

# Package ‘BeeGUTS’

October 12, 2022

**Title** General Unified Threshold Model of Survival for Bees using  
Bayesian Inference

**Version** 1.0.0

**Description** Tools to calibrate, validate, and make predictions with the  
General Unified Threshold model of Survival adapted for Bee species. The  
model is presented in the publication from Baas, J., Goussen, B., Miles, M.,  
Preuss, T.G., Roessing, I. (submitted) and is based on the GUTS framework  
Jager, T., Albert, C., Preuss, T.G. and Ashauer, R. (2011) <[doi:10.1021/es103092a](https://doi.org/10.1021/es103092a)>.  
The authors are grateful to Bayer A.G. for its financial support.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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**Biarch** true

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2.18.0)

**SystemRequirements** GNU make

**URL** <https://github.com/bgoussen/BeeGUTS>

**BugReports** <https://github.com/bgoussen/BeeGUTS/issues>

**Suggests** rmarkdown, knitr

**VignetteBuilder** knitr

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**Author** Benoit Goussen [aut, cre] (<<https://orcid.org/0000-0001-7204-7981>>),  
 Liubov Zakharova [ctb],  
 Romoli Carlo [ctb],  
 Bayer AG [cph]

**Maintainer** Benoit Goussen <benoit.goussen@ibacon.com>

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BeeGUTS-package	<i>'BeeGUTS' package; a package to perform GUTS modelling for Bee experiments.</i>
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## Description

Provide tools to analyse the survival toxicity tests performed for bee species. It can be used to fit a Toxicokinetic-Toxicodynamic (TKTD) model adapted for bee standard studies (acute oral, acute contact, and chronic oral studies). The TKTD model used is the General Unified Threshold model of Survival (GUTS).

The package follows the concept and assumptions presented in Baas et al (submitted)

## References

- Baas, J., Goussen, B., Miles, M., Preuss, T.G., Roessing, I. (submitted). BeeGUTS – new integrative TKTD model for honey bees approach moving from single point estimates of toxicity and exposure to a holistic link between exposure and effect.
- Jager, T., Albert, C., Preuss, T.G. and Ashauer, R. (2011). General Unified Threshold model of Survival - a toxicokinetic-toxicodynamic framework for ecotoxicology. doi: [10.1021/es103092a](https://doi.org/10.1021/es103092a)
- Jager, T. and Ashauer, R. (2018). Modelling survival under chemical stress. A comprehensive guide to the GUTS framework. Version 1.0 [https://leanpub.com/guts\\_book](https://leanpub.com/guts_book)
- EFSA PPR Scientific Opinion (2018). Scientific Opinion on the state of the art of Toxicokinetic/Toxicodynamic (TKTD) effect models for regulatory risk assessment of pesticides for aquatic organisms. <https://www.efsa.europa.eu/en/efsajournal/pub/5377>
- Stan Development Team (2020). RStan: the R interface to Stan. R package version 2.21.2. <https://mc-stan.org>

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betacyfluthrinChronic *Survival datasets for Honey bees exposed to constant concentration of Betacyfluthrin for 10 days.*

---

## Description

Survival datasets for *Honey bees* exposed to constant concentration of Betacyfluthrin for 10 days.

## Usage

```
data(betacyfluthrinChronic)
```

## Format

A list of class `beeSurvData` constructed by `dataGUTS` containing:

- `survData` A data frame containing the survival information over time for five treatments and a control in a wide format.
- `survData_long` A data frame containing the survival information over time for five treatments and a control in a long format.
- `concData` A data frame containing the concentration information over time for five treatments and a control in a wide format.
- `concData_long` A data frame containing the concentration information over time for five treatments and a control in a long format.
- `unitData` A character string containing the units of the concentration data.
- `typeData` A character string containing the type of data (here `Chronic_Oral`).
- `beeSpecies` A character string containing the species of bee of interest (here `Honey_Bee`).
- `concModel` A data frame containing the concentration information recalculated for the species of bee and test type of interest in a wide format.
- `concModel_long` A data frame containing the concentration information recalculated for the species of bee and test type of interest in a long format.

**References**

Bayer data.

---

concAC	<i>Recalculate the concentrations for the acute contact tests for bees</i>
--------	--

---

**Description**

Recalculate the concentrations for the acute contact tests for bees

**Usage**

```
concAC(cExt, expTime, k_ca = 0.4, ...)
```

**Arguments**

cExt	The concentration applied
expTime	The duration of the experiment in days
k_ca	Contact availability rate (d-1), default is 0.4
...	Not used

**Value**

A data frame containing a column with the time points and a column with the recalculated concentrations

**Examples**

```
conc <- concAC(cbind(3.1, 4, 6, 8), 4)
```

---

concAO	<i>Recalculate concentration for the acute oral tests for bees</i>
--------	--

---

**Description**

Recalculate concentration for the acute oral tests for bees

**Usage**

```
concAO(cExt, cTime = 0.25, expTime, k_sr = 0.625, ...)
```

**Arguments**

cExt	A dataframe of concentrations at time 0 concentration applied
cTime	The duration of exposure in days, default is 0.25 d
expTime	The duration of the experiment in days
k_sr	Stomach release rate (d-1), default is 0.625
...	Not used

**Value**

A data frame containing a column with the time points and a column with the recalculated concentrations

**Examples**

```
conc <- concA0(cExt = cbind(3.5, 6, 8, 10), cTime = 0.25, expTime = 4)
```

---

concCst	<i>Recalculate the concentrations for the chronic oral tests for bees from mg a.s./kg feed to <math>\mu</math>g/bee</i>
---------	---

---

**Description**

Recalculate the concentrations for the chronic oral tests for bees from mg a.s./kg feed to  $\mu$ g/bee

**Usage**

```
concCst(cExt, f_rate = c(25), targConc = 1, cstConcCal = TRUE, ...)
```

**Arguments**

cExt	The concentration dataframe in mg a.s./kg feed
f_rate	A vector containing the feeding rates of the bees in mg/bee/day. If the vector is of size 1, the same feeding rate is used for all test conditions. If the vector is of size >1, it should be of the same size as the number of condition and one feeding rate must be provided per condition. Default is 25 mg/bee/day
targConc	A numerical scalar representing the unit of the target concentration amongst (default = 1) <ul style="list-style-type: none"> <li>• 1 for <math>\mu</math>g a.s./bee</li> <li>• 2 for ng a.s./bee</li> <li>• 3 for mg a.s./bee</li> </ul>
cstConcCal	Logical. Indicate if concentrations should be recalculated from mg a.s./kg feed to Xg/bee
...	Not used

**Value**

A data frame containing a column with the time points and a column with the recalculated concentrations

**Examples**

```
cExt <- data.frame(SurvivalTime = c(0,10), Control = c(0,0),
  T1 = c(1, 1), T2 = c(5, 5), Dataset = c(1, 1))
conc <- concCst(cExt, targConc = 2)
```

---

 criteriaCheck

*Computes PPC and NRMSE as defined in EFSA 2018*


---

**Description**

Computes PPC and NRMSE as defined in EFSA 2018

**Usage**

```
criteriaCheck(x)
```

**Arguments**

x                    an object of class beeSurvFit or beeSurvPred

**Value**

The function returns a list with three items:

PPC	The criterion, in percent, compares the predicted median number of survivors associated to their uncertainty limits with the observed numbers of survivors. Based on experience, PPC resulting in more than 50% of the observations within the uncertainty limits indicate good model performance (EFSA 2018). A fit of 100% may hide too large uncertainties of prediction (so covering all data).
NRMSE	The criterion, in percent, is based on the classical root-mean-square error (RMSE), used to aggregate the magnitudes of the errors in predictions for various time-points into a single measure of predictive power. In order to provide a criterion expressed as a percentage, NRMSE is the normalised RMSE by the mean of the observations. EFSA (2018) recognised that a NRMSE of less than 50% indicates good model performance
SPPE	A list with the Survival Probability Prediction Error per dataset and condition. Each dataset is in a sublist.

@references EFSA PPR Scientific Opinion (2018) *Scientific Opinion on the state of the art of Toxicokinetic/Toxicodynamic (TKTD) effect models for regulatory risk assessment of pesticides for aquatic organisms* <https://www.efsa.europa.eu/en/efsajournal/pub/5377>

@example data(fitBetacyfluthrin\_Chronic) out <- criteriaCheck(fitBetacyfluthrin\_Chronic)

dataGUTS

*Read and format the data for the BeeGUTS model***Description**

Read data from a text or csv file and recalculate the exposure profile depending on the type of experiment (acute oral, acute contact, chronic oral).

**Usage**

```
dataGUTS(
  file_location = NULL,
  test_type = NULL,
  bee_species = "Honey_Bee",
  NA_string = getOption("datatable.na.strings", "NA"),
  ...
)
```

**Arguments**

**file\_location** List of Locations of text files containing each two datasets, one for the survival data, and one for the concentration data. Both datasets must be included in the same file and contain the same number of column in the same order. The following columns must be included in the survival dataset:

- Survival time  $\backslash[d\backslash]$ : a vector of time in days
- Control A vector of number of survivors for the control
- T1 - Tn A vector of number of survivors for the treatments T1 to Tn, one column per treatment.

A line containing the Concentration unit must be included directly after the end of the last row of the survival data.

The following columns must be included in the concentration dataset

- Concentration time  $\backslash[d\backslash]$ : a vector of time in days.
- Control A vector of concentrations for the control
- T1 - Tn A vector of concentration for the treatments T1 to Tn, one column per treatment.

For the Acute\_Oral and Acute\_Contact, only the initial exposure concentration at time 0 is required.

See detail section for example

**test\_type** list of test types amongst "Acute\_Oral", "Acute\_Contact", and "Chronic\_Oral" this list must have the same length of the list of file locations

**bee\_species** the bee type. At the moment only "Honey\_Bee" is supported

**NA\_string** a character vector of strings which are to be interpreted as NA values

**...** Optional arguments to be passed to the concentration reconstruction (e.g.

- `k_sr` = for the stomach release rate (d<sup>-1</sup>), default is 0.625,
- `k_ca` = contact availability rate (d<sup>-1</sup>), default is 0.4), or
- `cTime` = the duration of exposure in days for the acute oral tests, default is 0.25 d
- `cstConcCal` = logical, recalculate concentration in the Chronic\_Oral test from mg a.s./kg feed to Xg/bee (default is TRUE)
- `f_rate` = numerical vector, feeding rate used in the concentration recalculation in the Chronic\_Oral (default is 25 mg/bee/day)
- `targConc` = numerical scalar, target concentration unit in the recalculation in the Chronic\_Oral, 1 for µg/bee, 2 for ng/bee, 3 for mg/bee (default is 1).

### Details

The filename must begin with name of the chemical substance being tested and each word of the filename should be separated via an underscore '\_'.

#\* Example of formatting of the input file for a chronic oral study

Survival time [d]	Control	T1	T2	T3	T4	T5
0	120	120	120	120	120	120
1	120	118	117	112	115	94
2	120	118	115	112	98	88
3	120	118	114	106	83	27
4	119	118	113	103	67	9
5	119	118	112	100	43	3
Concentration unit: ug/bee/day						
Concentration time [d]	Control	T1	T2	T3	T4	T5
0	0	3	7	12	41	68
5	0	3	7	12	41	68

### Value

An object of class `beeSurvData`, which is a list with the following information:

<code>nDatasets</code>	Number of files passed to the function
<code>survData</code>	A table containing the survival data as entered by the user in the input file
<code>survData_long</code>	A data frame containing the survival data in long format for model purposes
<code>concData</code>	A table containing the concentration data as entered by the user in the input file
<code>concData_long</code>	A data frame containing concentration data in long format
<code>unitData</code>	A character vector containing the units of the data as entered in the line <code>Concentration unit</code> of the input file
<code>typeData</code>	A character vector containing the type of experiment
<code>beeSpecies</code>	A character vector containing the type bee
<code>concModel</code>	A data frame containing the concentration data as recalculated by the model
<code>concModel_long</code>	A data frame containing the concentration data as recalculated by the model in a long format

Each element of the list is itself a list to account for multiple files that can be passed as input.



## Examples

```
file_location <- system.file("extdata", "betacyfluthrin_chronic_ug.txt", package = "BeeGUTS")
lsData <- dataGUTS(file_location = c(file_location),
  test_type = c('Chronic_Oral'), cstConcCal = FALSE)
```

---

fitBeeGUTS	<i>Fit a GUTS model for bees survival analysis using Bayesian Inference (stan)</i>
------------	--

---

## Description

The function `fitBeeGUTS` estimates the parameters of a GUTS model for the stochastic death (SD) or individual tolerance (IT) death mechanisms for survival analysis using Bayesian inference.

## Usage

```
fitBeeGUTS(
  data,
  modelType = NULL,
  distribution = "loglogistic",
  priorsList = NULL,
  parallel = TRUE,
  nCores = parallel::detectCores() - 1L,
  nChains = 3,
  nIter = 2000,
  nWarmup = floor(nIter/2),
  thin = 1,
  adaptDelta = 0.95,
  odeIntegrator = "rk45",
  relTol = 1e-08,
  absTol = 1e-08,
  maxSteps = 1000,
  ...
)
```

## Arguments

<code>data</code>	An object of class <code>beeSurvData</code>
<code>modelType</code>	A model type between "SD" for Stochastic Death and "IT" for Individual Tolerance.
<code>distribution</code>	A distribution for the IT death mechanism. To be chosen between "loglogistic" and "lognormal". Default is "loglogistic"
<code>priorsList</code>	A list containing the prior distribution for the parameter considered. By default, when no priors are provided (default is NULL), priors are set automatically based on the experimental design (adapted from Delignette-Muller et al 2017)

<code>parallel</code>	Logical indicating whether parallel computing should be used or not. Default is TRUE
<code>nCores</code>	A positive integer specifying the number of cores to use. Default is one core less than maximum number of cores available
<code>nChains</code>	A positive integer specifying the number of MCMC chains to run. Default is 3.
<code>nIter</code>	A positive integer specifying the number of iteration to monitor for each MCMC chain. Default is 2000
<code>nWarmup</code>	A positive integer specifying the number of warmup iteration per chain. Default is half the number of iteration
<code>thin</code>	A positive integer specifying the interval between the iterations to monitor. Default is 1 (all iterations are monitored)
<code>adaptDelta</code>	A double, bounded between 0 and 1 and controlling part of the sampling algorithms. See the <code>control</code> in the function <code>stan::stan()</code> of the package <code>rstan</code> . The default is 0.95.
<code>odeIntegrator</code>	A string specifying the integrator used to solve the system of differential equations (ODE) in the <code>stan</code> module. To be chosen between "rk45" and "bdf". Default is "rk45".
<code>relTol</code>	A double, bounded between 0 and 1 and controlling the relative tolerance of the accuracy of the solutions generated by the integrator. A smaller tolerance produces more accurate solution at the expense of the computing time. Default is 1e-8
<code>absTol</code>	A double, bounded between 0 and 1 and controlling the absolute tolerance of the accuracy of the solutions generated by the integrator. A smaller tolerance produces more accurate solution at the expense of the computing time. Default is 1e-8
<code>maxSteps</code>	A double controlling the maximum number of steps that can be taken before stopping a runaway simulation. Default is 1000
<code>...</code>	Additional parameters to be passed to <code>sampling</code> from <code>stan</code>

### Details

The automated prior determination is modified from Delignette-Muller et al. by considering that the minimal concentration for the prior can be close to 0 (1e-6) whereas the original paper considered the lowest non-zero concentration. Similarly, the minimal `kd` considered for the prior calculation was reduced to allow more chance to capture slow kinetics.

### Value

The function `fitBeeGUTS` returns the parameter estimates of the General Unified Threshold model of Survival (GUTS) in an object of class `beeSurvFit`. This object is a list composed of the following:

<code>stanFit</code>	An object of S4 class <code>stanfit</code> . More information is available in the package <code>rstan</code> .
<code>data</code>	The data object provided as argument of the function

dataFit	A list of data passed to the Stan model object
setupMCMC	A list containing the setup used for the MCMC chains
modelType	A character vector specifying the type of GUTS model used between SD and IT
distribution	A character vector specifying the type of distribution used in case IT was used; NA otherwise
messages	A character vector containing warning messages

## References

Delignette-Muller, M.L., Ruiz P. and Veber P. (2017). Robust fit of toxicokinetic-toxicodynamic models using prior knowledge contained in the design of survival toxicity tests. doi: [10.1021/acs.est.6b05326](https://doi.org/10.1021/acs.est.6b05326)

## Examples

```
data(betacyfluthrinChronic)
fit <- fitBeeGUTS(betacyfluthrinChronic, modelType = "SD", nIter = 1000, nCores = 2)
```

---

```
fitBetacyfluthrin_Chronic
```

*Model calibration results datasets for Honey bees exposed to constant concentration of Betacyfluthrin for 10 days.*

---

## Description

Model calibration results datasets for *Honey bees* exposed to constant concentration of Betacyfluthrin for 10 days.

## Usage

```
data(fitBetacyfluthrin_Chronic)
```

## Format

A list of class `beeSurvFit` constructed by `fitBeeGUTS` containing:

`stanFit` A 'stanfit' object containing the results of the calibration.

`data` A 'beeSurvData' objects with the user data used for the calibration.

`dataFit` A list containing the priors and data formatted for the calibration algorithm.

`setupMCMC` A list containing the setup used for the MCMC.

`modelType` A character string containing the type of GUTS model used (here 'SD').

`distribution` A character string containing the distribution used (IT only, here 'NA').

`messages` A character string containing the error messages if  $R_{hat} > 1.1$  (here 'NA').

**References**

Bayer data.

---

LCx	<i>Predict the Lethal Concentration method at which <math>x</math> specified time-point for a beeSurvFit object</i>
-----	---

---

**Description**

Predict median and 95\

**Usage**

LCx(object, ...)

**Arguments**

object	An object used to select a method
...	Further arguments to be passed to generic methods

**Details**

When class of object is beeSurvFit, see [LCx.beeSurvFit](#).

**Value**

A LCx object containing the results of the lethal concentration predictions

---

LCx.beeSurvFit	<i>Predict the Lethal Concentration at which <math>x</math> specified time-point for a beeSurvFit object</i>
----------------	--

---

**Description**

Predict the Lethal Concentration at which  $x$  specified time-point for a beeSurvFit object

**Usage**

```
## S3 method for class 'beeSurvFit'
LCx(
  object,
  X = 50,
  testType = "Chronic_Oral",
  timeLCx = NULL,
  concRange = NULL,
  nPoints = 100,
  ...
)
```

**Arguments**

object	An object of class <code>beeSurvFit</code>
X	Percentage of individuals dying (e.g., 50 for the $LC_{50}$ )
testType	Test type for which the $LC_X$ is calculated amongst "Acute_Oral", "Acute_Contact", and "Chronic_Oral". Note that for "Acute_Oral" and "Acute_Contact", the concentration will be reconstructed as in the <code>dataGUTS</code> function (not recommended as this might not make sense for $LC_X$ estimations. Default is "Chronic_Oral"
timeLCx	A scalar giving the time at which $LC_x$ is predicted. If NULL, the latest time point of the experiment used in the calibration is used
concRange	A vector of length 2 with minimal and maximal value of the range of concentration. If NULL, the range is define between 0 and the highest tested concentration of the calibration experiment.
nPoints	Number of time point in <code>concRange</code> between 0 and the maximal concentration. 100 by default.
...	Further arguments to be passed to generic methods

**Value**

A `LCx` object containing the results of the lethal concentration predictions

**Examples**

```
data(fitBetacyfluthrin_Chronic)
out <- LCx(fitBetacyfluthrin_Chronic)
```

---

`plot.beeSurvData`      *Plotting method for beeSurvData objects*

---

**Description**

This is the generic `plot` S3 method for the `beeSurvData` class. It plots the number of survivors as a function of time as well as the reconstructed concentrations for "Acute\_Oral" and "Acute\_Contact" test types.

**Usage**

```
## S3 method for class 'beeSurvData'
plot(
  x,
  ...,
  xlab = "Time [d]",
  ylab1 = "Number of survivors",
  ylab2 = "Concentration",
  main = paste("Data from a", x$typeData, "test on", x$beeSpecies)
)
```

**Arguments**

x	An object of class beeSurvData
...	Additional parameters to generic plot function (not used)
xlab	A character string for the label of the x-axis
ylab1	A character string for the label of the y-axis of the survivor plots
ylab2	A character string for the label of the y-axis of the concentration plots
main	A character string for the title label plot

**Value**

A graphic with the input data

**Examples**

```
data(betacyfluthrinChronic)
plot(betacyfluthrinChronic)
```

---

plot.beeSurvFit	<i>Plotting method for beeSurvFit objects</i>
-----------------	---

---

**Description**

This is the generic plot S3 method for the beeSurvFit class. It plots the number of survivors as a function of time as well as the reconstructed concentrations for "Acute\_Oral" and "Acute\_Contact" test types.

**Usage**

```
## S3 method for class 'beeSurvFit'
plot(
  x,
  ...,
  xlab = "Time [d]",
  ylab1 = "Number of survivors",
  ylab2 = "Concentration",
  main = paste("Calibration results for a", x$data$typeData, "test on",
    x$data$beeSpecies)
)
```

**Arguments**

x	An object of class beeSurvFit
...	Additional parameters to generic plot functions (not used)
xlab	A character string for the label of the x-axis
ylab1	A character string for the label of the y-axis of the survivor plots
ylab2	A character string for the label of the y-axis of the concentration plots
main	A character string for the title label plot

**Value**

A graphic with the results of the fit

**Examples**

```
data(fitBetacyfluthrin_Chronic)
plot(fitBetacyfluthrin_Chronic)
```

---

plot.beeSurvPred      *Plotting method for beeSurvPred objects*

---

**Description**

This is the generic plot S3 method for the beeSurvPred class. It plots the predicted number of survivors for the exposure concentration entered by the user.

**Usage**

```
## S3 method for class 'beeSurvPred'
plot(
  x,
  ...,
  xlab = "Time [d]",
  ylab1 = "Survival probability",
  ylab2 = "Concentration",
  main = paste("Predictions results for a BeeGUTS", x$modelType, "calibrated for",
    x$beeSpecies)
)
```

**Arguments**

x	An object of class beeSurvPred
...	Additional parameters to generic plot functions (not used)
xlab	A character string for the label of the x-axis
ylab1	A character string for the label of the y-axis of the survivor plots
ylab2	A character string for the label of the y-axis of the concentration plots
main	A character string for the title label plot

**Value**

A graphic with results of the forward prediction

**Examples**

```

dataPredict <- data.frame(time = c(1:10, 1:10, 1:10),
                          conc = c(rep(5, 10), rep(10, 10), rep(15, 10)),
                          replicate = c(rep("rep1", 10), rep("rep2", 10), rep("rep3", 10)),
                          NSurv = c(rep(5, 10), rep(10, 10), rep(15, 10)))
data(fitBetacyfluthrin_Chronic)
prediction <- predict(fitBetacyfluthrin_Chronic, dataPredict)
plot(prediction)

```

---

```
plot.beeSurvValidation
```

*Plotting method for beeSurvValidation objects*

---

**Description**

This is the generic plot S3 method for the beeSurvValid class. It plots the number of survivors as a function of time as well as the reconstructed concentrations for "Acute\_Oral" and "Acute\_Contact" test types.

**Usage**

```

## S3 method for class 'beeSurvValidation'
plot(
  x,
  ...,
  xlab = "Time [d]",
  ylab1 = "Number of survivors",
  ylab2 = "Concentration",
  main = paste("Validation results for a BeeGUTS", x$typeData, "calibrated for",
              x$beeSpecies)
)

```

**Arguments**

x	An object of class beeSurvValid
...	Additional parameters to generic plot functions (not used)
xlab	A character string for the label of the x-axis
ylab1	A character string for the label of the y-axis of the survivor plots
ylab2	A character string for the label of the y-axis of the concentration plots
main	A character string for the title label plot

**Value**

A graphic with the results of the validation



**Examples**

```
data(betacyfluthrinChronic) # Load dataset for validation
data(fitBetacyfluthrin_Chronic)
validation <- validate(fitBetacyfluthrin_Chronic, betacyfluthrinChronic)
plot(validation)
```

---

plot.ppc

*Plotting method for ppc objects*

---

**Description**

Plotting method for ppc objects

**Usage**

```
## S3 method for class 'ppc'
plot(x, ...)
```

**Arguments**

x                    An object of class ppc.

...                  Further arguments to be passed to generic methods.

**Value**

an object of class ggplot.

**Examples**

```
data(fitBetacyfluthrin_Chronic)
out <- ppc(fitBetacyfluthrin_Chronic)
plot(out)
```

---

ppc	<i>Generates an object to be used in posterior predictive check for beeSurvFit, beeSurvPred</i>
-----	---

---

**Description**

Generates an object to be used in posterior predictive check for beeSurvFit, beeSurvPred

**Usage**

```
ppc(x)
```

**Arguments**

x                    an object used to select a method ppc

**Value**

a data.frame of class ppc

---

ppc.beeSurvFit	<i>Posterior predictive check method for beeSurvFit objects</i>
----------------	---

---

**Description**

Posterior predictive check method for beeSurvFit objects

**Usage**

```
## S3 method for class 'beeSurvFit'  
ppc(x)
```

**Arguments**

x                    an object of class beeSurvFit

**Value**

a data.frame of class ppc

**Examples**

```
data(fitBetacyfluthrin_Chronic)  
out <- ppc(fitBetacyfluthrin_Chronic)
```

---

predict.beeSurvFit      *Predict method for beeSurvFit objects*

---

### Description

This is the generic predict S3 method for the beeSurvFit class. It predict the survival over time for the concentration profiles entered by the user. No concentration reconstructions are performed here. Functions `odeGUTS::predict_ode()` from the morse package is used. This might be changed in a future update

### Usage

```
## S3 method for class 'beeSurvFit'
predict(object, dataPredict, ...)
```

### Arguments

object	An object of class beeSurvFit
dataPredict	Data to predict in the format as a dataframe containing the following column: <ul style="list-style-type: none"> <li>• time: A vector of time in days</li> <li>• conc: A vector of number of survivors of same length</li> <li>• replicate A vector replicate name</li> </ul>
...	Additional arguments to be parsed to the predict.survFit method from odeGUTS (e.g. <code>mcmc_size = 1000</code> is to be used to reduce the number of mcmc samples in order to speed up the computation. <code>mcmc_size</code> is the number of selected iterations for one chain. Default is 1000. If all MCMC is wanted, set argument to NULL. <code>hb_value = FALSE</code> the background mortality hb is set to a fixed value. If TRUE, parameter hb taken from the posterior (only works if one hb value was estimated. The default is FALSE. <code>hb_valueFORCED = 0</code> <code>hb_valueFORCED</code> If <code>hb_value</code> is FALSE, it fix hb. The default is 0

### Value

A beeSurvPred object containing the results of the forwards prediction

### Examples

```
dataPredict <- data.frame(time = c(1:5, 1:15),
                          conc = c(rep(5, 5), rep(15, 15)),
                          replicate = c(rep("rep1", 5), rep("rep2", 15)))
data(fitBetacyfluthrin_Chronic)
prediction <- predict(fitBetacyfluthrin_Chronic, dataPredict)
```

---

summary.beeSurvFit      *Summary of beeSurvFit objects*

---

### Description

This is the generic summary S3 method for the beeSurvFit class. It shows the quantiles of priors and posteriors on parameters.

This is the generic summary S3 method for the LCx class. It shows the median and 95% credible interval of the calculated LCx.

### Usage

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

### Arguments

object	An object of class LCx
...	Additional arguments to be parsed to the generic summary method (not used)

### Value

A summary of the beeSurvFit object  
A summary of the LCx object

### Examples

```
data(fitBetacyfluthrin_Chronic)  
summary(fitBetacyfluthrin_Chronic)  
  
data(fitBetacyfluthrin_Chronic)  
out <- LCx(fitBetacyfluthrin_Chronic)  
summary(out)
```

---

traceplot	<i>Plotting method for traces and densities for beeSurvFit objects</i>
-----------	--

---

### Description

This is the generic traceplot S3 method for the beeSurvFit class. It plots the traces with as well as the densities for the parameters of the GUTS IT or GUTS SD. The traceplot includes by default the warmup iterations, the density plot does not include them

### Usage

```
traceplot(object, ..., incWarmup_trace = TRUE, incWarmup_dens = FALSE)

## S3 method for class 'beeSurvFit'
traceplot(object, ..., incWarmup_trace = TRUE, incWarmup_dens = FALSE)
```

### Arguments

object	An object of class beeSurvFit to be plotted
...	Additional parameters to be parsed to generic rstan plot functions
incWarmup_trace	A logical indicating whether the warmup iterations should be plotted in the traceplot (default TRUE)
incWarmup_dens	A logical indicating whether the warmup iterations should be plotted in the density plot (default FALSE)

### Value

A graphic with the traceplots and densities of the fit

### Examples

```
data(fitBetacyfluthrin_Chronic)
traceplot(fitBetacyfluthrin_Chronic)
```

---

validate	<i>Validation method for beeSurvFit objects</i>
----------	---

---

### Description

This is a validation method for the beeSurvFit object. It perform forwards predictions for a specific concentration profile and compare these prediction to the respective experimental data.

### Usage

```
validate(object, dataValidate, ...)
```

**Arguments**

object	An object of class <code>beeSurvFit</code>
dataValidate	Data to validate in the format of the experimental data used for fit ( <code>dataGUTS</code> )
...	Additional arguments to be parsed to the <code>predict.survFit</code> method from <code>odeGUTS</code> (e.g. <code>mcmc_size = 1000</code> is to be used to reduce the number of mcmc samples in order to speed up the computation. <code>mcmc_size</code> is the number of selected iterations for one chain. Default is 1000. If all MCMC is wanted, set argument to <code>NULL.</code> , <code>hb_value = FALSE</code> the background mortality <code>hb</code> is taken into account from the posterior. If <code>FALSE</code> , parameter <code>hb</code> is set to a fixed value. The default is <code>FALSE</code> . <code>hb_valueFORCED = 0</code> <code>hb_valueFORCED</code> If <code>hb_value</code> is <code>FALSE</code> , it fix <code>hb</code> . The default is <code>0</code>

**Value**

An object of class `beeSurvValidation`.

---

`validate.beeSurvFit`    *Validate method for `beeSurvFit` objects*

---

**Description**

This is the generic `validate` S3 method for the `beeSurvFit` class. It predict the survival over time for the concentration profiles entered by the user.

**Usage**

```
## S3 method for class 'beeSurvFit'
validate(object, dataValidate, ...)
```

**Arguments**

object	An object of class <code>beeSurvFit</code>
dataValidate	Data to validate in the format of the experimental data used for fit ( <code>dataGUTS</code> )
...	Additional arguments to be parsed to the <code>predict.survFit</code> method from <code>odeGUTS</code> (e.g. <code>mcmc_size = 1000</code> is to be used to reduce the number of mcmc samples in order to speed up the computation. <code>mcmc_size</code> is the number of selected iterations for one chain. Default is 1000. If all MCMC is wanted, set argument to <code>NULL.</code> , <code>hb_value = FALSE</code> the background mortality <code>hb</code> is taken into account from the posterior. If <code>FALSE</code> , parameter <code>hb</code> is set to a fixed value. The default is <code>FALSE</code> . <code>hb_valueFORCED = 0</code> <code>hb_valueFORCED</code> If <code>hb_value</code> is <code>FALSE</code> , it fix <code>hb</code> . The default is <code>0</code>

**Value**

A `beeSurvValidation` object with the results of the validation

### **Examples**

```
data(betacyfluthrinChronic)
data(fitBetacyfluthrin_Chronic)
validation <- validate(fitBetacyfluthrin_Chronic, betacyfluthrinChronic)
```

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