Package ‘GUTS’

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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.
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GUTS-package .................................................... 2
diazinon .......................................................... 3
GUTS .............................................................. 3

Index 7
Description

GUTS (General Unified Theory 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.

Note

• Caution: This is a complete reimplementation of the former package. Please update your code.
• The package is under current development. Parts of the software are likely to change with future releases. Refer to the manual pages after updating your copy. Save your work before using this software.
• Extended help and an in-depth documentation can be found at the project web site http://guts.r-forge.r-project.org.

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References


See Also

   guts_setup, guts_calc_loglikelihood, guts_calc_survivalprobs, diazinon, Rcpp
**diazinon**  

*GUTS data set with survivors exposed to diazinon*

**Description**

3 experiments with survivors exposed to concentrations of diazinon. The list contains 12 variables.

**Usage**

```r
data("diazinon")
```

**Format**

A list containing 12 vectors, plus a description string.

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**Source**


**See Also**

GUTS

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**GUTS**  

*Fast Calculation of the Likelihood of a Stochastic Survival Model*

**Description**

GUTS (General Unified Theory of Survival) is a stochastic survival model for ecotoxicology. Use `guts_setup` to define exposure and survival time series as well as parameter values. Use `guts_calc_loglikelihood` to calculate the survival probabilities and the corresponding loglikelihood. `guts_calc_survivalprobs` is a convenience wrapper for calculate survival probabilities.

**Usage**

```r
guts_setup(C, Ct, y, yt, par = 0, dist = "lognormal",  
model = "Proper", N = 1000, M = 10000)

guts_calc_loglikelihood(gobj, pars)

guts_calc_survivalprobs(gobj, yts = 0)
```
Arguments

\( \text{C} \)  Numerical vector of concentrations. Vector must contain at least 2 values and be of the same length as \( \text{Ct} \).

\( \text{Ct} \)  Numerical vector of concentration time points. Vector must contain at least 2 values and be of the same length as \( \text{C} \). Numerics must start at 0, and contain unique values in ascending order. The last value of \( \text{Ct} \) must not be smaller than the last value of \( \text{yt} \), i.e., there must be information about concentrations when no survivor remains.

\( y \)  Integer vector (counts) of survivors. Vector must contain at least 2 values and be of the same length as \( \text{yt} \). \( y \) must not be ascending.

\( \text{yt} \)  Numerical 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. The last value of \( \text{yt} \) must not be larger than the last value of \( \text{Ct} \), i.e., there must be information about concentrations when no survivor remains.

\( \text{par} \)  Numerical vector of parameters. If \( \emptyset \), all parameters are set to 0. See details below.

\( \text{dist} \)  Distribution as character, either “lornormal” (default) or “delta”.

\( \text{model} \)  Model as character, either “Proper” (default) or “IT”.

\( N \)  Integer. Thresholds sample length. Must be greater than 2.

\( M \)  Integer. Time grid points. Must be greater than 1.

\( \text{gobj} \)  GUTS object. The object to be updated (and used for the calculation).

\( \text{pars} \)  Numeric vector of new parameters. See details below.

\( \text{yts} \)  Either a single positive integer or a vector of survivor time points. If \( \emptyset \), survivor information in \( \text{gobj} \) are used.

Details

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 modify fields.

However, parameters can also be updated using the function guts_calc_loglikelihood, and survivors and survivor time points are set when using the function guts_calc_survivalprobs.

Parameters:
For distribution “lognormal” and model “Proper”, 5 parameters are required:

- \( \text{hb} \): background mortality rate
- \( \text{ke} \): dominant rate constant
- \( \text{kk} \): killing rate
- \( \text{mn} \): mean of thresholds \( z \) from distribution \( \text{dist} \)
- \( \text{sd} \): standard deviation of thresholds \( z \) from distribution \( \text{dist} \)

The number of parameters is checked according to \( \text{dist} \) and type. For type “Proper”...
• ... if distribution is “lognormal”, 5 non-negative parameters are required. If \( sd \) is not 0, \( mn \) must not be 0.
• ... if distribution is “delta”, 4 non-negative parameters are required.

If dist is “delta” (also referred to as SD), \( sd \) is set internally and must not be provided. If model is “IT”, the number of required parameters is reduced by 1; the parameter “kk” is set internally and must not be provided.

Wrong number of parameters will give an error. Wrong parameter values (e.g., negative values) give a warning and set the loglikelihood to \(-Inf\).

**Distributions:**

Thresholds are created internally according to dist, model, N (and pars).

• If dist is set to “lognormal” (default), \( N \) ordered thresholds are created from the lognormal distribution with \( mn \), \( sd \). Note that \( mn \) and \( sd \) are parameters for the lognormal distribution, not its logarithm (differs from rlnorm in R)!
• If dist is set to “delta”, \( N \) thresholds are created from the delta distribution with \( mn \).
• For model type “SD” use distribution “delta” and model “Proper”.

**Value**

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

- C Concentrations.
- Ct Concentration time points.
- y Survivors.
- yt Survivor time points.
- par Parameters.
- dist Distribution.
- model Model.
- N Sample length.
- M Time grid points.
- results List of results.

The field results is a list containing the following fields:

- S Vector of Survivor probabilities.
- LL The loglikelihood.

guts_calc_loglikelihood and guts_calc_survivalprobs update objects directly and do not return a value. Use the fields object$results$ll and object$results$s to access the loglikelihood and survival probabilities.
Note

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References

See Also
diazinon, adaptMCMC, GUTS-package

Examples

data(diazinon)

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))
gts
# LL: -183.566.

guts_calc_survivalprobs( gts, 5 )
gts
# LL: 0, S: 1, 0.9293491, 0.8409267, 0.7987192, 0.4578539.

guts_calc_survivalprobs( gts, 6 )
gts
# LL: 0, S: 1, 0.9293336, 0.8409121, 0.7987059,
# 0.4577675, 0.3383011, 0.3213131.

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

*Topic datasets
  diazinon, 3
[[<- GUTS (GUTS-package), 2
$<- GUTS (GUTS-package), 2

adaptMCMC, 6
attr<- GUTS (GUTS-package), 2
attributes<- GUTS (GUTS-package), 2

diazinon, 2, 3, 6

GUTS, 3, 3
guts (GUTS), 3
GUTS-package, 2
guts_calc_loglikelihood, 2
guts_calc_loglikelihood (GUTS), 3
guts_calc_survivalprobs, 2
guts_calc_survivalprobs (GUTS), 3
guts_setup, 2
guts_setup (GUTS), 3

modguts (GUTS-package), 2
mostattributes<- GUTS (GUTS-package), 2

print.GUTS (GUTS-package), 2

Rcpp, 2