Package ‘synlik’  

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Synthetic Likelihood Methods for Intractable Likelihoods

Description

Package that provides Synthetic Likelihood methods for intractable likelihoods. The package is meant to be as general purpose as possible: as long as you are able to simulate data from your model you should be able to fit it.

Details

Package: synlik
Type: Package
Version: 0.1.2
Date: 2018-05-22
License: GPL (>=2)

The package allows users to create objects of class synlik (S4), which are essentially constituted of a simulator function and a function (summaries) that transforms the data into summary statistics. The simulator can output any kind of data (vector, list, etc) and this will be passed directly to the summaries function. This allow the package to fit a large variety of models.

Once the model of interest has been set up as a synlik object, it is possible several methods on it. The function most useful function is slik, which can be used to evaluate the synthetic likelihood. The slice.synlik function allows to obtain and plot slices of the synthetic likelihood with respect
to model parameters. It is possible to simulate data or statistics from the model using the generic `simulate`, and to check the normality of the statistics using the `checkNorm` function. Unknown parameters can be estimated by MCMC, through the `smcmc` function. This function will return an object of class `smcmc` (S4), which contains all the inputs and results of the MCMC procedure.

Many functions in the package support parallel simulation on multiple cores.

**Author(s)**

Matteo Fasiolo and Simon N. Wood

Maintainer: Matteo Fasiolo <matteo.fasiolo@gmail.com>

**References**


**See Also**

For some examples see the Vignettes (type `vignette("synlik")`).

**Examples**

```r
## Not run:
#### Here I put a simple example,
#### if you want to see more type: vignette("synlik")

## End(Not run)

#### Create synlik object
ricker_sl <- synlik(simulator = rickerSimul,
                    summaries = rickerStats,
                    param = c(logR = 3.8, logSigma = log(0.3), logPhi = log(10)),
                    extraArgs = list("nObs" = 50, "nBurn" = 50),
                    plotFun = function(input, ...){
                      plot(drop(input), type = 'l', ylab = "Pop", xlab = "Time", ...)
                    })

#### Simulate from the object
ricker_sl@data <- simulate(ricker_sl)
ricker_sl@extraArgs$obsData <- ricker_sl@data

#### Simulate statistics (each row is a vector of statistics)
simulate(ricker_sl, seed = 523, nsim = 10, stats = TRUE)

#### Plotting the data
plot(ricker_sl)

#### Checking multivariate normality of the statistics
```

```
checkNorm(ricker_sl)

#### Evaluate the likelihood
set.seed(4234)
slik(ricker_sl,
    param = c(logR = 3.8, logSigma = log(0.3), logPhi = log(10)),
    nsim    = 1e3)

#### Plotting a slice of the log-Likelihood possibly using multiple cores
slice(object = ricker_sl,
    ranges = list("logR" = seq(3.5, 3.9, by = 0.02),
                  "logPhi" = seq(2, 2.6, by = 0.02),
                  "logSigma" = seq(-2, -0.5, by = 0.05)),
    param = c(logR = 3.8, logSigma = log(0.3), logPhi = log(10)),
    nsim = 500, multicore = FALSE)

#### MCMC estimation possibly using multiple cores
set.seed(4235)
ricker_sl <- smcmc(ricker_sl,
    initPar = c(3.2, -1, 2.6),
    niter = 50,
    burn = 3,
    priorFun = function(input, ...) 0,
    propCov = diag(c(0.1, 0.1, 0.1))^2,
    nsim = 1e3,
    multicore = FALSE)

# Continue with additional 50 iterations
ricker_sl <- continue(ricker_sl, niter = 50)

# Plotting results on transformed scale (exponential)
trans <- rep("exp", 3)
names(trans) <- names(ricker_sl@param)

plot(ricker_sl)

---

ANYOrNULL-class  Dummy class

**Description**

Class unions for internal use only
bf

Nicholson’s 1954 blowfly data

Description

Data from figures 3 and 4 of Nicholson, 1954.

Usage

data(bf1)

Arguments

bf1 the dataset name

Details

bf1 is Nisbet and Gurney’s run 1, and Nicholson’s (1954) figure 3 (adult food limitation). The data are actually from the global population dynamics database at Silwood. They are daily: Nicholson’s figure 3 plots data every other day, but the text says that measurements were taken daily. However elsewhere they are reported every other day. Probably best to assume that they have been interpolated to daily.

bf2 and bf3 are digitized from Nicholson’s (1954) figure 4. bf2 is the upper series: larval food limitation, with 50g per day of larval food provided. bf3 is the lower series: same set up, half as much food. These are Nisbet and Gurney’s runs 2 and 3, respectively.

Value

matrix of replicate data series

Author(s)

Simon N. Wood, maintainer Matteo Fasiolo <matteo.fasiolo@ gmail.com>

References


See Also

blowfly
Examples

```r
library(synlik)
data(bf1)
data(bf2)
data(bf3)
par(mfrow=c(3,1),mar=c(4,4,1,1))
with(bf1,plot(day,pop,type="l"))
with(bf1,points(day,pop,pch=20,cex=.8))
abline(mean(bf1$pop),0,col=2); abline(median(bf1$pop),0,col=3);
with(bf2,plot(day,pop,type="l"))
with(bf2,points(day,pop,pch=20,cex=.8))
abline(mean(bf2$pop),0,col=2); abline(median(bf2$pop),0,col=3);
with(bf3,plot(day,pop,type="l"))
with(bf3,points(day,pop,pch=20,cex=.8))
abline(mean(bf3$pop),0,col=2); abline(median(bf3$pop),0,col=3);
```

---

blowSimul

*Simulates from the blowfly model*

Description

Simulator for the blowfly model proposed by Wood (2010).

Usage

```r
blowSimul(param, nsim, extraArgs, ...)
```

Arguments

- `param` vector of log-parameters: delta, P, N0, var.p, tau and var.d. The interpretation of these parameters is described in Wood (2010).
- `nsim` Number of simulations from the model.
- `extraArgs` A named list of additional arguments:
  - `nObs` = Length of each simulated time series.
  - `nBurn` = Number of initial steps to be discarded before saving the following `nObs` steps.
  - `steps` = Positive integer. If `steps == n` the observations correspond to `n` time steps.
- `...` Need for compatibility with synlik, but not used.

Value

A matrix `nsim` by `nObs`, where each row is a simulated path.

Author(s)

Simon Wood and Matteo Fasiolo <matteo.fasiolo@gmail.com>.
References


See Also

blow_sim

Examples

tmp <- blowSimul(param = log( c( "delta" = 0.16, "P" = 6.5, "N0" = 400, 
                              "var.p" = 0.1, "tau" = 14, "var.d" = 0.1) ) ), 
nsim = 2, 
extraArgs = list("nObs" = 200, "nBurn" = 1000, "steps" = 2))
matplot(t(tmp), type = 'l', ylab = "Y", xlab = "Time")

b

Blowfly model

Description

synlik object containing the blowfly model proposed by Wood (2010). The main components are the simulator blowSimul and the statistics blowStats, described in the same reference.

Author(s)

Simon Wood and Matteo Fasiolo <matteo.fasiolo@gmail.com>.

References


See Also

blowSimul
Examples

```r
data(blow_sl)
plot(blow_sl)
simulate(blow_sl, stats = TRUE)

slik(blow_sl,
    param = log( c("delta" = 0.16, "P" = 6.5, "N0" = 400,
        "var.p" = 0.1, "tau" = 14, "var.d" = 0.1) ),
    nsim = 1e3)

# Using Nicholson's data
data(bf1)
plot(blow_sl)

blow_sl@data <- bf1$pop
blow_sl@extraArgs$obsData <- bf1$pop #Important: blow_sl@blowStats uses the observed data

slik(blow_sl,
    param = log( c("delta" = 0.16, "P" = 6.5, "N0" = 400,
        "var.p" = 0.1, "tau" = 14, "var.d" = 0.1) ),
    nsim = 1e3)
```

---

**checkNorm**  
Checking the multivariate normal approximation.

---

**Description**

Given an object of class `synlik` this routine provides a graphical check of whether the distribution of the random summary statistics is multivariate normal.

**Usage**

```r
checkNorm(object, param = object@param, nsim = 1000, observed = NULL,
          cex.axis = 1, cex.lab = 1, ...)```

**Arguments**

- `object`  
  An object of class `synlik` or a matrix where each row is a random vector.
- `param`  
  A vector of model’s parameters at which the summary statistics will be simulated.
- `nsim`  
  Number of summary statistics to be simulated if object is of class `synlik`, otherwise it is not used.
- `observed`  
  A vector of observed summary statistics. By default NULL, so object@data will be used as observed statistics. It will be looked at only if object is a matrix.
- `cex.axis`  
  Axis scale expansion factor.
checkNorm

cex.lab  
Axis label expansion factor.

...  
additional arguments to be passed to object@simulator and object@summaries. In general I would avoid using it and including in object@extraArgs everything they need.

Details

The method is from section 7.5 of Krzanowski (1988). The replicate vectors of summary statistic S are transformed to variables which should be univariate chi squared r.v.s with DoF given by the number of rows of S. An appropriate QQ-plot is produced, and the proportion of the data differing substantially from the ideal line is reported. Deviations at the right hand end of the plot indicate that the tail behaviour of the Normal approximation is poor: in the context of synthetic likelihood this is of little consequence. Secondly, s is transformed to a vector which should be i.i.d. N(0,1) under multivariate normality, and a QQ plot is produced. Unfortunately this approach is not very useful unless the dimension of s is rather large. In simulations, perfectly MVN data produce highly variable results, so that the approach lacks any real power.

Value

Mainly produces plots and prints output. Also an array indicating proportion of simulated statistics smaller than observed.

Author(s)

Simon N. Wood, maintained by Matteo Fasiolo <matteo.fasiolo@gmail.com>.

References


Examples

```r
### Create Object
data(ricker_sl)

### Simulate from the object
ricker_sl@data <- simulate(ricker_sl)
ricker_sl@extraArgs$obsData <- ricker_sl@data

### Checking multivariate normality
checkNorm(ricker_sl)

# With matrix input
checkNorm(matrix(rnorm(200), 100, 2))
```
Description

Generic function, that given the results of an estimation procedure (ex. MCMC or maximum likelihood optimization) continues the procedure for some more iterations.

Usage

continue(object, ...)

## S4 method for signature 'smcmc'
continue(object, niter = object@niter, nsim = object@nsim,
propCov = object@propCov, targetRate = object@targetRate,
recompute = object@recompute, multicore = object@multicore,
ncores = object@ncores, cluster = NULL, control = object@control, ...)

Arguments

- **object**: An object representing the results of an estimation procedure which we wish to continue. For example it might represents an MCMC chain.
- **...**: additional arguments to be passed to slik function, see slik.
- **niter**: see smcmc-class.
- **nsim**: see smcmc-class.
- **propCov**: see smcmc-class.
- **targetRate**: see smcmc-class.
- **recompute**: see smcmc-class.
- **multicore**: see smcmc-class.
- **ncores**: see smcmc-class.
- **cluster**: an object of class c("SOCKcluster","cluster"). This allowes the user to pass her own cluster, which will be used if multicore == TRUE. The user has to remember to stop the cluster.
- **control**: see smcmc-class.

Details

When is("smcmc",object) == TRUE continues MCMC estimation of an object of class smcmc. All input parameters are defaulted to the corresponding slots in the input object, with the exception of cluster. The chain restarts were it ended, burn-in is set to zero, the same prior (if any) is used.

Value

An object of the same class as object, where the results of the estimation have been updated.
See Also

For examples, see smcmc-class.

---

**extractCorr**

*Extracting correlations from a covariance matrix*

**Description**

Extracting correlations from a covariance matrix

**Usage**

`extractCorr(mat)`

**Arguments**

- `mat` A covariance matrix.

**Value**

The correlation matrix embedded in `mat`.

**Examples**

```r
# 2 dimensional case
d <- 2
tmp <- matrix(rnorm(d^2), d, d)
mcov <- tcrossprod(tmp, tmp)

# Covariance matrix
mcov

# Correlation matrix
extractCorr(mcov)
```

---

**functionOrNULL-class**

*Dummy class*

**Description**

Class unions for internal use only
**internal_C**

*Internal C and C++ function*

**Description**

This functions are for internal use only.

**Author(s)**

Simon Wood and Matteo Fasiolo <matteo.fasiolo@gmail.com>.

---

**nlar**

*Estimate non-linear autoregressive coefficients*

**Description**

Function that, give time series data, transforms them into summary statistics using polynomial autoregression.

**Usage**

```
nlar(x, lag, power)
```

**Arguments**

- `x` a matrix. Each column contains a replicate series.
- `lag` vector of lags, for rhs terms.
- `power` vector of powers, for rhs terms.

**Value**

a matrix where each column contains the coefficients for a different replicate.

**Author(s)**

Simon N. Wood, maintainer Matteo Fasiolo <matteo.fasiolo@gmail.com>.
Examples

```r
library(synlik)
set.seed(10)
x <- matrix(runif(200),100,2)
beta <- nlar(x,lag=c(1,1),power=c(1,2))
y <- x[,1]
y <- y - mean(y)
z <- y[1:99]; y <- y[2:100]
lm(y~z+I(z^2)-1)
beta

## NA testing
x[5,1] <- x[45,2] <- NA
beta <- nlar(x,lag=c(1,1),power=c(1,2))
y <- x[,1]
y <- y - mean(y,na.rm=TRUE)
z <- y[1:99]; y <- y[2:100]
lm(y~z+I(z^2)-1)
beta

## higher order...
set.seed(10)
x <- matrix(runif(100),100,2)
beta <- nlar(x,lag=c(6,6,6,1,1),power=c(1,2,3,1,2))
k <- 2
y <- x[,] y <- y - mean(y)
ind <- (1+6):100
y6 <- y[ind-6]; y1 <- y[ind-1]; y <- y[ind]
beta0 <- coef(lm(y~y6+I(y6^2)+I(y6^3)+y1+I(y1^2)-1))
as.numeric(beta[,k]); beta0; beta0-as.numeric(beta[,k])
```

**numericOrNULL-class**  
*Dummy class*

**Description**  
Class unions for internal use only

**orderDist**  
*Summarize marginal distribution of (differenced) series.*

**Description**  
Summarizes (difference) distribution of replicate series, by regressing ordered differenced series on a reference series (which might correspond to observed data).
Usage

orderDist(x, z, np = 3, diff = 1)

Arguments

x a matrix. Each column contains a replicate series.
z vector of lags, for rhs terms.
np maximum power on rhs of regression.
diff order of differencing (zero for none).

Value

a matrix where each column contains the coefficients for a different replicate.

Author(s)

Simon N. Wood, maintainer Matteo Fasiolo <matteo.fasiolo@gmail.com>.

Examples

library(synlik)
set.seed(10)
n <- 100; nr <- 3
x <- matrix(runif(n*nr),n,nr)
z <- runif(n)
beta <- orderDist(x,z,np=3,diff=1)

zd <- z; xd <- x[,3]
zd <- diff(zd,1); xd <- diff(xd,1)
zd <- sort(zd); zd <- zd - mean(zd)
xd <- sort(xd); xd <- xd - mean(xd)
lm(xd~zd+I(zd^2)+I(zd^3)-1)

plot-smcmc

Plotting objects of class smcmc.

Description

Method for plotting an object of class smcmc.

Usage

## S4 method for signature 'smcmc,missing'
plot(x, trans = NULL, addPlot1 = NULL,
     addPlot2 = NULL, ...)

plot-smcmc

Plotting objects of class smcmc.
Arguments

- **x**: An object of class `smcmc`.
- **trans**: Name list or vector containing names of transforms for some parameters (ex: `list("par1" = "exp","par2" = "log")`). The transformations will be applied before plotting.
- **addPlot1**: Name of additional plotting function that will be called after the MCMC chain have been plotted. It has to have prototype `fun(nam,...)` where `nam` will be the parameter name. See "examples".
- **addPlot2**: Name of additional plotting function that will be called after the histograms have been plotted. It has to have prototype `fun(nam,...)` where `nam` will be the parameter name. See "examples".
- **...**: additional arguments to be passed to the plotting functions.

See Also

- `smcmc-class`, `plot`.

Examples

```r
data(ricker_smcmc)

# Functions for additional annotations (true parameters)
addline1 <- function(parNam, ...){
  abline(h = exp(ricker_smcmc@param[parNam]), lwd = 2, lty = 2, col = 3)
}
addline2 <- function(parNam, ...){
  abline(v = exp(ricker_smcmc@param[parNam]), lwd = 2, lty = 2, col = 3)
}

# Transformations (exponentials)
trans <- rep("exp", 3)
names(trans) <- names(ricker_smcmc@param)
plot(ricker_smcmc,
     trans = trans,
     addPlot1 = "addline1",
     addPlot2 = "addline2")
```

Description

It basically calls the slot `object@plotFun` with input `object@data`, if it has been provided by the user. Otherwise it tries to use the `plot(x = object@data,y,...)` generic.
Usage

```r
## S4 method for signature 'synlik,missing'
plot(x, y, ...)
```

Arguments

- `x`: An object of class `synlik`.
- `y`: Useless argument, only here for compatibility reasons.
- `...`: additional arguments to be passed to `object@plotFun`.

Author(s)

Matteo Fasiolo <matteo.fasiolo@gmail.com>

See Also

`synlik-class`, `plot`.

Examples

```r
data(ricker_sl)
# Using ricker_sl@plotFun
plot(ricker_sl)

# Using generic plot, doesn't work well because object@data is a matrix.
riccer_sl@plotFun <- NULL
plot(ricker_sl)
```

---

describe_simulate

### Description

Simulator for the stochastic Ricker model, as described by Wood (2010). The observations are \( Y_t \sim \text{Poiss}(\Phi \cdot N_t) \), and the dynamics of the hidden state are given by \( N_t = r \cdot N_{t-1} \cdot \exp(-N_{t-1} + e_t) \), where \( e_t \sim N(0, \Sigma^2) \).

Usage

```
riccerSimul(param, nsim, extraArgs, ...)
```
Arguments

param  vector of log-parameters: logR, logSigma, logPhi. Alternatively a matrix nsim by 3 were each row is a different parameter vector.

nsim  Number of simulations from the model.

eextraArgs  A named list of additional arguments:
  • nObs = Length of each simulated time series.
  • nBurn = Number of initial steps to be discarded before saving the following nObs steps.
  • randInit = if TRUE (default) the initial state N0 is runif(0,1), otherwise it is equal to extraArgs$initVal.
  • initVal = initial value N0, used only if extraArgs$randInit == TRUE.

Value

A matrix nsim by nObs, where each row is a simulated path.

Author(s)

Simon Wood and Matteo Fasiolo <matteo.fasiolo@gmail.com>.

References


See Also

ricker_sl

Examples

tmp <- rickerSimul(c(3.8, -1.2, 2.3), nsim = 2, extraArgs = list("nObs" = 50, "nBurn" = 200))
matplot(t(tmp), type = 'l', ylab = "Y", xlab = "Time")

parMat <- rbind(c(3.8, -1.2, 2.3), # Chaotic
                c(2.5, -1.2, 2.3)) # Not Chaotic

par(mfrow = c(2, 1))
tmp <- rickerSimul(parMat, nsim = 2, extraArgs = list("nObs" = 50, "nBurn" = 200))
plot(tmp[1, ], type = 'l', ylab = "Y", xlab = "Time")
plot(tmp[2, ], type = 'l', ylab = "Y", xlab = "Time")
**ricker_sl**

**Ricker model**

**Description**

*ricker_sl* is a `synlik` object containing the stochastic Ricker model, *ricker_smcmc* is a `smcmc` object which also contains the results of some MCMC iterations. The model is described in Wood (2010). The main components of the object are the simulator *rickerSimul* and the statistics *rickerStats*, described in the same reference.

**Author(s)**

Simon Wood and Matteo Fasiolo <matteo.fasiolo@gmail.com>.

**References**


**See Also**

*rickerSimul*

**Examples**

```r
data(ricker_sl)
plot(ricker_sl)
simulate(ricker_sl, stats = TRUE)

slik(ricker_sl, 
    param = c( logR = 3.8, logSigma = log(0.3), logPhi = log(10) ),
    nsim = 1e3)

# Using Nicholson's data
data(ricker_smcmc)
plot(ricker_smcmc)
```
robCov

Robust covariance matrix estimation

Description


Usage

robCov(sY, alpha = 2, beta = 1.25)

Arguments

sY A matrix, where each column is a replicate observation on a multivariate r.v.
alpha tuning parameter, see details.
beta tuning parameter, see details.

Details

Campbell (1980) suggests an estimator of the covariance matrix which downweights observations at more than some Mahalanobis distance $d_0$ from the mean. $d_0 = \sqrt{nrow(sY)} + alpha/sqrt(2)$. Weights are one for observations with Mahalanobis distance, $d$, less than $d_0$. Otherwise weights are $d_0*exp(-.5*(d-d_0)^2/beta)/d$. The defaults are as recommended by Campbell. This routine also uses pre-conditioning to ensure good scaling and stable numerical calculations.

Value

A list where:

- $E$: square root of the inverse covariance matrix, i.e. the inverse cov matrix is t($E)*E$;
- half.ldet.V: half the log of the determinant of the covariance matrix;
- mY: the estimated mean;
- sd: the estimated standard deviations of each variable.

Author(s)

Simon N. Wood, maintained by Matteo Fasiolo <matteo.fasiolo@gmail.com>.

References


Examples

p <- 5; n <- 100
Y <- matrix(rnorm(p*n), n)
robCov(Y)
Simulate data or statistics from an object of class `synlik`.

### Description

Simulate data or statistics from an object of class `synlik`.

### Usage

```r
## S4 method for signature 'synlik'
simulate(object, nsim, seed = NULL, param = object@param,
         stats = FALSE, clean = TRUE, verbose = TRUE, ...)
```

### Arguments

- **object**: An object of class `synlik`.
- **nsim**: Number of simulations from the model.
- **seed**: Random seed to be used. It is not passed to the simulator, but simply passed to `set.seed()` from within `simulate.synlik`.
- **param**: Vector of parameters passed to `object@simulator`.
- **stats**: If `TRUE` the function transforms the simulated data into statistics using `object@summaries`.
- **clean**: If `TRUE` the function tries to clean the statistics from NaNs or non-finite values. Given that `object@summaries` has to returns a numeric vector or a matrix where each row is a simulation, rows containing non-finite values will be discarded.
- **verbose**: If `TRUE` the function will complain if, for instance, the simulations contain lots of non-finite values.
- **...**: Additional arguments to be passed to `object@simulator` and `object@summaries`. In general I would avoid using it and including `object@extraArgs` everything they need.

### Value

If `stats == FALSE` the output will that of `object@simulator`, which depends on the simulator used by the user. If `stats == TRUE` the output will be a matrix where each row is vector of simulated summary statistics.

### Author(s)

Matteo Fasiolo <matteo.fasiolo@gmail.com>

### See Also

`synlik-class`, `simulate`
Examples

data(ricker_sl)

# Simulate data
simulate(ricker_sl, nsim = 2)

# Simulate statistics
simulate(ricker_sl, nsim = 2, stats = TRUE)

slAcf
Estimate auto-covariances for multiple datasets.

Description
Function that, given time series data, transforms them into auto-covariances with different lags.

Usage
slAcf(x, max.lag = 10)

Arguments

x a matrix. Each column contains a replicate series.

max.lag How many lags to use.

Value

a matrix where each column contains the coefficients for a different replicate. The first coefficient corresponds to lag == 0, hence it is the variance, the second is the covariance one step ahead and so on.

Author(s)

Simon N. Wood, maintainer Matteo Fasiolo <matteo.fasiolo@gmail.com>.

Examples
library(synlik)
set.seed(10)
x <- matrix(runif(1000),100,10)
acf <- slAcf(x)
slice

Plot slices of the synthetic log-likelihood.

Description

Plot slices of the synthetic log-likelihood.

Usage

slice(object, ranges, nsim, param = object@param, pairs = FALSE,
      draw = TRUE, trans = NULL, multicore = FALSE, ncores = detectCores() -
      1, cluster = NULL, ...)

Arguments

object synlik object.
ranges ranges of values along which we want the slices. If length(parName) == 1 than
range has a vector, while if length(parName) == 2 it have to be a named list of
2 vectors (ex: list("alpha" = 1:10,"beta" = 10:1)).
nsim Number of simulations used to evaluate the synthetic likelihood at each location.
param Named vector containing the value of the ALL parameters (including the sliced
one). Parameters that are not in parName will be fixed to the values in param.
pairs if TRUE the function will produce a 2D slice for every pair of parameters in
ranges. FALSE by default.
draw If TRUE the slice will be plotted.
trans Named vector or list of transformations to be applied to the parameters in parName
before plotting ex: trans = c(s = "exp",d = "exp")/
multicore If TRUE the object@simulator and object@summaries functions will be ex-
cuted in parallel. That is the nsim simulations will be divided in multiple cores.
ncores Number of cores to use if multicore == TRUE.
cluster An object of class c("SOCKcluster","cluster"). This allowes the user to
pass her own cluster, which will be used if multicore == TRUE. The user has to
remember to stop the cluster.
... additional arguments to be passed to slik(), see slik.

Value

Either a vector or matrix of log-synthetic likelihood estimates, depending on whether length(parNames)
== 1 or 2. These are returned invisibly.

Author(s)

Matteo Fasiolo <matteo.fasiolo@gmail.com>
Examples

data(ricker_sl)

# Plotting slices of the logLikelihood
slice(object = ricker_sl,
      ranges = list("logR" = seq(3.5, 3.9, by = 0.01),
                     "logPhi" = seq(2, 2.6, by = 0.01),
                     "logSigma" = seq(-2, -0.5, by = 0.01)),
      param = c(logR = 3.8, logSigma = log(0.3), logPhi = log(10)),
      nsim = 500)

## Not run:
# Plotting a contour of the logLikelihood
slice(object = ricker_sl,
      ranges = list("logR" = seq(3.5, 3.9, by = 0.01),
                     "logPhi" = seq(2, 2.6, by = 0.01),
                     "logSigma" = seq(-2, -0.5, by = 0.04)),
      pairs = TRUE,
      param = c(logR = 3.8, logSigma = log(0.3), logPhi = log(10)),
      nsim = 500, multicore = TRUE)

## End(Not run)

slik

Evaluates the synthetic log-likelihood.

Description

Evaluates the synthetic log-likelihood.

Usage

slik(object, param, nsim, multicore = FALSE, ncores = detectCores() - 1,
     cluster = NULL, ...)

Arguments

  object  An object of class synlik.
  param   Vector of parameters at which the synthetic likelihood will be evaluated.
  nsim    Number of simulation from the model.
  multicore (logical) if TRUE the object@simulator and object@summaries functions will be executed in parallel. That is the nsim simulations will be divided in multiple cores.
  ncores  (integer) number of cores to use if multicore == TRUE.
  cluster an object of class c("SOCKcluster","cluster"). This allowes the user to pass her own cluster, which will be used if multicore == TRUE. The user has to remember to stop the cluster.
... additional arguments to be passed to object@simulator and object@summaries. In general I would avoid using it and including object@extraArgs everything they need.

Value

The estimated value of the synthetic log-likelihood at param.

Author(s)

Matteo Fasiolo <matteo.fasiolo@gmail.com>

References


Examples

data(ricker_sl)
set.seed(643)
slik(ricker_sl, param = c(3.8, -1.2, 2.3), nsim = 500)

smcmc

MCMC parameter estimation for objects of class synlik.

Description

MCMC parameter estimation for objects of class synlik.

Usage

smcmc(object, initPar, niter, nsim, propCov, burn = 0,
priorFun = function(param, ...) 0, targetRate = NULL, recompute = FALSE,
multicore = !is.null(cluster), cluster = NULL, ncores = detectCores() - 1, control = list(), ...)

Arguments

object An object of class synlik.
initPar see smcmc-class.
niter see smcmc-class.
nsim see smcmc-class.
propCov see smcmc-class.
burn see smcmc-class.
priorFun see smcmc-class.
targetRate  see smcmc-class.
recompute  see smcmc-class.
multicore  see smcmc-class.
cluster  an object of class c("SOCKcluster","cluster"). This allows the user to pass her own cluster, which will be used if multicore == TRUE. The user has to remember to stop the cluster.
ncores  see smcmc-class.
control  see smcmc-class.
...  additional arguments to be passed to slik function, see slik.

Value
An object of class smcmc.

Author(s)
Matteo Fasiolo <matteo.fasiolo@gmail.com>, code for adaptive step from the adaptMCMC package.

References

---

Description
Object representing the results of MCMC estimation on an object of class synlik, from which it inherits.

Slots
initPar  Vector of initial parameters where the MCMC chain will start (numeric).
niter  Number of MCMC iterations (integer).
nsim  Number of simulations from the simulator at each step of the MCMC algorithm (integer).
burn  Number of initial MCMC iterations that are discarded (integer).
priorFun  Function that takes a vector of parameters as input and the log-density of the prior as output. If the output is not finite the proposed point will be discarded. (function). The function needs to have signature fun(x,...), where x represents the input parameters (function).
propCov  Matrix representing the covariance matrix to be used to perturb the parameters at each step of the MCMC chain (matrix).
**targetRate**  Target rate for the adaptive MCMC sampler. Should be in (0, 1), default is NULL (no adaptation). The adaptation uses the approach of Vihola (2011). (numeric)

**recompute**  If TRUE the synthetic likelihood will be evaluated at the current and proposed positions in the parameter space (thus doubling the computational effort). If FALSE the likelihood of the current position won’t be re-estimated (logical).

**multicore**  If TRUE the object@simulator and object@summaries functions will be executed in parallel. That is the nsim simulations will be divided in multiple cores (logical).

**ncores**  Number of cores to use if multicore == TRUE (integer).

**accRate**  Acceptance rate of the MCMC chain, between 0 and 1 (numeric).

**chains**  Matrix of size niter by length(initPar) where the i-th row contains the position of the MCMC algorithm in the parameter space at the i-th iteration (matrix).

**llkChain**  Vector of niter elements where the i-th element contains the estimate of the synthetic likelihood at the i-th iteration (numeric).

**control**  Control parameters used by the MCMC sampler:

- theta = controls the speed of adaption. Should be between 0.5 and 1. A lower gamma leads to faster adaption.
- adaptStart = iteration where the adaption starts. Default 0.
- adaptStop = iteration where the adaption stops. Default burn + niter
- saveFile = path to the file where the intermediate results will be stored (ex: ”~/Res.RData”).
- saveFreq = frequency with which the intermediate results will be saved on saveFile. Default 100.
- verbose = if TRUE intermediate posterior means will be printed.
- verbFreq = frequency with which the intermediate posterior means will be printed. Default 500.

**Author(s)**

Matteo Fasiolo <matteo.fasiolo@gmail.com>

**References**


**Examples**

```r
# Load "synlik" object
data(ricker_sl)

plot(ricker_sl)

# MCMC estimation
set.seed(4235)

ricker_sl <- smcmc(ricker_sl,
  initPar = c(3.2, -1, 2.6),
  niter = 50,
  burn = 3,
```
priorFun = function(input, ...) 1,
propCov = diag(c(0.1, 0.1, 0.1))^2,
nsim = 200,
m multicore = FALSE)

# Continue with additional 50 iterations
ricker_sl <- continue(ricker_sl, niter = 50)

plot(ricker_sl)

---

synlik-class

Description

Basic class for simulation-based approximate inference using Synthetic Likelihood methods.

Usage

synlik(...)

Arguments

... See section "Slots".

Slots

  param Named vector of parameters used by object@simulator (numeric).

  simulator Function that simulates from the model (function). It has to have prototype fun(param,nsim,extraArgs,...).
  If summaries() is not specified the simulator() has output a matrix with nsim rows, where each row is a vector of simulated statistics. Otherwise it can output any kind of object, and this output will be passed to summaries().

  summaries Function that transforms simulated data into summary statistics (function). It has to have prototype fun(x,extraArgs,...) and it has to output a matrix with nsim rows, where each row is a vector of simulated statistics. Parameter x contains the data.

  data Object containing the observed data or statistics (ANY).

  extraArgs List containing all the extra arguments to be passed to object@simulator and object@summaries (list).

  plotFun Function that will be used to plot object@data. Prototype should be fun(x,...)(function).

Author(s)

Matteo Fasiolo <matteo.fasiolo@gmail.com>
References


Examples

#### Create Object

```r
ricker_sl <- synlik(simulator = rickerSimul,
                     summaries = rickerStats,
                     param = c(logR = 3.8, logSigma = log(0.3), logPhi = log(10)),
                     extraArgs = list("nObs" = 50, "nBurn" = 50),
                     plotFun = function(input, ...)
                     plot(drop(input), type = 'l', ylab = "Pop", xlab = "Time", ...))
```

# Simulate from the object

```r
ricker_sl@data <- simulate(ricker_sl)

ricker_sl@extraArgs$obsData <- ricker_sl@data # Needed by WOOD2010 statistics

plot(ricker_sl)
```
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