Package ‘GUTS’

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Type Package

Title Fast Calculation of the Likelihood of a Stochastic Survival Model

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Description Given exposure and survival time series as well as parameter values, GUTS allows for the fast calculation of the survival probabilities as well as the logarithm of the corresponding likelihood.

License GPL (>= 2)

Depends R (>= 3.3.3), methods, Rcpp (>= 0.12.13)

LinkingTo Rcpp

LazyLoad yes

LazyData no

Encoding UTF-8

NeedsCompilation yes

Repository CRAN

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Description

GUTS (General Unified Threshold model of Survival) is a stochastic survival model for ecotoxicology. The package allows for the definition of exposure and survival time series as well as parameter values, and the fast calculation of the survival probabilities as well as the logarithm of the corresponding likelihood.

Details

Package: GUTS
Type: Package
License: GPL (>= 2)

A GUTS object is a special list of class “GUTS”. Functions guts_setup, guts_calc_loglikelihood and guts_calc_survivalprobs are available to create and work with GUTS objects. A data set diazinon is also included. See links for more details.

Author(s)

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References


See Also
guts_setup, guts_calc_loglikelihood, guts_calc_survivalprobs, diazinon, Rcpp
diazinon

GUTS data set with Gammarus pulex exposed to diazinon

Description

Data of 3 pulsed toxicity tests with the freshwater crustacean Gammarus pulex and diazinon, an organophosphate insecticide.

Usage

data("diazinon")

Format

A list containing 12 data vectors.

Author(s)

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Source


See Also

GUTS

GUTS

Fast Calculation of the Likelihood of a Stochastic Survival Model

Description

GUTS (General Unified Threshold model of Survival) is a stochastic survival model for ecotoxicology. The package allows for the definition of exposure and survival time series as well as parameter values, and the fast calculation of the survival probabilities as well as the logarithm of the corresponding likelihood.
Usage

guts_setup(C, Ct, y, yt, dist = "lognormal",
          model = "Proper", N = 1000, M = 10000)

guts_calc_loglikelihood(gobj, par)

guts_calc_survivalprobs(gobj, par)

Arguments

C          Numeric vector of concentrations. Vector must contain at least 2 values and be
          of the same length as Ct.
Ct         Numeric vector of concentration time points. Vector must contain at least 2
          values and be of the same length as C. Numerics must start at 0, and contain
          unique values in ascending order.
y          Integer vector (counts) of survivors. Vector must contain at least 2 values and
          be of the same length as yt. y must not be ascending.
yt         Numeric vector of survivor time points. Vector must contain at least 2 values
          and be of the same length as y. Numerics must start at 0, and contain unique
          values in ascending order. Survivor information at time points later than the
          latest concentration time point will be disregarded (with a warning).

dist       Distribution as character, either “lornormal” (default) or “delta”.
model      Model as character, either “Proper” (for full model, the default) or “IT” (for
          individual tolerance).

N          Integer. Thresholds sample length. Must be greater than 2.
M          Integer. Number of time grid points. Must be greater than 1.
gobj       GUTS object. The object to be updated (and used for the calculation).
par        Numeric vector of parameters. See details below.

Details

Functions:

Use guts_setup to define (or alter) a GUTS object. Various checks are applied to the data. On
success, a GUTS object will be created.

Use guts_calc_loglikelihood to calculate the survival probabilities and the corresponding log-
likelihood for a given set of parameters. The function is very fast and can be used in routines for
parameter estimation. The function returns the loglikelihood, however it also updates the fields
par, S and LL of the object.

Use guts_calc_survivalprobs is a convenience wrapper (calling guts_calc_loglikelihood) that
can be used for predictions; it returns the survival probabilities.

Parameters, Models, and Distributions:

GUTS uses the following parameters:

• hb: background mortality rate
• ke: dominant rate constant
• kk: killing rate
• mn: mean of thresholds z from distribution dist
• sd: standard deviation of thresholds z from distribution dist

For model “Proper”, the first 3 parameters are needed as well as the parameters for the distribution (mn and sd for “lognormal”, or mn for “delta”). For model “IT” (individual tolerance), the third parameter (kk) is set internally to infinity and must not be provided. For model type “SD” (stochastic death), use distribution “delta” and model “Proper” with the first 4 parameters.
The number of parameters is checked according to dist and model. Wrong number of parameters invoke an error, wrong parameter values (e.g., negative values) invoke a warning, and the loglikelihood is set to -Inf.

Thresholds are created internally according to dist, model, N (and par). If dist is “lognormal” (default), N ordered thresholds are created from the lognormal distribution with mn and sd. Note that mn and sd are parameters for the lognormal distribution (differs from rlnorm in R that uses mu and sigma)! If dist is “delta”, all N thresholds are equal to mn.

**Field and Attribute Access:**
Fields and attributes of an object of class “GUTS” are read-only. To prevent accidental change of fields or attributes, replacement functions were rewritten throwing an error when used. Always use function guts_setup to create objects or modify fields on existing objects. However, guts_calc_loglikelihood and guts_calc_survivalprobs update an object’s fields par (parameters), S (survival probabilities) and LL (the loglikelihood).

**Value**
guts_setup returns a list of class “GUTS” with the following fields:

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>Concentrations.</td>
</tr>
<tr>
<td>Ct</td>
<td>Concentration time points.</td>
</tr>
<tr>
<td>y</td>
<td>Survivors.</td>
</tr>
<tr>
<td>yt</td>
<td>Survivor time points.</td>
</tr>
<tr>
<td>dist</td>
<td>Distribution.</td>
</tr>
<tr>
<td>model</td>
<td>Model.</td>
</tr>
<tr>
<td>N</td>
<td>Sample length.</td>
</tr>
<tr>
<td>M</td>
<td>Time grid points.</td>
</tr>
<tr>
<td>par</td>
<td>Parameters.</td>
</tr>
<tr>
<td>S</td>
<td>Vector of survivor probabilities.</td>
</tr>
<tr>
<td>LL</td>
<td>The loglikelihood.</td>
</tr>
</tbody>
</table>

guts_calc_loglikelihood returns the loglikelihood.
guts_calc_survivalprobs returns the survival probabilities.

**Note**
The GUTS project web site can be found here: [http://guts.r-forge.r-project.org](http://guts.r-forge.r-project.org). For questions and discussion, please subscribe to the mailing list there.
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References

See Also
diazinon, GUTS-package

Examples
data(diazinon)

```r
gts <- guts_setup(C = diazinon$c1L, Ct = diazinon$ct1L, y = diazinon$y1L, yt = diazinon$yt1L)
guts_calc_loglikelihood(gts, c(0.05084761, 0.12641525, 1.61840054, 19.09911, 6.495246)) # -183.566.
guts_calc_survivalprobs(gts, rep(.5, 5)) # 1.000000e+00 1.737352e-05 ... 1.674316e-33
guts_calc_loglikelihood(gts, -1:3) # Warning.
gts
```

## Not run: guts_calc_survivalprobs( gts, 1:4 ) # Error.

## Not run: gts[["C"]] <- 1:3 # Error.
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