If 1, no CI is estimated.
metric.end.incubation	The expected metric at the end of incubation. Used to calibrate TSP size. If NULL, take the maximum Mean of the test parameter. If NA, use the actual final size. Can be a vector and is recycled if necessary.
col.stages	The color of the stages
col.PT	The color of the pivotal temperature
col.TSP	The color of the TSP
col.temperatures	The color of the temperatures
col.S	The color of the size or mass. Can be a vector (useful when series="all" option).
lty.temperatures	Type of line for temperatures
lwd.temperatures	Width of line for temperatures
ylimT	Range of temperatures to be displayed
ylimS	Range of size to be displayed
xlim	Range of incubation days to be displayed
show.stages	TRUE or FALSE, does the embryo stages should be displayed?
show.TSP	TRUE or FALSE, does the TSP borders should be displayed?
show.third	TRUE or FALSE, does the first and second third borders should be displayed?
GTRN.CI	How to estimate CI; can be NULL, "SE", "MCMC", or "Hessian"
show.metric	TRUE or FALSE, does the plot of embryo metric is shown?
show.fioritures	If FALSE, set show.PT, show.temperatures, show.stages, show.TSP, show.third to FALSE, GTRN.CI to NULL
show.temperatures	TRUE or FALSE, does the temperatures should be displayed?
show.PT	TRUE or FALSE, does the pivotal temperature should be displayed?
PT	Value for pivotal temperature, mean and SE
show.test	TRUE or FALSE, does the hatchling size should be displayed
add	If TRUE, all the curves are shown on the same graph
lab.third	Label for 2nd third of incubation
at.lab.third	Position of Label for 2nd third of incubation [default=10]; y-lim is scaled by at.lab.third
lab.PT	Label for Pivotal Temperature
lab.stages	Label for Stages

at.lab.TSP	Position of Label for TSP [default=8]; y-lim is scaled by at.lab.third
lab.TSP	Label for the TSP
mar	Parameter mar used for plot
xlab	Label for axis
ylabT	Label for temperature axis
ylabS	Label for size axis
progress	If FALSE, the progress bar is not shown (useful for use with sweave or knitr)
parallel	Should parallel computing be used ? TRUE or FALSE
NestsResult	A NestsResult file generated by searchR

Details

plot.NestsResult Plot the embryo growth

Value

Nothing

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(resultNest_4p_SSM4p)
plot(resultNest_4p_SSM4p, xlim=c(0,70), ylimT=c(22, 32), ylimS=c(0,45), series=1,
      SE=c(DHA=1.396525, DHH=4.101217, T12H=0.04330405, Rho25=1.00479),
      GTRN.CI = "SE", replicate.CI = 100,
      embryo.stages="Caretta caretta.SCL")
plot(resultNest_4p_SSM4p, xlim=c(0,70), ylimT=c(22, 32), ylimS=c(0,45), series=1,
      GTRN.CI = "Hessian", replicate.CI = 100,
      embryo.stages="Caretta caretta.SCL")
plot(resultNest_4p_SSM4p, xlim=c(0,70), ylimT=c(22, 32), ylimS=c(0,45), series=1,
      resultmcmc = resultNest_mcmc_4p_SSM4p,
      GTRN.CI = "MCMC", replicate.CI = 100,
      embryo.stages="Caretta caretta.SCL")
# to plot all the nest at the same time, use
plot(resultNest_4p_SSM4p, xlim=c(0,70), ylimT=c(22, 32), ylimS=c(0,45),
      series="all", show.fioritures=FALSE, add=TRUE,
      embryo.stages="Caretta caretta.SCL")
# to use color different for series
plot(resultNest_4p_SSM4p, xlim=c(0,70), ylimT=c(22, 32), ylimS=c(0,45), add=TRUE,
      series="all", show.fioritures=FALSE, col.S=c(rep("black", 5), rep("red", 6)),
      embryo.stages="Caretta caretta.SCL")

# to plot all the temperature profiles
```

```

par(mar=c(4, 4, 1, 1))
plot(resultNest_4p_SSM4p$data[[1]][, 1]/60/24,
      resultNest_4p_SSM4p$data[[1]][, 2], bty="n",
      las=1, xlab="Days of incubation",
      ylab=expression("Temperatures in "*degree*"C"),
      type="l", xlim=c(0,70),ylim=c(20, 35))

  for (i in 2:21) {
    par(new=TRUE)
    plot(resultNest_4p_SSM4p$data[[i]][, 1]/60/24,
          resultNest_4p_SSM4p$data[[i]][, 2], bty="n",
          las=1, xlab="", ylab="", type="l", xlim=c(0,70),
          ylim=c(20, 35), axes = FALSE)
  }

## End(Not run)

```

plot.tsd

Plot results of tsd() that best describe temperature-dependent sex determination

Description

Plot the estimates that best describe temperature-dependent sex determination.

Usage

```

## S3 method for class 'tsd'
plot(
  x,
  ...,
  show.observations = TRUE,
  show.model = TRUE,
  males.freq = TRUE,
  show.PTRT = TRUE,
  las.x = 1,
  las.y = 1,
  lab.PT = paste("Pivotal ", x$type),
  resultmcmc = NULL,
  chain = 1,
  l = 0.05,
  replicate.CI = 10000,
  range.CI = 0.95,
  mar = c(4, 4, 4, 1) + 0.4,
  temperatures.plot = seq(from = 25, to = 35, by = 0.1),
  durations.plot = seq(from = 40, to = 70, by = 0.1),
  lab.TRT = paste0("Transitional range of ", x$type, "s l=", x$l * 100, "%"),
  col.TRT = "gray",

```



```

col.TRT.CI = rgb(0.8, 0.8, 0.8, 0.5),
col.PT.CI = rgb(0.8, 0.8, 0.8, 0.5),
show.CI = TRUE,
warn = TRUE
)

```

Arguments

x	A result file generated by tsd()
...	Parameters for plot()
show.observations	Should the observations be shown
show.model	Should the model be shown
males.freq	Should the graph uses males relative frequency [TRUE] or females [FALSE]
show.PTRT	Should the P and TRT information be shown
las.x	las parameter for x axis
las.y	las parameter for y axis
lab.PT	Label to describe pivotal temperature
resultmcmc	A result of tsd_MHmcmc()
chain	What chain to be used is resultmcmc is provided
l	Sex ratio limits to define TRT are l and 1-l
replicate.CI	replicate.CI replicates from the hessian matrix to estimate CI
range.CI	The range of confidence interval for estimation, default=0.95
mar	The par("mar") parameter
temperatures.plot	Temperatures used for showing curves of sex ratio
durations.plot	Durations used for showing curves of sex ratio
lab.TRT	Label to describe transitional range of temperature
col.TRT	The color of TRT
col.TRT.CI	The color of CI of TRT based on range.CI
col.PT.CI	The color of CI of PT based on range.CI
show.CI	Do the CI for the curve should be shown
warn	Do the warnings must be shown ? TRUE or FALSE

Details

plot.tsd plot result of tsd() that best describe temperature-dependent sex determination

Value

Nothing

Author(s)

Marc Girondot

References

Girondot, M. 1999. Statistical description of temperature-dependent sex determination using maximum likelihood. *Evolutionary Ecology Research*, 1, 479-486.

Godfrey, M.H., Delmas, V., Girondot, M., 2003. Assessment of patterns of temperature-dependent sex determination using maximum likelihood model selection. *Ecoscience* 10, 265-272.

Hulin, V., Delmas, V., Girondot, M., Godfrey, M.H., Guillon, J.-M., 2009. Temperature-dependent sex determination and global change: are some species at greater risk? *Oecologia* 160, 493-506.

Girondot M., Submitted. On the concept of embryological thermosensitive period for sex determination in reptiles.

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD](#), [P_TRT\(\)](#), [TSP.list](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
CC_AtlanticSW <- subset(DatabaseTSD, RMU=="Atlantic, SW" &
                        Species=="Caretta caretta" & (!is.na(Sexed) & Sexed!=0))
tsdL <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
                                temperatures=Incubation.temperature-Correction.factor,
                                equation="logistic"))

plot(tsdL)

## End(Not run)
```

plotR

Show the fitted growth rate dependent on temperature and its density

Description

Show the fitted growth rate dependent on temperature and its density.

The curve "ML quantiles" is based on delta method.

The curve "ML" just shows the fitted model.

The curve "MCMC quantiles" uses the mcmc replicates to build the quantiles.

The curve "MCMC mean-SD" uses the mcmc replicates to build a symmetric credibility interval.

The parameter curves is case insensitive. If only parameters is given, curves must be ML.

Usage

```
plotR(  
  result = NULL,  
  resultmcmc = NULL,  
  parameters = NULL,  
  fixed.parameters = NULL,  
  temperatures = NULL,  
  curves = "ML quantiles",  
  set.par = 1,  
  ylim = c(0, 5),  
  xlim = c(20, 35),  
  hessian = NULL,  
  replicate.CI = 1000,  
  cex.lab = par("cex"),  
  cex.axis = par("cex"),  
  scaleY = "auto",  
  lty = 1,  
  ltyCI = 3,  
  lwd = 1,  
  lwdCI = 1,  
  col = "black",  
  col.polygon = "grey",  
  polygon = FALSE,  
  probs = 0.95,  
  colramp = colorRampPalette(c("white", rgb(red = 0.5, green = 0.5, blue = 0.5))),  
  bandwidth = c(0.1, 0.01),  
  pch = "",  
  main = "",  
  xlab = expression("Temperature in " * degree * "C"),  
  ylab = NULL,  
  bty = "n",  
  las = 1,  
  by.temperature = 0.1,  
  show.density = FALSE,  
  new = TRUE,  
  show.hist = FALSE,  
  ylimH = NULL,  
  atH = NULL,  
  ylabH = "Temperature density",  
  breaks = "Sturges",  
  log.hist = FALSE,  
  mar = NULL  
)
```

Arguments

result	A result object or a list of result objects
resultmcmc	A result object from GRTN_MHmcmc() function

parameters	A set of parameters - Has the priority over result
fixed.parameters	A set of fixed parameters
temperatures	A set of temperatures - Has the priority over result
curves	What curves to show: "MCMC quantiles" or "MCMC mean-SD" based on mcmc or "ML" or "ML quantiles" for maximum-likelihood
set.par	1 or 2 to designate with set of parameters to show
ylim	Range of values for y-axis
xlim	Range of values for x-axis
hessian	An hessian matrix
replicate.CI	Number of replicates to estimate confidence interval with Hessian if delta method failed
cex.lab	cex value for axis
cex.axis	cex value for axis
scaleY	Scaling factor for y axis or "auto"
lty	The type of lines
ltyCI	The type of lines
lwd	The type of lines
lwdCI	The type of lines
col	The color of the lines
col.polygon	The color of the polygon
polygon	If TRUE, confidence interval is shown as a polygon with color
probs	Confidence or credibility interval to show
colramp	Ramp function accepting an integer as an argument and returning n colors.
bandwidth	numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. bandwidth is subsequently passed to function bkde2D.
pch	Character for outlayers
main	Title of the graph
xlab	Label for x axis
ylab	Label for y axis
bty	Box around the pot
las	Orientation for labels in y axis
by.temperature	Step to built the temperatures
show.density	TRUE or FALSE for use with Hessian or MCMC
new	Should the graphics be a new one (TRUE) or superimposed to a previous one (FALSE)
show.hist	TRUE or FALSE
ylimH	Scale of histogram using ylimH=c(min, max)

atH	Position of ticks for scale of histogram
ylabH	Label for histogram scale
breaks	See ?hist
log.hist	Should the y scale for hist is log ?
mar	The value of par("mar"). If null, it will use default depending on show.dist. If NA, does not change par("mar").

Details

plotR shows the fitted growth rate dependent on temperature and the density of the mcmc

Value

The value of scaleY to be used with other plotR function

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
plotR(result = resultNest_4p_SSM4p,
       resultmcmc=resultNest_mcmc_4p_SSM4p,
       curves = "MCMC quantiles")
#####
plotR(resultmcmc=resultNest_mcmc_4p_SSM4p,
       curves = "MCMC quantiles", show.density=TRUE)
#####
plotR(resultmcmc=resultNest_mcmc_4p_SSM4p,
       curves = "MCMC quantiles", polygon=TRUE)
#####
plotR(resultmcmc=resultNest_mcmc_6p_SSM6p, ylim=c(0,4),
       curves = "MCMC quantiles", polygon=TRUE, col.polygon = rgb(0, 1, 0, 1))
plotR(resultmcmc=resultNest_mcmc_4p_SSM4p,
       curves = "MCMC quantiles", polygon=TRUE, col.polygon = rgb(1, 0, 0, 0.5), new=FALSE)
legend("topleft", legend=c("SSM 4 parameters", "SSM 6 parameters"),
       pch=c(15, 15), col=c(rgb(1, 0, 0, 0.5), rgb(0, 1, 0, 1)))
#####
sy <- plotR(resultmcmc=resultNest_mcmc_4p_SSM4p,
            curves = "MCMC quantiles", show.density=FALSE)
plotR(resultmcmc=resultNest_mcmc_6p_SSM6p, col="red",
       curves = "MCMC quantiles", show.density=FALSE,
       new=FALSE, scaleY=sy)
#####
sy <- plotR(result=resultNest_6p_SSM6p, curves="ML",
            show.hist = TRUE, new = TRUE)
plotR(result=resultNest_4p_SSM4p, curves="ML", scaleY=sy,
       show.hist = FALSE, new = FALSE, col="red")
#####
```

```

plotR(result=resultNest_6p_SSM6p, curves="ML",
      show.hist = TRUE, ylim=c(0,1), atH=c(0, 0.1, 0.2))
#####
plotR(result = resultNest_4p_SSM4p,
      resultmcmc=resultNest_mcmc_4p_SSM4p,
      show.density = TRUE,
      curves = "MCMC quantiles")
#####
plotR(result=resultNest_4p_SSM4p,
      ylim=c(0, 4), curves="ML quantiles", scaleY=1E5)
#####
plotR(result=resultNest_4p_SSM4p, show.hist = TRUE,
      ylim=c(0, 4), curves="ML quantiles", scaleY=1E5)
#####
plotR(resultmcmc=resultNest_mcmc_4p_SSM4p,
      ylim=c(0, 4), curves = "MCMC quantiles", show.density=TRUE, scaleY=1E5)

## End(Not run)

```

plot_transition	<i>Show fonction used for transition</i>
-----------------	--

Description

Plot the transition function

Usage

```
plot_transition(result = NULL, parameters = NULL, sizes = c(0, 40), ...)
```

Arguments

result	A result object
parameters	Set of parameters. If both result and parameters are indicated, parameters have priority.
sizes	The range of possible sizes
...	Parameters for plot() such as main= or ylim=

Details

plot_transition show fonction used for transition

Value

Nothing

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
data(resultNest_4p_SSM4p)
# Get a set of parameters without transition
x1 <- resultNest_4p_SSM4p$par
# Generate a set of parameters with transition
x2 <- switch.transition(x1)
x2 <- x2[names(x2)!="transition_P"]
x2["transition_S"] <- 4
pfixed <- c(rK=2.093313, transition_P=20)
resultNest_4p_transition <- searchR(parameters=x2, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_transition)
# show the model for smallest size
plotR(resultNest_4p_transition, ylim=c(0,0.3))
# show the model for larger sizes
plotR(resultNest_4p_transition, set.par=2, ylim=c(0,0.3))
# plot model for both together
plotR(resultNest_4p_transition, set.par=c(1,2), ylim=c(0,0.3),
      col=c("red", "black"), legend=list("Initial", "End"))
plot_transition(result=resultNest_4p_transition, las=1, sizes=c(0,40))
compare_AIC(one.model=list(resultNest_4p_SSM4p), two.models=list(resultNest_4p_transition))
# Note that the model with fitted transition_P is trivial. Embryos grow fast until
# they reach hatchling size and then growth rate becomes null!

## End(Not run)
```

predict.HatchingSuccess

Return prediction based on a model fitted with HatchingSuccess.fit()

Description

Set of functions to study the hatching success.
 If replicates is 0, it returns only the fitted model.
 If replicates is null and resultmcmc is not null, it will use all the mcmc data.
 if replicates is lower than the number of iterations in resultmcmc, it will use sequence of data regularly thinned.

Usage

```
## S3 method for class 'HatchingSuccess'
predict(
  object,
  ...,
```

```

    temperature = NULL,
    probs = c(0.025, 0.5, 0.975),
    replicates = NULL,
    resultmcmc = NULL,
    chain = 1
  )

```

Arguments

<code>object</code>	The return of a fit done with <code>HatchingSuccess.fit()</code> .
<code>...</code>	Not used
<code>temperature</code>	A vector of temperatures.
<code>probs</code>	Quantiles.
<code>replicates</code>	Number of replicates to estimate the confidence interval.
<code>resultmcmc</code>	Results obtained using <code>HatchingSuccess.MHmcmc()</code>
<code>chain</code>	Chain to use in <code>resultmcmc</code>

Details

`predict.HatchingSuccess` returns prediction based on a model fitted with `HatchingSuccess.fit()`

Value

Return a matrix with prediction based on a model fitted with `HatchingSuccess.fit()`

Author(s)

Marc Girondot

See Also

Other Hatching success: [HatchingSuccess.MHmcmc_p\(\)](#), [HatchingSuccess.MHmcmc\(\)](#), [HatchingSuccess.fit\(\)](#), [HatchingSuccess.lnL\(\)](#), [HatchingSuccess.model\(\)](#), [logLik.HatchingSuccess\(\)](#), [nobs.HatchingSuccess\(\)](#), [plot.HatchingSuccess\(\)](#)

Examples

```

## Not run:
library(embryogrowth)
totalIncubation_Cc <- subset(DatabaseTSD,
                             Species=="Caretta caretta" &
                             Note != "Sinusoidal pattern" &
                             !is.na(Total) & Total != 0)

par <- c(S.low=0.5, S.high=0.3,
         P.low=25, deltaP=10, MaxHS=0.8)

HatchingSuccess.lnL(x=par, data=totalIncubation_Cc)

```



```

g <- HatchingSuccess.fit(par=par, data=totalIncubation_Cc)

HatchingSuccess.lnL(par=g$par, data=totalIncubation_Cc)

plot(g)

## End(Not run)

```

predict.tsd

Estimate sex ratio according to constant incubation temperature

Description

Estimate sex ratio according to constant incubation temperature

The data.frame has the temperatures or durations in columns and the quantiles in rows.

Note that incubation duration is a very bad proxy for sex ratio. See Georges, A., Limpus, C. J. & Stoutjesdijk, R. 1994. Hatchling sex in the marine turtle *Caretta caretta* is determined by proportion of development at a temperature, not daily duration of exposure. *J. Exp. Zool.*, 270, 432-444.

If replicate.CI is 0 or NULL, point estimate for maximum likelihood is returned.

Usage

```

## S3 method for class 'tsd'
predict(
  object,
  temperatures = NULL,
  durations = NULL,
  SD.temperatures = NULL,
  SD.durations = NULL,
  resultmcmc = NULL,
  chain = 1,
  replicate.CI = 10000,
  probs = c(0.025, 0.5, 0.975),
  ...
)

```

Arguments

object	A result file generated by tsd
temperatures	A vector of temperatures
durations	A vector of durations
SD.temperatures	SD of temperatures
SD.durations	SD of durations
resultmcmc	A result of tsd_MHmcmc()

chain	What chain to be used is resultmcmc is provided
replicate.CI	Number of replicates to estimate CI
probs	The quantiles to be returned, default=c(0.025, 0.5, 0.975)
...	Not used

Details

predict.tsd Estimate sex ratio according to constant incubation temperature

Value

A data.frame with informations about sex-ratio

Author(s)

Marc Girondot

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD](#), [P_TRT\(\)](#), [TSP.list](#), [plot.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
m <- c(10, 14, 7, 4, 3, 0, 0)
f <- c(0, 1, 2, 4, 15, 10, 13)
t <- c(25, 26, 27, 28, 29, 30, 31)
result <- tsd(males=m, females=f, temperatures=t)
plot(result)
predict(result, temperatures=c(25, 31), replicate.CI = 10000)
predict(result, temperatures=c(25, 31), SD.temperatures = c(1, 2), replicate.CI = 10000)
d <- c(72, 70, 65, 63, 62, 60, 59)
result <- tsd(males=m, females=f, durations=d)
predict(result, durations=c(67, 68), replicate.CI = 10000)

## End(Not run)
```

Description

Estimate the parameters that best describe the thermal reaction norm for sex ratio when temperature-dependent sex determination occurs.

It can be used also to evaluate the relationship between incubation duration and sex ratio.

The parameter l was defined in Girondot (1999). The TRT is defined from the difference between the two boundary temperatures giving sex ratios of l and $1 - l$.

In Girondot (1999), l was 0.05 and then the TRT was defined as being the range of temperatures producing from 5 If l is null, TRT is not estimated and only sex ratio is estimated.

if replicate.CI is null or 0, no replicate is used and only point estimate is done.

Standard error is calculated using resampling based on the Hessian matrix with Cholesky decomposition or using MCMC chain if resultmcmc is provided. In the former case, a replicate.CI random sample of the MCMC results will be used.

Usage

```
P_TRT(
  x = NULL,
  resultmcmc = NULL,
  fixed.parameters = NULL,
  chain = 1,
  equation = NULL,
  l = 0.05,
  replicate.CI = NULL,
  temperatures = NULL,
  durations = NULL,
  SD.temperatures = NULL,
  SD.durations = NULL,
  probs = c(0.025, 0.5, 0.975),
  warn = TRUE
)
```

Arguments

x	Set of parameters or a result of tsd()
resultmcmc	A result of tsd_MHmcmc()
fixed.parameters	Set of fixed parameters
chain	What chain to be used is resultmcmc is provided
equation	What equation should be used. Must be provided if x is not a result of tsd()
l	Sex ratio limits to define TRT are l and $1-l$. If NULL, TRT is not estimated.
replicate.CI	If a result of tsd() is provided, use replicate.CI replicates from the hessian matrix to estimate CI
temperatures	If provided returns the sex ratio and its quantiles for each temperature
durations	If provided returns the sex ratio and its quantiles for each duration

SD.temperatures	SD of temperatures
SD.durations	SD of durations
probs	Probabilities used to estimate quantiles
warn	Do the warnings must be shown ? TRUE or FALSE

Details

P_TRT estimates the transitional range of temperatures based on a set of parameters

Value

A list with a P_TRT object containing a matrix with lower and higher bounds for TRT, TRT and P and a P_TRT_quantiles object with quantiles for each and a sexratio_quantiles object

Author(s)

Marc Girondot

References

- Girondot, M. 1999. Statistical description of temperature-dependent sex determination using maximum likelihood. *Evolutionary Ecology Research*, 1, 479-486.
- Godfrey, M.H., Delmas, V., Girondot, M., 2003. Assessment of patterns of temperature-dependent sex determination using maximum likelihood model selection. *Ecoscience* 10, 265-272.
- Hulin, V., Delmas, V., Girondot, M., Godfrey, M.H., Guillon, J.-M., 2009. Temperature-dependent sex determination and global change: are some species at greater risk? *Oecologia* 160, 493-506.

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD](#), [TSP.list](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library("embryogrowth")
CC_AtlanticSW <- subset(DatabaseTSD, RMU=="Atlantic, SW" &
                        Species=="Caretta caretta" & Sexed!=0)
tsdL <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
                               temperatures=Incubation.temperature-Correction.factor,
                               equation="logistic"))

P_TRT(tsdL)
P_TRT(tsdL, replicate.CI=1000)
P_TRT(tsdL, replicate.CI=1000, temperatures=20:35)
P_TRT_out <- P_TRT(tsdL, replicate.CI=1000, temperatures=c(T1=20, T2=35))
attributes(P_TRT_out$sexratio_quantiles)$temperatures
P_TRT(tsdL$par, equation="logistic")
pMCMC <- tsd_MHmcmc_p(tsdL, accept=TRUE)
# Take care, it can be very long
```

```
result_mcmc_tsd <- tsd_MHmcmc(result=tsdL,  
parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,  
n.adapt = 0, thin=1, trace=FALSE, adaptive=TRUE)  
P_TRT(result_mcmc_tsd, equation="logistic")  
  
## End(Not run)
```

resultNest_3p_Dallwitz

Fit using the nest database

Description

Fit using the nest database

Usage

```
resultNest_3p_Dallwitz
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database

Author(s)

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

References

Girondot, M., Monsinjon, J., Guillon, J.-M., Submitted. Delimitation of the embryonic thermosensitive period for sex determination using an embryo growth model reveals a potential bias for sex ratio prediction in turtles.

Examples

```
## Not run:  
library(embryogrowth)  
data(nest)  
formatted <- FormatNests(nest)  
x <- structure(c(4.88677476830268, 20.4051904475743, 31.5173105860335),  
.Names = c("Dallwitz_b1", "Dallwitz_b2", "Dallwitz_b3"))  
pfixed <- c(rK=1.208968)  
resultNest_3p_Dallwitz <- searchR(parameters=x, fixed.parameters=pfixed,  
temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,  
test=c(Mean=39.33, SD=1.92))
```

```
plotR(result=resultNest_3p_Dallwitz, show.hist = TRUE,
      ylim=c(0, 8), curves="ML quantiles")

## End(Not run)
```

resultNest_3p_Weibull *Result of the fit using the nest database using Weibull function*

Description

Fit using the nest database using Weibull function. The model is:
`rT <- dweibull(T, shape=abs(parms["k"]),`
`scale=abs(parms["lambda"])*parms["scale"]*1E-5`

Usage

```
resultNest_3p_Weibull
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database using Weibull function

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# Weibull model
x <- ChangeSSM(temperatures = (200:350)/10,
               parameters = resultNest_4p_SSM4p$par,
               initial.parameters = structure(c(73.4009010417375, 304.142079511996,
                                               27.4671689276281),
                                             .Names = c("k", "lambda", "scale")),
               control=list(maxit=1000))
```

```

pfixed <- c(rK=2.093313)
resultNest_3p_Weibull <- searchR(parameters=x$par, fixed.parameters=pfixed,
                                temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
                                test=c(Mean=39.33, SD=1.92))
plotR(resultNest_3p_Weibull, ylim=c(0, 3))
plotR(resultNest_3p_Weibull, ylim=c(0, 3), ylimH = c(0, 0.9), show.hist=TRUE)
compare_AIC(SSM=resultNest_4p_SSM4p, Weibull=resultNest_3p_Weibull)

## End(Not run)

```

resultNest_4p_normal *Result of the fit using the nest database using asymmetric normal function*

Description

Fit using the nest database using asymmetric normal function

Usage

```
resultNest_4p_normal
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database using asymmetric normal function

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```

## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
x <- ChangeSSM(temperatures = (200:350)/10,
               parameters = resultNest_4p_SSM4p$par,
               initial.parameters = structure(c(3, 7, 11, 32),
                                             .Names = c("Scale", "sdL", "sdH", "Peak")),
               control=list(maxit=1000))

```

```

pfixed <- c(rK=2.093313)
resultNest_4p_normal <- searchR(parameters=x$par, fixed.parameters=pfixed,
                               temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
                               test=c(Mean=39.33, SD=1.92))
plotR(resultNest_4p_normal, ylim=c(0, 3))
plotR(resultNest_4p_normal, ylim=c(0, 3), ylimH = c(0, 0.9), show.hist=TRUE)
compare_AIC(SSM=resultNest_4p_SSM4p, Asymmetric.normal=resultNest_4p_normal)

## End(Not run)

```

resultNest_4p_SSM *Fit using the nest database*

Description

Fit using the nest database

Usage

```
resultNest_4p_SSM
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database

Author(s)

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

References

Girondot, M., Monsinjon, J., Guillon, J.-M., Submitted. Delimitation of the embryonic thermosensitive period for sex determination using an embryo growth model reveals a potential bias for sex ratio prediction in turtles.

Examples

```

## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
x <- structure(c(109.683413821537, 614.969219372661, 306.386903812694,
                229.003478775323), .Names = c("DHA", "DHH", "T12H", "Rho25"))
pfixed <- c(rK=1.208968)
resultNest_4p_SSM <- searchR(parameters=x, fixed.parameters=pfixed,

```



```

temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
test=c(Mean=39.33, SD=1.92))
plotR(result=resultNest_4p_SSM, show.hist = TRUE,
      ylim=c(0, 8), curves="ML quantiles")

## End(Not run)

```

resultNest_4p_SSM4p *Fit using the nest database*

Description

Fit using the nest database

Usage

```
resultNest_4p_SSM4p
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```

## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(118.431040984352, 498.205702157603, 306.056280989839,
118.189669472381), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
resultNest_4p_SSM4p <- searchR(parameters=x, fixed.parameters=pfixed,

```

```
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
plotR(result=resultNest_4p_SSM4p, show.hist = TRUE,
      ylim=c(0, 4), curves="ML quantiles")

## End(Not run)
```

resultNest_4p_transition

Result of the fit using the nest database using transition

Description

Fit using the nest database using transition

Usage

```
resultNest_4p_transition
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database using transition

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
data(resultNest_4p_transition)

## End(Not run)
```

resultNest_4p_trigo *Result of the fit using the nest database using trigonometric function*

Description

Fit using the nest database using trigonometric function

Usage

```
resultNest_4p_trigo
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database using trigonometric function

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
x <- ChangeSSM(temperatures = (200:350)/10,
               parameters = resultNest_4p_SSM4p$par,
               initial.parameters = structure(c(3, 20, 40, 32),
               .Names = c("Max", "LengthB", "LengthE", "Peak")),
               control=list(maxit=1000))
pfixed <- c(rK=2.093313)
resultNest_4p_trigo <- searchR(parameters=x$par, fixed.parameters=pfixed,
                              temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
                              test=c(Mean=39.33, SD=1.92))
plotR(resultNest_4p_trigo, ylim=c(0, 3))
plotR(resultNest_4p_trigo, ylim=c(0, 3), ylimH = c(0, 0.9), show.hist=TRUE)
compare_AIC(SSM=resultNest_4p_SSM4p, trigonometric=resultNest_4p_trigo)

## End(Not run)
```

resultNest_4p_weight *Fit using the nest database with weight*

Description

Fit using the nest database with weight

Usage

```
resultNest_4p_weight
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database with weight

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
w <- weightmaxentropy(formatted, control_plot=list(xlim=c(20,36)))
x <- structure(c(118.768297442004, 475.750095909406, 306.243694918151,
116.055824800264), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
# K or rK are not used for dydt.linear or dydt.exponential
resultNest_4p_weight <- searchR(parameters=x,
fixed.parameters=pfixed, temperatures=formatted,
derivate=dydt.Gompertz, M0=1.7, test=c(Mean=39.33, SD=1.92),
method = "BFGS", weight=w)
data(resultNest_4p_weight)
plotR(resultNest_4p_weight, ylim=c(0,0.50), xlim=c(15, 35))

## End(Not run)
```

resultNest_5p_Dallwitz

Fit using the nest database

Description

Fit using the nest database

Usage

```
resultNest_5p_Dallwitz
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database

Author(s)

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

References

Girondot, M., Monsinjon, J., Guillon, J.-M., Submitted. Delimitation of the embryonic thermosensitive period for sex determination using an embryo growth model reveals a potential bias for sex ratio prediction in turtles.

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
x <- structure(c(4.91191231405918, 12.7453211281394, 31.2670410811077,
  5.7449376569153, -0.825689964543813), .Names = c("Dallwitz_b1",
  "Dallwitz_b2", "Dallwitz_b3", "Dallwitz_b4", "Dallwitz_b5"))
pfixed <- c(rK=1.208968)
resultNest_5p_Dallwitz <- searchR(parameters=x, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
  test=c(Mean=39.33, SD=1.92))
plotR(result=resultNest_5p_Dallwitz, show.hist = TRUE,
  ylim=c(0, 8), curves="ML quantiles")

## End(Not run)
```

resultNest_6p_SSM *Fit using the nest database*

Description

Fit using the nest database

Usage

```
resultNest_6p_SSM
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database

Author(s)

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

References

Girondot, M., Monsinjon, J., Guillon, J.-M., Submitted. Delimitation of the embryonic thermosensitive period for sex determination using an embryo growth model reveals a potential bias for sex ratio prediction in turtles.

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
x <- structure(c(104.954347370542, 3447.10062406071, 661.269363920423,
  96.3871849546537, 306.456389026151, 232.105840347154), .Names = c("DHA",
  "DHH", "DHL", "DT", "T12L", "Rho25"))
pfixed <- c(rK=1.208968)
resultNest_6p_SSM <- searchR(parameters=x, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
  test=c(Mean=39.33, SD=1.92))
plotR(result=resultNest_6p_SSM, show.hist = TRUE,
  ylim=c(0, 8), curves="ML")

## End(Not run)
```

resultNest_6p_SSM6p *Fit using the nest database*

Description

Fit using the nest database

Usage

```
resultNest_6p_SSM6p
```

Format

A list with fitted information about data(nest)

Details

Result of the fit using the nest database

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(115.770032186805, 428.649144244891, 503.716700005443,
12.2641939339981, 306.305498098871, 116.380086027401),
.Names = c("DHA", "DHH", "DHL", "DT", "T12L", "Rho25"))
pfixed <- c(rK=2.093313)
resultNest_6p_SSM6p <- searchR(parameters=x, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))

## End(Not run)
```

 resultNest_mcmc_4p_SSM4p

Result of the mcmc using the nest database

Description

Fit using the nest database

Usage

```
resultNest_mcmc_4p_SSM4p
```

Format

A list of class mcmcComposite with mcmc result for data(nest) with 4 parameters and Gompertz model of growth

Details

Result of the mcmc using the nest database

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(118.431040984352, 498.205702157603, 306.056280989839,
118.189669472381), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
resultNest_4p_SSM4p <- searchR(parameters=x, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_SSM4p)
pMCMC <- TRN_MHmcmc_p(resultNest_4p_SSM4p, accept=TRUE)
```



```

# Take care, it can be very long, sometimes several days
resultNest_mcmc_4p_SSM4p <- GRTRN_MHmcmc(result=resultNest_4p_SSM4p,
  adaptive = TRUE,
  parametersMCMC=pMCMC, n.iter=10000, n.chains = 1, n.adapt = 0,
  thin=1, trace=TRUE)
data(resultNest_mcmc_4p_SSM4p)
1-rejectionRate(as.mcmc(resultNest_mcmc_4p_SSM4p))
as.parameters(resultNest_mcmc_4p_SSM4p)
layout(mat=matrix(1:4, nrow = 2))
plot(resultNest_mcmc_4p_SSM4p, parameters = "all", scale.prior = TRUE, las = 1)
layout(mat=1)
plotR(resultNest_4p_SSM4p, resultmcmc=resultNest_mcmc_4p_SSM4p, ylim=c(0,4),
  main="Schoolfield, Sharpe & Magnuson 4-parameters", show.density=TRUE)

## End(Not run)

```

resultNest_newp

Fit using the nest database with anchored parameters

Description

Fit using the nest database with anchored parameters

Usage

```
resultNest_newp
```

Format

A list with fitted information from data(nest) with anchored parameters

Details

Result of the fit using the nest database with anchored parameters

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
newp <- GenerateAnchor(nests=formatted, number.anchors=7)
pfixed <- c(rK=2.093313)
resultNest_newp <- searchR(parameters=newp, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
  test=c(Mean=39.33, SD=1.92))
data(resultNest_newp)
plotR(resultNest_newp)

## End(Not run)
```

result_mcmc_newp

Result of the mcmc using the nest database with anchored parameters

Description

Fit using the nest database with anchored parameters

Usage

```
result_mcmc_newp
```

Format

A list of class mcmcComposite with mcmc result for data(nest) with anchored parameters

Details

Result of the mcmc using the nest database with anchored parameters

Author(s)

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

References

Girondot, M., & Kaska, Y. (2014). A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology*, 45, 96-102. doi: 10.1016/j.jtherbio.2014.08.005

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
newp <- GenerateAnchor(nests=formatted, number.anchors=7)
pfixed <- c(rK=2.093313)
resultNest_newp <- searchR(parameters=newp, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
  test=c(Mean=39.33, SD=1.92))
data(resultNest_newp)
pMCMC <- TRN_MHmcmc_p(resultNest_newp, accept=TRUE)
# Take care, it can be very long, sometimes several days
result_mcmc_newp <- GRTRN_MHmcmc(result=resultNest_newp,
  parametersMCMC=pMCMC, n.iter=10000, n.chains = 1, n.adapt = 0,
  thin=1, trace=TRUE)
data(result_mcmc_newp)
data(resultNest_4p_SSM4p)
newp <- GenerateAnchor(nests=resultNest_4p_SSM4p, number.anchors=7)
# Here the confidence interval is built based on anchored parameters
plotR(resultNest_4p_SSM4p, parameters=newp, SE=result_mcmc_newp$SD,
  ylim=c(0,4), ylimH=c(0,0.4), show.hist=TRUE, curves="ML quantiles")
# Here the confidence interval is built based on parametric SSM equation
data(resultNest_4p_SSM4p)
plotR(resultNest_4p_SSM4p, SE=result_mcmc_4p_SSM4p$SD,
  ylim=c(0,4), ylimH=c(0,0.4), show.hist=TRUE, curves="ML quantiles")
plot(result_mcmc_newp, las=1, xlim=c(0,30), parameters="294",
breaks=c(0, 1.00095, 2.0009, 3.00085, 4.0008, 5.00075, 6.0007, 7.00065, 8.0006, 9.00055,
10.0005, 11.00045, 12.0004, 13.00035, 14.0003, 15.00025, 16.0002, 17.00015, 18.0001,
19.00005, 20))
plot(result_mcmc_newp, las=1, xlim=c(0,30), parameters="296.3333333333333")
plot(result_mcmc_newp, las=1, xlim=c(0,30), parameters=3)

## End(Not run)
```

searchR

Fit the parameters that best represent nest incubation data.

Description

Fit the parameters that best represent data.

test can be a data.frame with two columns Mean and SD and rownames with the nest name.

If SD is na, then least square criteria is used for fitting.

Function to fit thermal reaction norm can be expressed as :

- a 4-parameters Schoolfield, Sharpe, and Magnuson model (1981) with DHH, DHA, T12H, and Rho25;

- a 6-parameters Schoolfield, Sharpe, and Magnuson model (1981) with T12L, DT, DHH, DHL, DHA, and Rho25;
- Each of these two first models can be combined as low and high sets of parameters by adding the _L suffix to one set. Then you must add also transition_S and transition_P parameters and then the growth rate is $1/(1+\exp((1/\text{transition_S})*(P-\text{transition_P})))$ with P being the proportion of development;
- The Rho25_b control the effect of hygrometry (or Rho25_b_L) (It is not fully functional still);
- a Weibull function with k (shape), lambda (scale) and theta parameters;
- a normal function with Peak, Scale, and sd parameters;
- an asymmetric normal function with Peak, Scale, sdH and sdL parameters;
- a symmetric trigonometric function with Length, Peak, and Max;
- an asymmetric trigonometric function with LengthB, LengthE, Peak, and Max.
- Dallwitz-Higgins model (1992) can be used using Dallwitz_b1, Dallwitz_b2, Dallwitz_b3, Dallwitz_b4 and Dallwitz_b5 parameters.
- If Dallwitz_b4 is not included, Dallwitz_b4 = 6 will be used.
- If Dallwitz_b5 is not included, Dallwitz_b5 = 0.4 will be used.
- It is possible also to add the parameter epsilon and then the model becomes $X + \text{epsilon}$ with X being any of the above model;
- It is possible also to add the parameter epsilon_L and then the model becomes $X_L + \text{epsilon_L}$ with X_L being any of the above model with suffix _L;
- If the name of the parameter is a number, then the model is a polynomial anchored with the rate being the parameter value at this temperature (the name). see ChangeSSM() function.

Usage

```
searchR(
  parameters = stop("Initial set of parameters must be provided"),
  fixed.parameters = NULL,
  temperatures = stop("Formatted temperature must be provided !"),
  derivate = dydt.Gompertz,
  test = c(Mean = 39.33, SD = 1.92),
  M0 = 1.7,
  saveAtMaxiter = FALSE,
  fileName = "intermediate",
  weight = NULL,
  control = list(trace = 1, REPORT = 100, maxit = 500)
)
```

Arguments

parameters	A set of parameters used as initial point for searching
fixed.parameters	A set of parameters that will not be changed
temperatures	Timeseries of temperatures after formatted using FormatNests()

derivate	Function used to fit embryo growth: dydt.Gompertz, dydt.exponential or dydt.linear
test	A vector with Mean and SD of size of hatchlings, ex. test=c(Mean=39, SD=3). Can be a data.frame also. See description
M0	Measure of hatchling size or mass proxi at laying date
saveAtMaxiter	If True, each time number of iteration reach maxiter, current data are saved in file with filename name
fileName	The intermediate results are saved in file with fileName.Rdata name
weight	A named vector of the weight for each nest for likelihood estimation
control	List for control parameters for optimx

Details

searchR fits the parameters that best represent nest incubation data.

Value

A result object

Author(s)

Marc Girondot

References

- Angilletta, M.J., 2006. Estimating and comparing thermal performance curves. *Journal of Thermal Biology* 31, 541-545.
- Dallwitz, M.J., Higgins, J.P., 1992. User's guide to DEVAR. A computer program for estimating development rate as a function of temperature. *CSIRO Aust Div Entomol Rep* 2, 1-23.
- Georges, A., Beggs, K., Young, J.E., Doody, J.S., 2005. Modelling development of reptile embryos under fluctuating temperature regimes. *Physiological and Biochemical Zoology* 78, 18-30.
- Girondot, M., Kaska, Y., 2014. A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology* 45, 96-102.
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Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "DT", "DHA", "DHH", "DHL", "Rho25"
# K for Gompertz must be set as fixed parameter or being a constant K
```

```

# or relative to the hatchling size rK
x <- structure(c(105.966881676793, 613.944134764125, 306.449533440186,
  118.193882815108), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
resultNest_4p_SSM4p <- searchR(parameters=x, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
  test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_SSM4p)
plot(resultNest_4p_SSM4p, xlim=c(0,70), ylimT=c(22, 32), ylimS=c(0,45), series=1,
  embryo.stages="Caretta caretta.SCL")
x <- structure(c(106.567809092008, 527.359011254683, 614.208632495199,
  2720.94506457237, 306.268259715624, 120.336791245212), .Names = c("DHA",
  "DHH", "DHL", "DT", "T12L", "Rho25"))
pfixed <- c(rK=2.093313)

# exemple of data.frame for test
ttest <- data.frame(Mean=rep(25.5, formatted$IndiceT["NbTS"]),
  SD=rep(0.75, formatted$IndiceT["NbTS"]),
  row.names=names(formatted)[1:formatted$IndiceT["NbTS"]])
resultNest_6p_SSM6p <- searchR(parameters=x, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
  test=ttest)

data(resultNest_6p_SSM6p)
pMCMC <- TRN_MHmcmc_p(resultNest_6p_SSM6p, accept=TRUE)
# Take care, it can be very long, sometimes several days
resultNest_mcmc_6p_SSM6p <- GRTRN_MHmcmc(result=resultNest_6p_SSM6p,
  parametersMCMC=pMCMC, n.iter=10000, n.chains = 1, n.adapt = 0,
  thin=1, trace=TRUE)
# compare_AIC() is a function from the package "HelpersMG"
compare_AIC(test1=resultNest_4p_SSM4p, test2=resultNest_6p_SSM6p)
##### with new parametrization
data(resultNest_4p_SSM4p)
x0 <- resultNest_4p_SSM4p$par
t <- hist(resultNest_4p_SSM4p, plot=FALSE)
x <- c(3.4, 3.6, 5.4, 5.6, 7.6, 7.5, 3.2)
names(x) <- seq(from=range(t$temperatures)[1], to=range(t$temperatures)[2],
  length.out=7)
newx <- ChangeSSM(temperatures = (200:350)/10, parameters = x0,
  initial.parameters = x,
  control=list(maxit=5000))
pfixed <- c(rK=2.093313)
resultNest_newp <- searchR(parameters=newx, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
  test=c(Mean=39.33, SD=1.92))
plotR(resultNest_newp, ylim=c(0, 3), xlimR=c(23, 34), ylimH=c(0, 0.3), show.hist.TRUE)
compare_AIC(test4p=resultNest_4p_SSM4p,
  test6p=resultNest_6p_SSM6p,
  testAnchor=resultNest_newp)

#####
# example with thermal reaction norm fitted from Weibull function

```

```
#####
x <- ChangeSSM(temperatures = (200:350)/10,
               parameters = resultNest_4p_SSM4p$par,
               initial.parameters = structure(c(73.4009010417375, 304.142079511996,
                                               27.4671689276281),
                                             .Names = c("k", "lambda", "scale")),
               control=list(maxit=1000))
pfixed <- c(rK=2.093313)
resultNest_3p_Weibull <- searchR(parameters=x$par, fixed.parameters=pfixed,
                                temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
                                test=c(Mean=39.33, SD=1.92))
plotR(list(resultNest_4p_SSM4p, resultNest_3p_Weibull), ylim=c(0,3), col=c("Black", "red"))
compare_AIC(SSM4p=resultNest_4p_SSM4p, Weibull=resultNest_3p_Weibull)

#####
# example with thermal reaction norm fitted from asymmetric normal function
#####

x <- ChangeSSM(temperatures = (200:350)/10,
               parameters = resultNest_4p_SSM4p$par,
               initial.parameters = structure(c(3, 7, 11, 32),
                                             .Names = c("Scale", "sdL", "sdH", "Peak")),
               control=list(maxit=1000))
pfixed <- c(rK=2.093313)
resultNest_4p_normal <- searchR(parameters=x$par, fixed.parameters=pfixed,
                                temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
                                test=c(Mean=39.33, SD=1.92))

#####
# example with thermal reaction norm fitted from trigonometric model
#####

x <- ChangeSSM(temperatures = (200:350)/10,
               parameters = resultNest_4p_SSM4p$par,
               initial.parameters = structure(c(3, 20, 40, 32),
                                             .Names = c("Max", "LengthB", "LengthE", "Peak")),
               control=list(maxit=1000))
pfixed <- c(rK=2.093313)
resultNest_4p_trigo <- searchR(parameters=x$par, fixed.parameters=pfixed,
                                temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
                                test=c(Mean=39.33, SD=1.92))

#####
# example with thermal reaction norm fitted from Dallwitz model
# From Girondot, M., Monsinjon, J., Guillon, J.-M., Submitted. Delimitation of the
# embryonic thermosensitive period for sex determination using an embryo growth model
# reveals a potential bias for sex ratio prediction in turtles.
# rK = 1.208968
# M0 = 0.3470893
# See the example in stages datasets
#####
```

```

x <- structure(c(4.88677476830268, 20.4051904475743, 31.5173105860335),
.Names = c("Dallwitz_b1", "Dallwitz_b2", "Dallwitz_b3"))
pfixed <- c(rK=1.208968)
resultNest_3p_Dallwitz <- searchR(parameters=x, fixed.parameters=pfixed,
                                temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
                                test=c(Mean=39.33, SD=1.92))
plotR(resultNest_3p_Dallwitz, ylim=c(0,8))

x <- structure(c(4.91191231405918, 12.7453211281394, 31.2670410811077,
5.7449376569153, -0.825689964543813), .Names = c("Dallwitz_b1",
"Dallwitz_b2", "Dallwitz_b3", "Dallwitz_b4", "Dallwitz_b5"))
pfixed <- c(rK=1.208968)
resultNest_5p_Dallwitz <- searchR(parameters=x, fixed.parameters=pfixed,
                                temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
                                test=c(Mean=39.33, SD=1.92))
plotR(resultNest_5p_Dallwitz, ylim=c(0,8))

xp <- resultNest_6p_SSM6p$par
xp["Rho25"] <- 233
pfixed <- c(rK=1.208968)
resultNest_6p_SSM <- searchR(parameters=xp, fixed.parameters=pfixed,
                              temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
                              test=c(Mean=39.33, SD=1.92))
plotR(resultNest_6p_SSM, ylim=c(0,8))

xp <- ChangeSSM(parameters = resultNest_3p_Dallwitz$par,
                initial.parameters = resultNest_4p_SSM4p$par)
pfixed <- c(rK=1.208968)
resultNest_4p_SSM <- searchR(parameters=xp$par, fixed.parameters=pfixed,
                              temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
                              test=c(Mean=39.33, SD=1.92))
plotR(resultNest_4p_SSM, ylim=c(0,8))

compare_AIC(Dallwitz3p=resultNest_3p_Dallwitz, Dallwitz5p=resultNest_5p_Dallwitz,
            SSM4p=resultNest_4p_SSM, SSM6p=resultNest_6p_SSM)

#####
# Example with thermal reaction norm of proportion of development
# fitted from Dallwitz model
# see Woolgar, L., Trocini, S., Mitchell, N., 2013. Key parameters describing
# temperature-dependent sex determination in the southernmost population of loggerhead
# sea turtles. Journal of Experimental Marine Biology and Ecology 449, 77-84.
#####

x <- structure(c(1.48207559695689, 20.1100310234046, 31.5665036287242),
.Names = c("Dallwitz_b1", "Dallwitz_b2", "Dallwitz_b3"))
resultNest_PropDev_3p_Dallwitz <- searchR(parameters=x, fixed.parameters=NULL,
                                          temperatures=formatted, derivate=dydt.linear, M0=0,
                                          test=c(Mean=1, SD=NA))
plotR(resultNest_PropDev_3p_Dallwitz, ylim=c(0, 1.5), curves="ML")
plot(x=resultNest_PropDev_3p_Dallwitz, ylimS=c(0,1), xlim=c(0,60), series=2,
     embryo.stages="Generic.ProportionDevelopment")

```



```

x <- structure(c(1.48904182113431, 10.4170365155993, 31.2591665490154,
6.32355497589913, -1.07425378667104), .Names = c("Dallwitz_b1",
"Dallwitz_b2", "Dallwitz_b3", "Dallwitz_b4", "Dallwitz_b5"))
resultNest_PropDev_5p_Dallwitz <- searchR(parameters=x, fixed.parameters=NULL,
      temperatures=formatted, derivate=dydt.linear, M0=0,
      test=c(Mean=1, SD=NA))
plotR(resultNest_PropDev_5p_Dallwitz, ylim=c(0, 1.5))
plot(x=resultNest_PropDev_5p_Dallwitz, ylimS=c(0,1), xlim=c(0,60), series=2,
      embryo.stages="Generic.ProportionDevelopment")

plotR(resultNest_PropDev_3p_Dallwitz, ylim=c(0, 1.5), curves="ML")
plotR(resultNest_PropDev_5p_Dallwitz, ylim=c(0, 1.5), curves="ML", new=FALSE, col="red")
compare_AICc(Dallwitz3p=resultNest_PropDev_3p_Dallwitz,
      Dallwitz5p=resultNest_PropDev_5p_Dallwitz)

## End(Not run)

```

stages

Database of of embryonic development and thermosensitive period of development for sex determination

Description

Database of embryonic development and thermosensitive period of development for sex determination.

Usage

stages

Format

A list with dataframes including attributes

Details

Database of embryonic development and thermosensitive period of development for sex determination

Author(s)

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References

- Pieau, C., Dorizzi, M., 1981. Determination of temperature sensitive stages for sexual differentiation of the gonads in embryos of the turtle, *Emys orbicularis*. *Journal of Morphology* 170, 373-382.
- Yntema, C.L., Mrosovsky, N., 1982. Critical periods and pivotal temperatures for sexual differentiation in loggerhead sea turtles. *Canadian Journal of Zoology-Revue Canadienne de Zoologie* 60, 1012-1016.
- Kaska, Y., Downie, R., 1999. Embryological development of sea turtles (*Chelonia mydas*, *Caretta caretta*) in the Mediterranean. *Zoology in the Middle East* 19, 55-69.
- Greenbaum, E., 2002. A standardized series of embryonic stages for the emydid turtle *Trachemys scripta*. *Canadian Journal of Zoology-Revue Canadienne de Zoologie* 80, 1350-1370.
- Magalhães, M.S., Vogt, R.C., Sebben, A., Dias, L.C., de Oliveira, M.F., de Moura, C.E.B., 2017. Embryonic development of the Giant South American River Turtle, *Podocnemis expansa* (Testudines: Podocnemididae). *Zoomorphology*.

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD.P_TRT\(\)](#), [TSP.list](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
data(stages)
names(stages)
levels(as.factor(stages$Species))
# Version of database
stages$Version[1]
kaska99.SCL <- subset(stages, subset=(Species == "Caretta caretta"),
  select=c("Stage", "SCL_Mean_mm", "SCL_SD_mm", "Days_Begin", "Days_End"))

kaska99.SCL[kaska99.SCL$Stage==31, "Days_Begin"] <- 51
kaska99.SCL[kaska99.SCL$Stage==31, "Days_End"] <- 62
kaska99.SCL <- na.omit(kaska99.SCL)
kaska99.SCL[which(kaska99.SCL$Stage==31), "Stage"] <- c("31a", "31b", "31c")
kaska99.SCL <- cbind(kaska99.SCL,
  Days_Mean=(kaska99.SCL[, "Days_Begin"]+kaska99.SCL[, "Days_End"])/2)
kaska99.SCL <- cbind(kaska99.SCL,
  Days_SD=(kaska99.SCL[, "Days_End"]-kaska99.SCL[, "Days_Begin"])/4)
Gompertz <- function(x, par) {
  K <- par["K"]
  rT <- par["rT"]
  X0 <- par["X0"]
  y <- abs(K)*exp(log(abs(X0)/abs(K))*exp(-rT*x))
  return(y)
}

ML.Gompertz <- function(x, par) {
  par <- abs(par)
```

```

y <- Gompertz(x, par)
return(sum(-dnorm(y, mean=kaska99.SCL[, "SCL_Mean_mm"],
                 sd=kaska99.SCL[, "SCL_SD_mm"], log=TRUE)))
}

parIni <- structure(c(48.66977358, 0.06178453, 0.38640902),
                  .Names = c("K", "rT", "X0"))

fitsize.SCL <- optim(parIni, ML.Gompertz, x=kaska99.SCL[, "Days_Mean"], hessian = TRUE)

# Estimation of standard error of parameters using Hessian matrix
sqrt(diag(solve(fitsize.SCL$hessian)))

# Estimation of standard error of parameters using Bayesian concept and MCMC
pMCMC <- structure(list(Density = c("dunif", "dunif", "dunif"),
                      Prior1 = c(0, 0, 0), Prior2 = c(90, 1, 2),
                      SDProp = c(1, 1, 1),
                      Min = c(0, 0, 0), Max = c(90, 1, 2),
                      Init = fitsize.SCL$par),
                  .Names = c("Density", "Prior1", "Prior2", "SDProp", "Min", "Max", "Init"),
                  row.names = c("K", "rT", "X0"), class = "data.frame")

Bayes.Gompertz <- function(data, x) {
  x <- abs(x)
  y <- Gompertz(data, x)
  return(sum(-dnorm(y, mean=kaska99.SCL[, "SCL_Mean_mm"],
                  sd=kaska99.SCL[, "SCL_SD_mm"], log=TRUE)))
}

mcmc_run <- MHalgoGen(n.iter=50000, parameters=pMCMC, data=kaska99.SCL[, "Days_Mean"],
                    likelihood=Bayes.Gompertz, n.chains=1, n.adapt=100, thin=1, trace=1,
                    adaptive = TRUE)

plot(mcmc_run, xlim=c(0, 90), parameters="K")
plot(mcmc_run, xlim=c(0, 1), parameters="rT")
plot(mcmc_run, xlim=c(0, 2), parameters="X0")

1-rejectionRate(as.mcmc(mcmc_run))

par <- mcmc_run$resultMCMC[[1]]

outsp <- t(apply(par, MARGIN = 1, FUN=function(x) Gompertz(0:70, par=x)))

rangqtiles <- apply(outsp, MARGIN=2, function(x) {quantile(x, probs=c(0.025, 0.5, 0.975))})

par(mar=c(4, 4, 2, 1))
plot_errbar(x=kaska99.SCL[, "Days_Mean"], y=kaska99.SCL[, "SCL_Mean_mm"],
            errbar.y = 2*kaska99.SCL[, "SCL_SD_mm"], bty="n", las=1,
            ylim=c(0, 50), xlab="Days", ylab="SCL mm",
            xlim=c(0, 70), x.plus = kaska99.SCL[, "Days_End"],
            x.minus = kaska99.SCL[, "Days_Begin"])

lines(0:70, rangqtiles["2.5%", ], lty=2)

```

```

lines(0:70, rangqtiles["97.5%", ], lty=2)
lines(0:70, rangqtiles["50%", ], lty=3)

text(x=50, y=10, pos=4, labels=paste("K=", format(x = fitsize.SCL$par["K"], digits = 4)))
text(x=50, y=12.5, pos=4,
     labels=paste("rK=", format(x = fitsize.SCL$par["K"]/39.33, digits = 4)))
text(x=50, y=15, pos=4, labels=paste("X0=", format(x = fitsize.SCL$par["X0"], digits = 4)))
title("Univariate normal distribution")

# Using a multivariate normal distribution

library(mvtnorm)

ML.Gompertz.2D <- function(x, par) {
  par <- abs(par)
  y <- Gompertz(x, par)
  L <- 0
  for (i in seq_along(y)) {
    sigma <- matrix(c(kaska99.SCL$SCL_SD_mm[i]^2, 0, 0, kaska99.SCL$Days_SD[i]^2),
                    nrow=2, byrow=TRUE,
                    dimnames=list(c("SCL_SD_mm", "Days_SD"), c("SCL_SD_mm", "Days_SD")))
    L <- L -dmvnorm(x=c(SCL_SD_mm=kaska99.SCL$SCL_Mean_mm[i],
                      Days_SD=kaska99.SCL$Days_Mean[i]),
                  mean= c(SCL_SD_mm=y[i], Days_SD=kaska99.SCL$Days_Mean[i]),
                  sigma=sigma, log=TRUE)
  }
  return(L)
}

parIni <- structure(c(48.66977358, 0.06178453, 0.38640902),
                  .Names = c("K", "rT", "X0"))

fitsize.SCL.2D <- optim(parIni, ML.Gompertz.2D, x=kaska99.SCL[, "Days_Mean"], hessian = TRUE)

# Estimation of standard error of parameters using Hessian matrix
sqrt(diag(solve(fitsize.SCL.2D$hessian)))

# Estimation of standard error of parameters using Bayesian concept and MCMC
Bayes.Gompertz.2D <- function(data, x) {
  x <- abs(x)
  y <- Gompertz(data, x)
  L <- 0
  for (i in seq_along(y)) {
    sigma <- matrix(c(kaska99.SCL$SCL_SD_mm[i]^2, 0, 0, kaska99.SCL$Days_SD[i]^2),
                    nrow=2, byrow=TRUE,
                    dimnames=list(c("SCL_SD_mm", "Days_SD"), c("SCL_SD_mm", "Days_SD")))
    L <- L - dmvnorm(x=c(SCL_SD_mm=kaska99.SCL$SCL_Mean_mm[i],
                      Days_SD=kaska99.SCL$Days_Mean[i]),
                  mean= c(SCL_SD_mm=y[i], Days_SD=kaska99.SCL$Days_Mean[i]),
                  sigma=sigma, log=TRUE)
  }
  return(L)
}

```

```

pMCMC <- structure(list(Density = c("dunif", "dunif", "dunif"),
  Prior1 = c(0, 0, 0), Prior2 = c(90, 1, 2),
  SDProp = c(1, 1, 1),
  Min = c(0, 0, 0), Max = c(90, 1, 2),
  Init = fitsize.SCL.2D$par),
  .Names = c("Density", "Prior1", "Prior2", "SDProp", "Min", "Max", "Init"),
  row.names = c("K", "rT", "X0"), class = "data.frame")
mcmc_run.2D <- MHalgoGen(n.iter=50000, parameters=pMCMC, data=kaska99.SCL[, "Days_Mean"],
  likelihood=Bayes.Gompertz.2D, n.chains=1, n.adapt=100, thin=1, trace=1,
  adaptive = TRUE)

plot(mcmc_run.2D, xlim=c(0, 90), parameters="K")
plot(mcmc_run.2D, xlim=c(0, 1), parameters="rT")
plot(mcmc_run.2D, xlim=c(0, 2), parameters="X0")

1-rejectionRate(as.mcmc(mcmc_run.2D))

par <- mcmc_run.2D$resultMCMC[[1]]

outsp <- t(apply(par, MARGIN = 1, FUN=function(x) Gompertz(0:70, par=x)))

rangqtiles <- apply(outsp, MARGIN=2, function(x) {quantile(x, probs=c(0.025, 0.5, 0.975))})

par(mar=c(4, 4, 2, 1))
plot_errbar(x=kaska99.SCL[, "Days_Mean"], y=kaska99.SCL[, "SCL_Mean_mm"],
  errbar.y = 2*kaska99.SCL[, "SCL_SD_mm"], bty="n", las=1,
  ylim=c(0, 50), xlab="Days", ylab="SCL mm",
  xlim=c(0, 70), x.plus = kaska99.SCL[, "Days_End"],
  x.minus = kaska99.SCL[, "Days_Begin"])

lines(0:70, rangqtiles["2.5%", ], lty=2)
lines(0:70, rangqtiles["97.5%", ], lty=2)
lines(0:70, rangqtiles["50%", ], lty=3)

text(x=50, y=10, pos=4,
  labels=paste("K=", format(x = fitsize.SCL.2D$par["K"], digits = 4)))
text(x=50, y=12.5, pos=4,
  labels=paste("rK=", format(x = fitsize.SCL.2D$par["K"]/39.33, digits = 4)))
text(x=50, y=15, pos=4,
  labels=paste("X0=", format(x = fitsize.SCL.2D$par["X0"], digits = 4)))
title("Multivariate normal distribution")

## End(Not run)

```

Description

Estimate the parameters that best describe the sexualisation thermal reaction norm within the TSP. The Temperatures parameter is a character string which can be:

- TimeWeighted.temperature.mean
- GrowthWeighted.temperature.mean
- GrowthRateWeighted.temperature.mean
- TSP.TimeWeighted.temperature.mean
- TSP.GrowthWeighted.temperature.mean
- TSP.GrowthRateWeighted.temperature.mean
- TSP.STRNWeighted.temperature.mean
- TSP.GrowthWeighted.STRNWeighted.temperature.mean
- TSP.GrowthRateWeighted.STRNWeighted.temperature.mean
- MiddleThird.TimeWeighted.temperature.mean
- MiddleThird.GrowthWeighted.temperature.mean
- MiddleThird.GrowthRateWeighted.temperature.mean

If information for sex is not known for some timeseries, set NA for Sexed.

Sexed, Males and Females must be vectors with names. The names must be the same as the names of timeseries of temperatures in EmbryoGrowthTRN.

Only two of these 3 parameters are required: Males, Females and Sexed

Note: four species have predefined embryo stages. embryo.stages parameter can take the values:

- Caretta caretta.SCL
- Chelonia mydas.SCL
- Emys orbicularis.SCL
- Emys orbicularis.mass
- Podocnemis expansa.SCL
- Generic.ProportionDevelopment

Usage

```
STRN(
  Initial_STRN = NULL,
  fixed.parameters = NULL,
  EmbryoGrowthTRN = stop("Embryo Growth Thermal Reaction Norm must be provided"),
  TSP.borders = NULL,
  embryo.stages = "Generic.ProportionDevelopment",
  TSP.begin = 0,
  TSP.end = 0.5,
  tsd = NULL,
  equation = "logistic",
```

```

Sexed = NULL,
Males = NULL,
Females = NULL,
Temperatures = "TSP.GrowthWeighted.STRNWeighted.temperature.mean",
SE = TRUE,
parallel = TRUE,
itnmax = 1000,
method = c("Nelder-Mead", "BFGS"),
control = list(trace = 1, REPORT = 10),
zero = 1e-09
)

```

Arguments

Initial_STRN	Values for initial model of Sexualisation Thermal Reaction Norm
fixed.parameters	Value for Sexualisation Thermal Reaction Norm model that will not be changed
EmbryoGrowthTRN	The Embryo Growth Thermal Reaction Norm obtained with searchR()
TSP.borders	The limits of TSP in stages. See embryo.stages parameter.
embryo.stages	The embryo stages. At least TSP.borders stages must be provided to estimate TSP borders. See note.
TSP.begin	Where TSP begin during the stage of beginning? In relative proportion of the stage.
TSP.end	Where TSP begin during the stage of ending? In relative proportion of the stage.
tsd	The model used to predict sex ratio, obtained from tsd()
equation	If tsd parameter is not provided, equation and parameters for tsd model must be provided.
Sexed	The number of sexed embryos with names identifying timeseries
Males	The number of males embryos with names identifying timeseries
Females	The number of females embryos with names identifying timeseries
Temperatures	The temperature from out of info.nests to be used
SE	Should standard error of parameters and Hessian matrix be estimated ? TRUE or FALSE
parallel	Should parallel computing for info.nests() be used
itnmax	Maximum number of iterations for each method
method	Methods to be used with optimx
control	List for control parameters for optimx
zero	The value to replace a null sex ratio

Details

STRN estimates the parameters that best describe the sexualisation thermal reaction norm within the TSP

Value

The list with object return by `optim()`

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
MedIncubation_Cc <- subset(DatabaseTSD, Species=="Caretta caretta" &
  RMU=="Mediterranean" & Sexed!=0)
Med_Cc <- with(MedIncubation_Cc, tsd(males=Males, females=Females,
  temperatures=Incubation.temperature, par=c(P=29.5, S=-0.01)))
plot(Med_Cc, xlim=c(25, 35))
males <- c(7, 0, 0, 0, 0, 5, 6, 3, 5, 3, 2, 3, 0, 0, 0, 0, 0, 0, 0, 0)
names(males) <- rev(rev(names(resultNest_4p_SSM4p$data))[-(1:2)])
sexed <- rep(10, length(males))
names(sexed) <- rev(rev(names(resultNest_4p_SSM4p$data))[-(1:2)])
Initial_STRN <- resultNest_4p_SSM4p$par[c("DHA_STRN", "DHH_STRN", "T12H_STRN")]
Initial_STRN <- structure(c(582.567096666926, 2194.0806711639, 3475.28414940385),
  .Names = c("DHA_STRN", "DHH_STRN", "T12H_STRN"))

fp <- c(Rho25_STRN=100)
fitSTRN <- STRN(Initial_STRN=Initial_STRN,
  EmbryoGrowthTRN=resultNest_4p_SSM4p, tsd=Med_Cc,
  embryo.stages="Caretta caretta.SCL",
  Sexed=sexed, Males=males,
  fixed.parameters=fp,
  SE=TRUE,
  Temperatures="TSP.GrowthWeighted.STRNWeighted.temperature.mean")
plotR(fitSTRN, curves = "ML quantiles", ylim=c(0,2))
CTE <- info.nests(NestsResult=resultNest_4p_SSM4p,
  SexualisationTRN=fitSTRN,
  SexualisationTRN.CI="Hessian",
  embryo.stages="Caretta caretta.SCL",
  CI="Hessian",
  replicate.CI=100,
  progress=TRUE,
  warnings=TRUE,
  out="summary")$summary
# CTE with growth-weighted temperature average
plot(Med_Cc, xlim=c(25, 35))
points(x=CTE$TSP.GrowthWeighted.temperature.mean, y=males/sexed,
  col="red", pch=19)
legend("topright", legend=c("CTE with growth-weighted TRN"),
  pch=19, col=c("red"))
# CTE with sexualisation TRN and growth-weighted temperature average
plot(Med_Cc, xlim=c(25, 35))
points(x=CTE$TSP.GrowthWeighted.STRNWeighted.temperature.mean, y=males/sexed,
  col="red", pch=19)
legend("topright", legend=c("CTE with growth-weighted TRN and Sex. TRN"),
```



```

      pch=19, col=c("red"))
xx <- seq(from=20, to=35, by=0.1)
plot(x=xx,
      y=log10(getFromNamespace(".SSM", ns="embryogrowth")(xx,
      c(fitSTRN$par, fitSTRN$fixed.parameters))[[1]]),
      type="l", bty="n", xlim=c(20, 35), ylim=c(-20, 20),
      xlab="Temperature", ylab="Sexualisation thermal reaction norm (log10)")

# Using only the sexualisation thermal reaction norm within TSP to calculate CTE

Initial_STRN <- resultNest_4p_SSM4p$par[c("DHA_STRN", "DHH_STRN", "T12H_STRN")]
Initial_STRN <- structure(c(3678.94960547096, -301.436485427701, 912.595953854977),
      .Names = c("DHA_STRN", "DHH_STRN", "T12H_STRN"))
fp <- c(Rho25_STRN=100)
fitSTRN_2 <- STRN(Initial_STRN=Initial_STRN,
      EmbryoGrowthTRN=resultNest_4p_SSM4p, tsd=Med_Cc,
      embryo.stages="Caretta caretta.SCL",
      Sexed=sexed, Males=males,
      fixed.parameters=fp,
      Temperatures="TSP_STRNWeighted.temperature.mean")
CTE <- info.nests(NestsResult=resultNest_4p_SSM4p,
      SexualisationTRN=fitSTRN_2,
      SexualisationTRN.CI="Hessian",
      embryo.stages="Caretta caretta.SCL",
      CI="Hessian",
      replicate.CI=100,
      progress=TRUE,
      warnings=TRUE,
      out="summary")$summary

# CTE with sexualisation TRN
plot(Med_Cc, xlim=c(25, 35))
points(x=CTE$TSP_STRNWeighted.temperature.mean, y=males/sexed,
      col="red", pch=19)
legend("topright", legend=c("CTE with Sexualisation TRN"),
      pch=19, col=c("red"))
xx <- seq(from=20, to=35, by=0.1)
plot(x=xx,
      y=getFromNamespace(".SSM", ns="embryogrowth")(xx,
      c(fitSTRN$par, fitSTRN$fixed.parameters))[[1]]),
      type="l", bty="n", xlim=c(20, 35), ylim=c(0, 1E-18),
      xlab="Temperature", ylab="Sexualisation thermal reaction norm")

## End(Not run)

```

STRN_MHmcmc

Metropolis-Hastings algorithm for Sexualisation Thermal Reaction Norm

Description

Run the Metropolis-Hastings algorithm for Sexualisation Thermal Reaction Norm.
The number of iterations is $n.iter+n.adapt+1$ because the initial likelihood is also displayed.

I recommend that `thin=1` because the method to estimate SE uses resampling. If initial point is maximum likelihood, `n.adapt = 0` is a good solution. To get the SE of the point estimates from `result_mcmc <-STRN_MHmcmc(result=try)`, use: `result_mcmc$SD` coda package is necessary for this function. The dataSTRN is a named list with the following objects:

- EmbryoGrowthTRN= result of [searchR](#)
- tsd= result of [tsd](#)
- sexed= vector with number of sexed embryos
- males= vector with number of males (could be also females=)
- Temperatures= a text of the temperatures name used as CTE

The Temperatures text for CTE can be:

- TimeWeighted.temperature.mean
- TSP.TimeWeighted.temperature.mean
- TSP.GrowthWeighted.temperature.mean
- TSP.STRNWeighted.temperature.mean
- TSP.GrowthWeighted.STRNWeighted.temperature.mean
- MiddleThird.TimeWeighted.temperature.mean

They are explained in the [info.nests](#) function.

This function is not still fully described as it has not been published still.

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 processes at time limited.

Usage

```
STRN_MHmcmc(
  result = NULL,
  n.iter = 10000,
  parametersMCMC = NULL,
  n.chains = 1,
  n.adapt = 0,
  thin = 1,
  trace = NULL,
  traceML = FALSE,
  batchSize = sqrt(n.iter),
  dataSTRN = NULL,
  adaptive = FALSE,
```

```

    adaptive.lag = 500,
    adaptive.fun = function(x) { ifelse(x > 0.234, 1.3, 0.7) },
    parallel = TRUE,
    intermediate = NULL,
    filename = "intermediate.Rdata",
    previous = NULL
  )

```

Arguments

result	An object obtained after a STRN fit
n.iter	Number of iterations for each step
parametersMCMC	A set of parameters used as initial point for searching with information on priors
n.chains	Number of replicates
n.adapt	Number of iterations before to store outputs
thin	Number of iterations between each stored output
trace	TRUE or FALSE or period, shows progress
traceML	TRUE or FALSE to show ML
batchSize	Number of observations to include in each batch fo SE estimation
dataSTRN	A named list data used to estimate likelihoods (see further in description)
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
parallel	Should parallel computing for info.nests() be used
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

STRN_MHmcmc runs the Metropolis-Hastings algorithm for STRN (Bayesian MCMC)

Value

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

Author(s)

Marc Girondot

Examples

```

## Not run:
library(embryogrowth)
MedIncubation_Cc <- subset(DatabaseTSD, Species=="Caretta caretta" &
  RMU=="Mediterranean" & Sexed!=0)
Med_Cc <- with(MedIncubation_Cc, tsd(males=Males, females=Females,
  temperatures=Incubation.temperature, par=c(P=29.5, S=-0.01)))
plot(Med_Cc, xlim=c(25, 35))
males <- c(7, 0, 0, 0, 0, 5, 6, 3, 5, 3, 2, 3, 0, 0, 0, 0, 0, 0, 0, 0)
names(males) <- rev(rev(names(resultNest_4p_SSM4p$data))[-(1:2)])
sexed <- rep(10, length(males))
names(sexed) <- rev(rev(names(resultNest_4p_SSM4p$data))[-(1:2)])
Initial_STRN <- resultNest_4p_SSM4p$par[c("DHA", "DHH", "T12H")]
Initial_STRN <- structure(c(3460.21379985491, 588.062535503578, 2347.70617453574),
  .Names = c("DHA", "DHH", "T12H"))

fp <- c(Rho25=100)
fitSTRN <- STRN(Initial_STRN, EmbryoGrowthTRN=resultNest_4p_SSM4p, tsd=Med_Cc,
  Sexed=sexed, Males=males,
  fixed.parameters=fp,
  Temperatures="TSP.GrowthWeighted.STRNWeighted.temperature.mean")
pMCMC <- TRN_MHmcmc_p(fitSTRN, accept=TRUE)
pMCMC[, "Density"] <- "dunif"
pMCMC[, "Prior2"] <- pMCMC[, "Max"] <- 10000
pMCMC[, "Prior1"] <- pMCMC[, "Min"] <- 1
outMCMC <- STRN_MHmcmc(result = fitSTRN, n.iter = 50000, parametersMCMC = pMCMC,
  n.chains = 1, n.adapt = 0, thin = 1, trace = TRUE,
  dataSTRN = list(EmbryoGrowthTRN = resultNest_4p_SSM4p,
    Temperatures = "TSP.STRNWeighted.temperature.mean",
    fixed.parameters=fitSTRN$fixed.parameters,
    zero=1E-9,
    tsd=Med_Cc,
    Sexed=sexed, Males=males),
  adaptive = TRUE, adaptive.lag = 500,
  intermediate = 1000,
  filename = "intermediate_mcmcSTRN.Rdata")

plot(outMCMC, parameters=1)
plot(outMCMC, parameters=2)
plot(outMCMC, parameters=3)
1-rejectionRate(as.mcmc(x = outMCMC))
# Take care,you computer will be 100% busy as all cores will be used intensively
outMCMC_parallel <- parallel::mclapply(1:detectCores(), function(x) {
  STRN_MHmcmc(result = fitSTRN, n.iter = 50000/detectCores(),
    parametersMCMC = pMCMC,
    n.chains = 1, n.adapt = 0, thin = 1, trace = TRUE,
    dataSTRN = list(EmbryoGrowthTRN = resultNest_4p_SSM4p,
      Temperatures = "TSP.STRNWeighted.temperature.mean",
      fixed.parameters=fitSTRN$fixed.parameters,
      tsd=Med_Cc, zero=1E-9,
      Sexed=sexed, Males=males),
    parallel=FALSE,
    adaptive = TRUE, adaptive.lag = 500,
    intermediate = NULL)

```

```

})
outMCMC_parallel_merge <- outMCMC_parallel[[1]]
for (i in 2:length(outMCMC_parallel)) {
  outMCMC_parallel_merge <- merge(outMCMC_parallel_merge, outMCMC_parallel[[i]])
}
plot(outMCMC_parallel_merge, parameters=1)
plot(outMCMC_parallel_merge, parameters=2)
plot(outMCMC_parallel_merge, parameters=3)

plotR(parameters = fitSTRN$par, fixed.parameters=fitSTRN$fixed.parameters,
       curves = "MCMC quantiles", ylim=c(0, 5), resultmcmc = outMCMC_parallel_merge,
       ylab="Relative contribution to sexualisation", xlim=c(28, 29))

## End(Not run)

```

summary.Nests

Summarize the information from a Nests object.

Description

Summarize the information from a Nests object:
- Name of the nests, total incubation length and average temperature

Usage

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

Arguments

object	A object obtained after FormatNests()
...	Not used

Details

summary.Nests Summarize the information from a Nests object

Value

None

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest, previous=NULL)
summary(formatted)

## End(Not run)
```

switch.transition *Add a transition parameter on a set of parameters or remove it*

Description

Add a transition parameter on a set of parameters or remove it

Usage

```
switch.transition(parameters = stop("A set of parameters must be supplied"))
```

Arguments

parameters A vector with parameters

Details

switch.transition Add a transition parameter on a set of parameters or remove it

Value

A vector with parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
data(resultNest_6p_SSM6p)
# Get a set of parameters without transition
x1 <- resultNest_6p_SSM6p$par
# Generate a set of parameters with transition
x2 <- switch.transition(x1)
# Generate a set of parameters without transition
x3 <- switch.transition(x3)

## End(Not run)
```

tempConst	<i>Timeseries of constant temperatures for nests</i>
-----------	--

Description

Timeseries of temperatures for nests

Usage

```
tempConst
```

Format

A dataframe with raw data.

Details

Timeseries of constant temperatures for nests

Author(s)

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

References

Girondot, M., Kaska, Y., 2014. A model to predict the thermal reaction norm for the embryo growth rate from field data. *Journal of Thermal Biology* 45, 96-102.

Examples

```
## Not run:
library(embryogrowth)
# Same as:
# GenerateConstInc(durations = rep(104*60*24, 11),
# temperatures = 25:35,
# names = paste0("T",25:35))
data(tempConst)
tempConst_f <- FormatNests(tempConst)

data(nest)
formatted <- FormatNests(nest)
x <- structure(c(109.683413821537, 614.969219372661, 306.386903812694,
  229.003478775323), .Names = c("DHA", "DHH", "T12H", "Rho25"))

# See the stages dataset examples for justification of M0 and rK

pfixed <- c(rK=1.208968)
resultNest_4p_SSM <- searchR(parameters=x, fixed.parameters=pfixed,
  temperatures=formatted, derivate=dydt.Gompertz, M0=0.3470893,
```

```

test=c(Mean=39.33, SD=1.92))

plotR(result=resultNest_4p_SSM, show.hist = TRUE,
      ylim=c(0, 8), curves="ML quantiles")

# Now use the fitted parameters from resultNest_4p_SSM with
# the constant incubation temperatures:

plot(resultNest_4p_SSM, temperatures=tempConst_f,
stopatatest=TRUE, series="T30", xlim=c(0,50),
ylimT=c(22, 32), test=c(Mean=39.33, SD=1.92),
embryo.stages="Caretta caretta.SCL")

plot(resultNest_4p_SSM, temperatures=tempConst_f,
stopatatest=TRUE, series="T25", xlim=c(0,120),
ylimT=c(22, 32), test=c(Mean=39.33, SD=1.92),
embryo.stages="Caretta caretta.SCL")

## End(Not run)

```

test.parallel	<i>Estimate the likelihood of a set of parameters for nest incubation data with or without parallel computing option</i>
---------------	--

Description

Estimate the likelihood of a set of parameters for nest incubation data with or without parallel computing option. It uses the user time from the print result of system.time() function.

Usage

```
test.parallel(result = stop("A ResultNest object must be provided"))
```

Arguments

result A object obtained after searchR or likelihoodR

Details

test.parallel estimates the likelihood of a set of parameters for nest incubation data with or without parallel computing option

Value

The gain or loss of computing time using parallel version

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(resultNest_4p_SSM4p)
test.parallel(resultNest_4p_SSM4p)

## End(Not run)
```

TRN_MHmcmc_p	<i>Generates set of parameters to be used with GRTRN_MHmcmc() or STRN_MHmcmc()</i>
--------------	--

Description

Interactive script used to generate set of parameters to be used with GRTRN_MHmcmc() or STRN_MHmcmc().

Usage

```
TRN_MHmcmc_p(
  result = NULL,
  parameters = NULL,
  fixed.parameters = NULL,
  accept = FALSE
)
```

Arguments

result	An object obtained after a SearchR fit
parameters	A set of parameters. Replace the one from result
fixed.parameters	A set of fixed parameters. Replace the one from result
accept	If TRUE, the script does not wait user information

Details

TRN_MHmcmc_p generates set of parameters to be used with GRTRN_MHmcmc() or STRN_MHmcmc()

Value

A matrix with the parameters

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
# The initial parameters value can be:
# "T12H", "DHA", "DHH", "Rho25"
# Or
# "T12L", "T12H", "DHA", "DHH", "DHL", "Rho25"
x <- structure(c(118.768297442004, 475.750095909406, 306.243694918151,
116.055824800264), .Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
resultNest_4p_SSM4p <- searchR(parameters=x, fixed.parameters=pfixed,
temperatures=formatted, derivate=dydt.Gompertz, M0=1.7,
test=c(Mean=39.33, SD=1.92))
data(resultNest_4p_SSM4p)
pMCMC <- TRN_MHmcmc_p(resultNest_4p_SSM4p, accept=TRUE)

## End(Not run)
```

tsd

Estimate the parameters that best describe temperature-dependent sex determination

Description

Estimate the parameters that best describe the thermal reaction norm for sex ratio when temperature-dependent sex determination occurs.

It can be used also to evaluate the relationship between incubation duration and sex ratio.

The parameter l was defined in Girondot (1999). The TRT is defined from the difference between the two boundary temperatures giving sex ratios of l and $1 - l$, respectively:

For logistic model (Girondot, 1999), it follows

$$TRT_l = abs(S K_l)$$

where K_l is a constant equal to $2 \log\left(\frac{l}{1-l}\right)$.

In Girondot (1999), l was 0.05 and then the TRT was defined as being the range of temperatures producing from 5% to 95% of each sex.

For other models, TRT is calculated numerically.

The basic model is logistic one. This model has the particularity to have a symmetric shape around P .

The other models have been built to alleviate this constraint. Hill and A-logistic models can be asymmetric, but it is impossible to control independently the low and high transitions.

Hulin model is asymmetric but the control of asymmetry is difficult to manage. If asymmetric model is selected, it is always better to use flexit model.

$$ifdose < P then (1 + (2^K 1 - 1) * exp(4 * S1 * (P - x)))^{1/K1}$$

$$ifdose > Pthen 1 - ((1 + (2^{K2} - 1) * exp(4 * S2 * (x - P)))^{1/K2})$$

with:

$$S1 = S / ((4/K1) * (2^{K1} - 1))^{1/K1 + 1} * (2^{K1} - 1)$$

$$S2 = S / ((4/K2) * (2^{K2} - 1))^{1/K2 + 1} * (2^{K2} - 1)$$

Usage

```
tsd(
  df = NULL,
  males = NULL,
  females = NULL,
  N = NULL,
  temperatures = NULL,
  durations = NULL,
  l = 0.05,
  parameters.initial = c(P = NA, S = -2, K = 0, K1 = 1, K2 = 0),
  males.freq = TRUE,
  fixed.parameters = NULL,
  equation = "logistic",
  replicate.CI = 10000,
  range.CI = 0.95,
  replicate.NullDeviance = 1000,
  control = list(maxit = 1000),
  print = TRUE
)
```

Arguments

df	A dataframe with at least two columns named males, females or N and temperatures, Incubation.temperature or durations column
males	A vector with male numbers
females	A vector with female numbers
N	A vector with total numbers
temperatures	The constant incubation temperatures used to fit sex ratio
durations	The duration of incubation or TSP used to fit sex ratio
l	Sex ratio limits to define TRT are l and 1-l (see Girondot, 1999)
parameters.initial	Initial values for P, S or K search as a vector, ex. c(P=29, S=-0.3)
males.freq	If TRUE data are shown as males frequency
fixed.parameters	Parameters that will not be changed
equation	Could be "logistic", "Hill", "A-logistic", "Hulin", "Double-A-logistic", "flexit" or "GSD"
replicate.CI	Number of replicates to estimate confidence intervals

range.CI	The range of confidence interval for estimation, default=0.95
replicate.NullDeviance	Number of replicates to estimate null distribution of deviance
control	List of parameters used in optim.
print	Should the results be printed at screen? TRUE (default) or FALSE

Details

tsd estimates the parameters that best describe temperature-dependent sex determination

Value

A list the pivotal temperature, transitional range of temperatures and their SE

Author(s)

Marc Girondot

References

Girondot, M. 1999. Statistical description of temperature-dependent sex determination using maximum likelihood. *Evolutionary Ecology Research*, 1, 479-486.

Godfrey, M.H., Delmas, V., Girondot, M., 2003. Assessment of patterns of temperature-dependent sex determination using maximum likelihood model selection. *Ecoscience* 10, 265-272.

Hulin, V., Delmas, V., Girondot, M., Godfrey, M.H., Guillon, J.-M., 2009. Temperature-dependent sex determination and global change: are some species at greater risk? *Oecologia* 160, 493-506.

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD, P_TRT\(\)](#), [TSP.list](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
CC_AtlanticSW <- subset(DatabaseTSD, RMU=="Atlantic, SW" &
  Species=="Caretta caretta" & (!is.na(Sexed) & Sexed!=0) &
  !is.na(Correction.factor))
tsdL <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
  temperatures=Incubation.temperature-Correction.factor,
  equation="logistic", replicate.CI=NULL))
tsdH <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
  temperatures=Incubation.temperature-Correction.factor,
  equation="Hill", replicate.CI=NULL))
tsdR <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
  temperatures=Incubation.temperature-Correction.factor,
  equation="A-logistic", replicate.CI=NULL))
tsdF <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
  temperatures=Incubation.temperature-Correction.factor,
```

```

                                equation="Flexit", replicate.CI=NULL))
tsdDR <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
                                temperatures=Incubation.temperature-Correction.factor,
                                equation="Double-A-logistic", replicate.CI=NULL))
gsd <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
                                temperatures=Incubation.temperature-Correction.factor,
                                equation="GSD", replicate.CI=NULL))
compare_AIC(Logistic_Model=tsdL, Hill_model=tsdH, Alogistic_model=tsdR,
            flexit=tsdF,
            DoubleAlogistic_model=tsdDR, GSD_model=gsd)
compare_AICc(Logistic_Model=tsdL, Hill_model=tsdH, Alogistic_model=tsdR,
            DoubleAlogistic_model=tsdDR, GSD_model=gsd, factor.value = -1)
compare_BIC(Logistic_Model=tsdL, Hill_model=tsdH, Alogistic_model=tsdR,
            DoubleAlogistic_model=tsdDR, GSD_model=gsd, factor.value = -1)
#####
eo <- subset(DatabaseTSD, Species=="Emys orbicularis", c("Males", "Females",
            "Incubation.temperature"))

eo_Hill <- with(eo, tsd(males=Males, females=Females,
            temperatures=Incubation.temperature,
            equation="Hill"))
eo_Hill <- tsd(df=eo, equation="Hill", replicate.CI=NULL)
eo_logistic <- tsd(eo, replicate.CI=NULL)
eo_Alogistic <- with(eo, tsd(males=Males, females=Females,
            temperatures=Incubation.temperature,
            equation="a-logistic", replicate.CI=NULL))
### The Hulin model is a modification of A-logistic (See Hulin et al. 2009)

##### Caution
### It should not be used anymore as it can produce unexpected results
par <- eo_Alogistic$par
names(par)[which(names(par)=="K")] <- "K2"
par <- c(par, K1=0)
eo_Hulin <- with(eo, tsd(males=Males, females=Females,
            parameters.initial=par,
            temperatures=Incubation.temperature,
            equation="Hulin", replicate.CI=NULL))

### The Double-A-logistic model is a A-logistic model with K1 and K2 using respectively
### below and above P

##### Caution
### The curve is not smooth at pivotal temperature

par <- eo_Alogistic$par
names(par)[which(names(par)=="K")] <- "K2"
par <- c(par, K1=as.numeric(par["K2"])*0.8)
par["K2"] <- par["K2"]*0.8
eo_Double_Alogistic <- with(eo, tsd(males=Males, females=Females,
            parameters.initial=par,
            temperatures=Incubation.temperature,
            equation="Double-a-logistic", replicate.CI=NULL))

```

```

### The flexit model is modeled with K1 and K2 using respectively
### below and above P and smooth transition at P; S is the slope at P

par <- c(eo_logistic$par["P"], 1/4*eo_logistic$par["S"], K1=1, K2=1)
eo_flexit <- with(eo, tsd(males=Males, females=Females,
                        parameters.initial=par,
                        temperatures=Incubation.temperature,
                        equation="flexit", replicate.CI=NULL))

compare_AIC(Logistic=eo_logistic, Hill=eo_Hill, Alogistic=eo_Alogistic,
            Hulin=eo_Hulin, Double_Alogistic=eo_Double_Alogistic,
            flexit=eo_flexit)
## Note that SE for lower limit of TRT is wrong
plot(eo_flexit)
## To get correct confidence interval, check \code{tsd_MHmcmc()}.

### Note the asymmetry of the Double-A-logistic and flexit models
predict(eo_Double_Alogistic,
        temperatures=c(eo_Double_Alogistic$par["P"]-0.2, eo_Double_Alogistic$par["P"]+0.2))
predict(eo_Double_Alogistic)

(p <- predict(eo_flexit,
              temperatures=c(eo_flexit$par["P"]-0.3, eo_flexit$par["P"]+0.3)))
p["50%", 1]-0.5; 0.5-p["50%", 2]
predict(eo_flexit)

### It can be used also for incubation duration
CC_AtlanticSW <- subset(DatabaseTSD, RMU=="Atlantic, SW" &
                        Species=="Caretta caretta" & Sexed!=0)
tsdL_IP <- with (CC_AtlanticSW, tsd(males=Males, females=Females,
                                   durations=IP.mean,
                                   equation="logistic", replicate.CI=NULL))
plot(tsdL_IP, xlab="Incubation durations in days")
# Example with Chelonia mydas
cm <- subset(DatabaseTSD, Species=="Chelonia mydas" & !is.na(Sexed), c("Males", "Females",
                                                                    "Incubation.temperature", "RMU"))
tsd(subset(cm, subset=RMU=="Pacific, SW"))
tsd(subset(cm, subset=RMU=="Pacific, Northwest"))
tsd(subset(cm, subset=RMU=="Atlantic, S Caribbean"))

### Eretmochelys imbricata
Ei_PacificSW <- subset(DatabaseTSD, RMU=="Pacific, SW" &
                      Species=="Eretmochelys imbricata")
Ei_AtlanticW <- subset(DatabaseTSD, RMU=="Atlantic, W (Caribbean and E USA)" &
                      Species=="Eretmochelys imbricata")
Ei_AtlanticSW <- subset(DatabaseTSD, RMU=="Atlantic, SW" &
                       Species=="Eretmochelys imbricata")
Ei_PacSW <- tsd(Ei_PacificSW)
Ei_AtlW <- tsd(Ei_AtlanticW)
Ei_AtlSW <- tsd(Ei_AtlanticSW)

plot(Ei_PacSW, xlim=c(27, 33), show.PTRT = FALSE, main=expression(italic("Eretmochelys imbricata")))
par(new=TRUE)

```



```

Podocnemis_expansa_Valenzuela_2001 <- subset(Podocnemis_expansa,
      Reference=="Valenzuela, 2001")
PeL2001 <- tsd(df=Podocnemis_expansa_Valenzuela_2001)
# The pivotal temperature is 32.133 °C (CI 95% 31.495;32.766)
# In Valenzuela, 2001: "Using data from the present study alone,
# the critical temperature was 32.2 °C by both methods and the 95%
# confidence limits were 31.4 °C and 32.9 °C."
# Data are close but not identical to what was published.

# The pivotal temperature calculated by maximum likelihood and by inverse
# prediction from logistic regression, was 32.6°C using raw data from
# 1991 (N. Valenzuela, unpublished data) and from this study. The lower
# and upper 95% confidence limits of the pivotal temperature were 32.2°C
# and 33.2°C,

Podocnemis_expansa_Valenzuela_1997 <- subset(Podocnemis_expansa,
      subset=(((Reference=="Lance et al., 1992; Valenzuela et al., 1997") |
      (Reference=="Valenzuela, 2001")) &
      (!is.na(Sexed)) & (Sexed != 0)))

PeL1997 <- tsd(df=Podocnemis_expansa_Valenzuela_1997)

## End(Not run)

```

tsd_MHmcmc

Metropolis-Hastings algorithm for Sex ratio

Description

Run the Metropolis-Hastings algorithm for tsd.
 Deeply modified from a MCMC script by Olivier Martin (INRA, Paris-Grignon).
 The number of iterations is $n.iter+n.adapt+1$ because the initial likelihood is also displayed.
 I recommend that $thin=1$ because the method to estimate SE uses resampling.
 If initial point is maximum likelihood, $n.adapt = 0$ is a good solution.
 To get the SE from `result_mcmc <- tsd_MHmcmc(result=try)`, use:
`result_mcmc$BatchSE` or `result_mcmc$TimeSeriesSE`
 The batch standard error procedure is usually thought to be not as accurate as the time series methods.
 Based on Jones, Haran, Caffo and Neath (2005), the batch size should be equal to $\sqrt{n.iter}$.
 Jones, G.L., Haran, M., Caffo, B.S. and Neath, R. (2006) Fixed Width Output Analysis for Markov chain Monte Carlo, *Journal of the American Statistical Association*, 101:1537-1547.
 coda package is necessary for this function.
 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 processes at time limited.

Usage

```
tsd_MHmcmc(
  result = stop("A result of tsd() fit must be provided"),
  n.iter = 10000,
  parametersMCMC = NULL,
  n.chains = 1,
  n.adapt = 0,
  thin = 1,
  trace = FALSE,
  traceML = FALSE,
  batchSize = sqrt(n.iter),
  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

result	An object obtained after a SearchR fit
n.iter	Number of iterations for each step
parametersMCMC	A set of parameters used as initial point for searching with information on priors
n.chains	Number of replicates
n.adapt	Number of iterations before to store outputs
thin	Number of iterations between each stored output
trace	TRUE or FALSE or period, shows progress
traceML	TRUE or FALSE to show ML
batchSize	Number of observations to include in each batch fo SE estimation
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

tsd_MHmcmc runs the Metropolis-Hastings algorithm for tsd (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 Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD.P_TRT\(\)](#), [TSP.list](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
eo <- subset(DatabaseTSD, Species=="Emys orbicularis", c("Males", "Females",
              "Incubation.temperature"))

eo_logistic <- tsd(eo)
pMCMC <- tsd_MHmcmc_p(eo_logistic, accept=TRUE)
# Take care, it can be very long
result_mcmc_tsd <- tsd_MHmcmc(result=eo_logistic,
  parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,
  n.adapt = 0, thin=1, trace=FALSE, adaptive=TRUE)
# summary() permits to get rapidly the standard errors for parameters
summary(result_mcmc_tsd)
plot(result_mcmc_tsd, parameters="S", scale.prior=TRUE, xlim=c(-3, 3), las=1)
plot(result_mcmc_tsd, parameters="P", scale.prior=TRUE, xlim=c(25, 35), las=1)

plot(eo_logistic, resultmcmc = result_mcmc_tsd)

1-rejectionRate(as.mcmc(result_mcmc_tsd))
raftery.diag(as.mcmc(result_mcmc_tsd))
heidel.diag(as.mcmc(result_mcmc_tsd))
library(car)
o <- P_TRT(x=eo_logistic, resultmcmc=result_mcmc_tsd)
outEo <- dataEllipse(x=o$P_TRT[, "PT"],
                    y=o$P_TRT[, "TRT"],
                    levels=c(0.95),
                    draw=FALSE)
plot(x = o$P_TRT[, "PT"],
     y=o$P_TRT[, "TRT"],
     pch=".", las=1, bty="n",
     xlab="Pivotal temperature",
     ylab=paste0("TRT ", as.character(100*eo_logistic$l), "%"),
     xlim=c(28.4, 28.6),
     ylim=c(0.8, 1.8))
lines(outEo[, 1], outEo[, 2], col="green", lwd=2)
legend("topleft", legend = c("Emys orbicularis", "95% confidence ellipse"),
      pch=c(19, NA), col=c("black", "green"), lty=c(0, 1), lwd=c(0, 2))

logistic <- function(x, P, S) {
  return(1/(1+exp((1/S)*(P-x))))
}

q <- as.quantile(result_mcmc_tsd, fun=logistic,
```

```

        xlim=seq(from=25, to=35, by=0.1), nameparxlim="x")
plot(x=seq(from=25, to=35, by=0.1), y=q[1, ], type="l", las=1,
     xlab="Temperatures", ylab="Male proportion", bty="n")
lines(x=seq(from=25, to=35, by=0.1), y=q[2, ])

## End(Not run)

```

tsd_MHmcmc_p

Generates set of parameters to be used with tsd_MHmcmc()

Description

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

Usage

```

tsd_MHmcmc_p(
  result = stop("An output from tsd() must be provided"),
  accept = FALSE
)

```

Arguments

<code>result</code>	An object obtained after a <code>tsd</code> fit
<code>accept</code>	If TRUE, the script does not wait user information

Details

`tsd_MHmcmc_p` generates set of parameters to be used with `tsd_MHmcmc()`

Value

A matrix with the parameters

Author(s)

Marc Girondot

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD](#), [P_TRT\(\)](#), [TSP.list](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
eo <- subset(DatabaseTSD, Species=="Emys orbicularis", c("Males", "Females",
              "Incubation.temperature"))
eo_logistic <- with(eo, tsd(males=Males, females=Females,
              temperatures=Incubation.temperature))
pMCMC <- tsd_MHmcmc_p(eo_logistic, accept=TRUE)
# Take care, it can be very long
result_mcmc_tsd <- tsd_MHmcmc(result=eo_logistic,
parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,
n.adapt = 0, thin=1, trace=FALSE, adaptive=TRUE)
# summary() permits to get rapidly the standard errors for parameters
summary(result_mcmc_tsd)
plot(result_mcmc_tsd, parameters="S", scale.prior=TRUE, xlim=c(-3, 3), las=1)
plot(result_mcmc_tsd, parameters="P", scale.prior=TRUE, xlim=c(25, 35), las=1)

eo_flexit <- with(eo, tsd(males=Males, females=Females,
              parameters.initial=c(eo_logistic$par["P"],
              1/(4*eo_logistic$par["S"])),
              K1=1, K2=1),
              temperatures=Incubation.temperature,
              equation="flexit", replicate.CI=NULL))
pMCMC <- tsd_MHmcmc_p(eo_flexit, accept=TRUE)
result_mcmc_tsd <- tsd_MHmcmc(result=eo_flexit,
parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,
n.adapt = 0, thin=1, trace=FALSE, adaptive=TRUE)
# summary() permits to get rapidly the standard errors for parameters
summary(result_mcmc_tsd)
plot(result_mcmc_tsd, parameters="S", scale.prior=TRUE, xlim=c(-3, 3), las=1)
plot(result_mcmc_tsd, parameters="P", scale.prior=TRUE, xlim=c(25, 35), las=1)
plot(result_mcmc_tsd, parameters="K1", scale.prior=TRUE, xlim=c(-10, 10), las=1)
plot(result_mcmc_tsd, parameters="K2", scale.prior=TRUE, xlim=c(-10, 10), las=1)

plot(eo_flexit, resultmcmc = result_mcmc_tsd)

## End(Not run)
```

TSP.list

Database of thermosensitive period of development for sex determination

Description

Database of thermosensitive period of development for sex determination.

This database can be used with the functions `plot()` or `info.nests()`.

The attributes `TSP.begin.stages` and `TSP.end.stages` for each dataframe give respectively the first and the last stages for TSP. Then the metrics for the limits of TSP are the average sizes before and after the TSP (see example, below).

If the metric for the stages before the TSP or after the TSP is not known, it will use the available information.

Usage

```
TSP.list
```

Format

A list with dataframes including attributes

Details

Database of thermosensitive period of development for sex determination

Author(s)

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

References

Mrosovsky, N., Pieau, C., 1991. Transitional range of temperature, pivotal temperatures and thermosensitive stages for sex determination in reptiles. *Amphibia-Reptilia* 12, 169-179.

See Also

Other Functions for temperature-dependent sex determination: [DatabaseTSD.version\(\)](#), [DatabaseTSD](#), [P_TRT\(\)](#), [plot.tsd\(\)](#), [predict.tsd\(\)](#), [stages](#), [tsd_MHmcmc_p\(\)](#), [tsd_MHmcmc\(\)](#), [tsd\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
data(TSP.list)
names(TSP.list)
reference <- "Emys_orbicularis.mass"
metric <- TSP.list[[reference]]
TSP.begin <- attributes(TSP.list[[reference]])$TSP.begin.stages
TSP.end <- attributes(TSP.list[[reference]])$TSP.end.stages
# Metric at the beginning of the TSP
del <- ifelse(all(metric$stages == TSP.begin - 1)==FALSE, 0, 1)
(metric$metric[metric$stages == TSP.begin - del] +
  metric$metric[metric$stages == TSP.begin]) / 2
# Metric at the end of the TSP
del <- ifelse(all(metric$stages == TSP.begin + 1)==FALSE, 0, 1)
(metric$metric[metric$stages == TSP.end] +
  metric$metric[metric$stages == del + TSP.end]) / 2

## End(Not run)
```

uncertainty.datalogger

Uncertainty of average temperatures obtained using temperature data logger

Description

Calculate the uncertainty of average temperature dependent on the characteristics of a data logger and sampling rate.

The temperature is supposed to be uniformly distributed with min and max being -accuracy and +accuracy.

Usage

```
uncertainty.datalogger(  
  max.time = 0,  
  sample.rate = 0,  
  accuracy = 0.5,  
  resolution = 1,  
  replicates = 10000,  
  method = function(x) { 2 * qnorm(0.975) * sd(x) }  
)
```

Arguments

max.time	being the maximum time to record in minutes
sample.rate	The sample rates in minutes
accuracy	The accuracy of the data logger in °C
resolution	The resolution of the data logger in °C
replicates	The number of replicates to estimate uncertainty.
method	The fonction that will be used to return the uncertainty.

Details

uncertainty.datalogger Calculate the uncertainty of the average temperature calculated using data gathered by a data logger.

Value

The function will return the uncertainty of the average temperature for the considered period as being the 95

Author(s)

Marc Girondot

See Also

Other Data loggers utilities: [calibrate.datalogger\(\)](#), [movement\(\)](#)

Examples

```
## Not run:
library(embryogrowth)
# Example using the hypothesis of Gaussian distribution
uncertainty.datalogger(sample.rate=30, accuracy=1, resolution=0.5,
  method=function(x) {2*qnorm(0.975)*sd(x)})
# Example without hypothesis about distribution, using quantiles
uncertainty.datalogger(sample.rate=30, accuracy=1, resolution=0.5,
  method=function(x) {quantile(x, probs=c(0.975))-
    quantile(x, probs=c(0.025))})

par(mar=c(4, 4, 1, 1))
plot(x=10:120, uncertainty.datalogger(sample.rate=10:120,
  accuracy=0.5,
  resolution=1),
  las=1, bty="n", type="l",
  xlab="Sample rate in minutes",
  ylab=expression("Uncertainty in "*degree*"C"),
  ylim=c(0, 0.15), xlim=c(0, 120))
lines(x=10:120, uncertainty.datalogger(sample.rate=10:120,
  accuracy=1,
  resolution=0.5), col="red")
lines(x=10:120, uncertainty.datalogger(sample.rate=10:120,
  accuracy=1,
  resolution=1), col="blue")
lines(x=10:120, uncertainty.datalogger(sample.rate=10:120,
  accuracy=0.5,
  resolution=0.5), col="yellow")
legend("topleft", legend=c("Accuracy=0.5, resolution=0.5",
  "Accuracy=0.5, resolution=1",
  "Accuracy=1, resolution=0.5",
  "Accuracy=1, resolution=1"), lty=1,
  col=c("yellow", "black", "red", "blue"),
  cex=0.6)

## End(Not run)
```

web.tsd

Run a shiny application for basic functions of tsd function

Description

Run a shiny application for basic functions of tsd function.

Usage

```
web.tsd()
```

Details

web.tsd runs a shiny application for basic functions of tsd function

Value

Nothing

Author(s)

Marc Girondot

Examples

```
## Not run:  
library(embryogrowth)  
web.tsd()  
  
## End(Not run)
```

weightmaxentropy	<i>Search for the weights of the nests which maximize the entropy of nest temperatures distribution</i>
------------------	---

Description

Search for the weights of the nests which maximize the entropy of nest temperatures distribution. Entropy is measured by Shanon index.
Entropy method must be entropy.empirical because it is the only method insensitive to scaling.
If no weight is given, the initial weight is uniformly distributed.
Use control_optim=list(trace=0) for not show progress of search report.

Usage

```
weightmaxentropy(  
  temperatures = stop("Temperature data must be provided !"),  
  weight = NULL,  
  entropy.method = entropy::entropy.empirical,  
  plot = TRUE,  
  control_optim = list(trace = 0, maxit = 500),  
  control_plot = NULL,  
  control_entropy = NULL,  
  col = c("black", "red")  
)
```


Arguments

temperatures	Timeseries of temperatures formatted using FormatNests()
weight	A named vector of the initial weight search for each nest for likelihood estimation
entropy.method	Entropy function, for example entropy::entropy.empirical. See package entropy for description
plot	Do the plot of temperatures before and after weight must be shown ? TRUE or FALSE
control_optim	A list with control paramaters for optim function
control_plot	A list with control paramaters for plot function
control_entropy	A list with control paramaters for entropy function
col	Colors for unweighted and weighted distributions

Details

Search for the weights of the nests which maximize the entropy of nest temperatures distribution

Value

A named vector of weights

Author(s)

Marc Girondot

Examples

```
## Not run:
library(embryogrowth)
data(nest)
formatted <- FormatNests(nest)
w <- weightmaxentropy(formatted, control_plot=list(xlim=c(20,36)))
x <- structure(c(120.940334922916, 467.467455887442,
306.176613681557, 117.857995419495),
.Names = c("DHA", "DHH", "T12H", "Rho25"))
# pfixed <- c(K=82.33) or rK=82.33/39.33
pfixed <- c(rK=2.093313)
# K or rK are not used for dydt.linear or dydt.exponential
resultNest_4p_weight <- searchR(parameters=x,
fixed.parameters=pfixed, temperatures=formatted,
derivate=dydt.Gompertz, M0=1.7, test=c(Mean=39.33, SD=1.92),
method = "BFGS", weight=w)
data(resultNest_4p_weight)
plotR(resultNest_4p_weight, ylim=c(0,0.50), xlim=c(15, 35))
# Standard error of parameters can use the GRTRN_MHmcmc() function

## End(Not run)
```

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