Package 'rbioacc'

February 27, 2024

Title Inference and Prediction of ToxicoKinetic (TK) Models

Version 1.2.1

Description The MOSAICbioacc application is a turnkey package providing bioaccumulation
factors (BCF/BMF/BSAF) from a toxicokinetic (TK) model fitted to
accumulation-depuration data. It is designed to fulfil the requirements
of regulators when examining applications for market authorization of active
substances. See Ratier et al. (2021) <doi:10.1101/2021.09.08.459421>.

URL https://gitlab.in2p3.fr/mosaic-software/rbioacc

BugReports https://gitlab.in2p3.fr/mosaic-software/rbioacc/-/issues

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(>= 5.0.1), rstan (>= 2.26.0), StanHeaders (>= 2.26.0)

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rbioacc-package	*The 'rbioacc' package.*

Description

A DESCRIPTION OF THE PACKAGE

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References

Stan Development Team (NA). RStan: the R interface to Stan. R package version NA. https://mc-stan.org

See Also

Useful links:

- https://gitlab.in2p3.fr/mosaic-software/rbioacc
- Report bugs at https://gitlab.in2p3.fr/mosaic-software/rbioacc/-/issues

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.fonte   *A simple implementation of to pivot_longer of tidyr*

Description

A simple implementation of to pivot_longer of tidyr

Usage

```
.fonte(df, names_to, values_to)
```

Arguments

df   A data frame to pivot.

names_to   A string specifying the name of the column to create from the data stored in the
                    column names of df.

values_to   A string specifying the name of the column to create from the data stored in cell
                    values.

Value

The data frame with a "lengthens" shape: more rows, less columns

---

.index_col_exposure   *Return column matching "expw", "exps", "expf", "exppw" of a*
                        `data.frame`

Description

Return column matching "expw", "exps", "expf", "exppw" of a `data.frame`

Usage

```
.index_col_exposure(data_frame)
```

Arguments

data_frame   a dataframe

Value

A vector of numeric

`.index_col_metabolite`	*Return column matching "concX" of a* `data.frame` *where X is metabolite*

Description

Return column matching "concX" of a `data.frame` where X is metabolite

Usage

```
.index_col_metabolite(data_frame)
```

Arguments

`data_frame`	a dataframe

Value

A vector of numeric

`.is_equal_rmInf`	*Check if two vectors* `x` *and* `y` *are equal after remove* `Inf`

Description

Check if two vectors `x` and `y` are equal after remove `Inf`

Usage

```
.is_equal_rmInf(x, y)
```

Arguments

`x`	A vector
`y`	A vector

Value

A logical value

---

bioacc_metric   *Biaccumulation metrics*

Description

Biaccumulation metrics

Usage

```
bioacc_metric(fit, ...)

## S3 method for class 'fitTK'
bioacc_metric(fit, type = "k", route = "all", ...)
```

Arguments

fit	An stanFit object
...	Further arguments to be passed to generic methods
type	A string with the type of metric: k for the kinetics BioConcentration Factor, ss for the steady state BioConcentration Factor.
route	Provide exposure route: all

Value

a data frame

Chironomus_benzoapyrene

Data on Chironomus exposed to benzoapyrene

Description

Data on Chironomus exposed to benzoapyrene

Usage

```
data(Chironomus_benzoapyrene)
```

Chiro_Creuzot *Data on Chironomus with several exposure routes.*

Description

Data on Chironomus with several exposure routes.

Usage

```
data(Chiro_Creuzot)
```

Format

A dataframe with 24 observations on the following four variables:

time A vector of class `numeric` with the time points in days.

expw A vector of class `numeric` with the exposure in water.

expw A vector of class `numeric` with the exposure in pore water.

replicate A vector of class `integer` for replicate identification.

conc A vector of class `numeric` with concentration in organism.

concm1 A vector of class `numeric` with metabolite concentration in organism.

concm2 A vector of class `numeric` with metabolite concentration in organism.

---

corrMatrix *Correlations between parameters: colored matrix*

Description

Correlations between parameters: colored matrix

Usage

```
corrMatrix(fit)
```

Arguments

fit   An object of class `fitTK`

Value

A heatmap of class `ggplot`.

---

corrPlot   *Correlations between parameters: pairs plot*

Description

Correlations between parameters: pairs plot

Usage

```
corrPlot(fit, plots = c("all", "deterministic", "stochastic"))
```

Arguments

fit	An object of class `fitTK`
plots	A string selecting the parameters. Defaults is `"all"` and select all parameters. Deterministc parameters can be selected by setting `"deterministic"` and stochastic parameter with `"stochastic"`

Value

A pairsplot of class `ggmatrix` containing planes of parameter pairs (lower triangle), marginal posterior distribution of each parameter (diagonal) and Pearson correlation coefficients (upper triangle)

---

df_ppc   *PPC data.frame*

Description

This is the generic ppc S3 method for plots of the predicted values along with 95\ versus the observed values for `fitTK` objects.

Usage

```
df_ppc(fit, ...)

## S3 method for class 'fitTK'
df_ppc(fit, ...)

ppc(fit, ...)

## S3 method for class 'fitTK'
ppc(fit, ...)
```

Arguments

`fit`	And object returned by fitTK
`...`	Additional arguments

Details

The black points show the observed number of survivors (pooled replicates, on X-axis) against the corresponding predicted number (Y-axis). Predictions come along with 95\ intervals, which are depicted in green when they contain the observed value and in red otherwise. Samples with equal observed value are shifted on the X-axis. For that reason, the bisecting line (y = x), is represented by steps when observed values are low. That way we ensure green intervals do intersect the bisecting line.

Value

A data frame with median and 95\

a plot of class `ggplot`

`df_PriorPost`	*Data frame of Posterior over Prior*

Description

Data frame of Posterior over Prior

Data frame of Posterior over Prior

Usage

```
df_PriorPost(fit, ...)

## S3 method for class 'fitTK'
df_PriorPost(fit, select = "all", ...)
```

Arguments

`fit`	An object of class `fitTK` returned by the function `fitTK()`.
`...`	Additional arguments
`select`	A string selecting the parameters. Defaults is `"all"` and select all parameters.Deterministc parameters can be selected by setting `"deterministic"` and stochastic parameter with `"stochastic"`

Value

An object of class `data.frame`

---

equations   *Equations of the mathematical model used for the fit*

Description

Equations of the mathematical model used for the fit

Usage

```
equations(fit, object)
```

Arguments

fit   An object of class fitTK

object   The data.frame used as the base as the fit object

Value

A vector of strings each containing an equation

---

exposure_names   *Retrieve exposure routes names from object*

Description

Retrieve exposure routes names from object

Usage

```
exposure_names(object)
```

Arguments

object   a data frame.

Value

A vector of string

Exposure_Sialis_lutaria
Data on Sialis lutaria exposure time series

Description

Data on Sialis lutaria exposure time series

Usage

```
data(Exposure_Sialis_lutaria)
```

---

fitTK
Posterior predictive check

Description

Posterior predictive check

Bayesian inference of TK model with Stan

Bayesian inference of TK model with variable exposure profile (BETA version)

Usage

```
fitTK(stanTKdata, ...)

## S3 method for class 'stanTKdataCST'
fitTK(stanTKdata, ...)

## S3 method for class 'stanTKdataVAR'
fitTK(stanTKdata, ...)
```

Arguments

stanTKdata   List of Data require for computing

...   Arguments passed to rstan::sampling (e.g. iter, chains).

Value

An object of class fitTK containing two object: stanTKdata the data set used for inference and stanfit returned by rstan::sampling

Gammarus_azoxistrobine_1d_Rosch2017
Data on Gammarus exposed to azoxistrobine

Description

Data on Gammarus exposed to azoxistrobine

Usage

```
data(Gammarus_azoxistrobine_1d_Rosch2017)
```

Internal_Sialis_lutaria
Data on Sialis lutaria internal time series

Description

Data on Sialis lutaria internal time series

Usage

```
data(Internal_Sialis_lutaria)
```

Male_Gammarus_Merged	*Male* Gammarus fossarum *exposed to Hg spiked water. Three exposure concentrations were tested in triplicates. The duration of the accumulation phase is 4 days for 0.0000708021 and 0.000283208 $\mu g.mL\hat{}-1$ exposure concentrations, and 7 days for 0.000141604 $\mu g.mL\hat{}-1$ exposure concentration.*

Description

Male Gammarus fossarum exposed to Hg spiked water. Three exposure concentrations were tested in triplicates. The duration of the accumulation phase is 4 days for 0.0000708021 and 0.000283208 $\mu g.mL^{-1}$ exposure concentrations, and 7 days for 0.000141604 $\mu g.mL^{-1}$ exposure concentration.

Usage

```
data(Male_Gammarus_Merged)
```

Format

A dataframe with 72 observations on the following four variables:

time A vector of class numeric with the time points in days.

expw A vector of class numeric with Hg exposure in water in $\mu g.mL^{-1}$.

replicate A vector of class integer for replicate identification.

conc A vector of class numeric with Hg concentration in organism in $\mu g.mL^{-1}$.

References

Ciccia, T. (2019). Accumulation et devenir du mercure chez l'espèce sentinelle Gammarus fossarum : de l'expérimentation au développement d'un modèle toxicocinétique multi-compartiments. Rapport de stage de Master 2, INRAE.

Male_Gammarus_seanine_growth

> *Male* Gammarus pulex *exposed to seanine spiked water. A single exposure concentration was tested. The duration of the accumulation phase is 1.417 days. Three metabolites were quantified. The growth of organism was included.*

Description

Male Gammarus pulex exposed to seanine spiked water. A single exposure concentration was tested. The duration of the accumulation phase is 1.417 days. Three metabolites were quantified. The growth of organism was included.

Usage

```
data(Male_Gammarus_seanine_growth)
```

Format

A dataframe with 22 observations on the following four variables:

time A vector of class numeric with the time points in days.

expw A vector of class numeric with seanine exposure in water in $\mu g.mL^{-1}$.

replicate A vector of class integer for replicate identification.

conc A vector of class numeric with concentration in organism.

concm1 A vector of class numeric with metabolite concentration in organism.

concm2 A vector of class numeric with metabolite concentration in organism.

concm3 A vector of class numeric with metabolite concentration in organism.

growth A vector of class numeric with growth of the organism.

References

Ashauer, R. et al. (2012). Significance of xenobiotic metabolism for bioaccumulation kinetics of organic chemicals in Gammarus pulex. Environmental Science Technology, 46: 3498-3508.

Male_Gammarus_Single	*Bio-accumulation data set for* Gammarus fossarum *exposed to Hg spiked water.*

Description

Male *Gammarus fossarum* exposed to Hg spiked water. A single exposure concentration was tested. The duration of the accumulation phase is 4 days.

Usage

```
data(Male_Gammarus_Single)
```

Format

A dataframe with 23 observations on the following four variables:

time A vector of class numeric with the time points in days.

expw A vector of class numeric with Hg exposure in water in $\mu g.mL^{-1}$.

replicate A vector of class integer for replicate identification.

conc A vector of class numeric with Hg concentration in organism in $\mu g.mL^{-1}$.

References

Ciccia, T. (2019). Accumulation et devenir du mercure chez l'espèce sentinelle Gammarus fossarum : de l'expérimentation au développement d'un modèle toxicocinétique multi-compartiments. Rapport de stage de Master 2, INRAE.

---

mcmcTraces	*Traces of MCMC iterations*

Description

Traces of MCMC iterations

Usage

```
mcmcTraces(fit, plots = "all")
```

Arguments

fit   An object of class `fitTK`

plots   A string selecting the parameters. Defaults is `"all"` and select all parameters. Deterministc parameters can be selected by setting `"deterministic"` and stochastic parameter with `"stochastic"`

Value

A traceplot of class `ggplot`.

---

modelData   *Create a list giving data and parameters to use in the model inference.*

Description

Create a list giving data and parameters to use in the model inference.

Usage

```
modelData(object, ...)

## S3 method for class 'data.frame'
modelData(object, time_accumulation, elimination_rate = NA, ...)
```

Arguments

object   An object of class `data.frame`

...   Further arguments to be passed to generic methods

time_accumulation
              A scalar givin accumulation time

elimination_rate
              A scalar for the elimination rate. Default is `NA`. To remove elimination rate, set
              `elimination_rate = 0`.

Value

A `list` with data and parameters require for model inference.

---

modelData_ode   *Create a list giving data and parameters to use in the model inference.*

Description

Create a list giving data and parameters to use in the model inference.

Usage

```
modelData_ode(
  df_exposure,
  df_internal,
  y0 = 1,
  t0 = -0.001,
  unifMax = 10,
  time_accumulation = NULL,
  minK = -5,
  maxK = 5,
  ...
)

modelData_ode(
  df_exposure,
  df_internal,
  y0 = 1,
  t0 = -0.001,
  unifMax = 10,
  time_accumulation = NULL,
  minK = -5,
  maxK = 5,
  ...
)
```

Arguments

df_exposure	Dataframe of exposure with 2 column (time and value)
df_internal	Dataframe of internal concentration with 2 column (time and value)
y0	Initial concentration
t0	initial time point
unifMax	Hyperparameter value
time_accumulation	
	Time of accumulation
minK	Hyperparameter value
maxK	Hyperparameter value
...	Additional arguments

Value

A `list` with data and parameters require for model inference.

Oncorhynchus_two	*Data on Oncorhynchus exposition*

Description

Data on Oncorhynchus exposition

Usage

```
data(Oncorhynchus_two)
```

---

plot.bioaccMetric	*Plot function for object of class* bioaccMetric

---

Description

Plot function for object of class `bioaccMetric`

Usage

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

Arguments

x	a data frame
...	Additional arguments

Value

A plot of class `ggplot`

---

plot.fitTK *Plotting method for* fitTK *objects*

Description

This is the generic `plot` S3 method for the `fitTK`. It plots the fit obtained for each variable in the original dataset.

Usage

```
## S3 method for class 'fitTK'
plot(x, time_interp = NULL, ...)
```

Arguments

x   And object returned by fitTK

time_interp   A vector with additional time point to interpolate. Time point of the original
               data set are conserved.

...   Additional arguments

Value

a plot of class ggplot

---

plot.predictTK *Plotting method for* predictTK *objects*

Description

This is the generic `plot` S3 method for the `predictTK`.

Usage

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

## S3 method for class 'predictTKstan'
plot(x, add_data = FALSE, ...)
```

Arguments

x   An object of class predictTK returned by predict

...   Additional arguments

add_data   logical TRUE or FALSE to add the orignal data of the fit object x

Value

A plot of class `ggplot`

`plot_exposure`	*Plot exposure profile*

Description

Plot exposure profile

Usage

```
plot_exposure(object)
```

Arguments

`object`	a data frame with exposure column

Value

a plot of class `ggplot`

`plot_PriorPost`	*Plot Posterior over Prior*

Description

Plot Posterior over Prior

Plot Posterior over Prior

Usage

```
plot_PriorPost(x, ...)

## S3 method for class 'fitTK'
plot_PriorPost(x, select = "all", ...)

## S3 method for class 'df_PP'
plot_PriorPost(x, select = "all", ...)
```

Arguments

`x`	A data.frame of class `df_PP` returned by the function `df_PriorPost()`.
`...`	addition arguments
`select`	A string selecting the parameters. Defaults is `"all"` and select all parameters. Deterministic parameters can be selected by setting `"deterministic"` and stochastic parameter with `"stochastic"`.

Value

A plot of class ggplot.

A plot of class ggplot.

---

predict.fitTK   *Prediction function using* fitTK *object*

Description

Use when parameter are manually given by the user.

Usage

```
## S3 method for class 'fitTK'
predict(object, data, mcmc_size = NULL, fixed_init = TRUE, ...)

predict_stan(
  object,
  data,
  mcmc_size = NULL,
  fixed_init = TRUE,
  time_interp = NULL,
  iter = 1000,
  ...
)

predict_manual(
  param,
  data,
  time_accumulation = NULL,
  C0 = 0,
  G0 = NA,
  gmax = NA
)
```

Arguments

object	An object of stanfit
data	A data set with one column time and 1 to 4 exposure
mcmc_size	Size of mcmc chain if needed to be reduced
fixed_init	If TRUE fix the initial conditions of internal concentration. columns with name in expw, exps, expf and exppw
...	Additional arguments
time_interp	A vector with additional time point to interpolate. Time point of the original data set are conserved.

iter	Number of time steps
param	A dataframe with name of parameters kee, keg, ku1, ku2, ..., km1, km2, ... and kem1, kem2, ..., sigmaConc, sigmaCmet (if metabolites) and sigmaGrowth (if growth). The parameter kee is mandatory.
time_accumulation	
	the time of accumulation.
C0	Gives the initial conditions of internal concentration.
G0	initial condition of G0 (require if keg is provided)
gmax	gmax (require if keg is provided) columns with name in expw, exps, expf and exppw

Value

An object of class `predictTK`

An object of class `predictTK`

---

psrf	*Potential Scale Reduction Factors (PSRF) of the parameters*

Description

Potential Scale Reduction Factors (PSRF) of the parameters

Usage

```
psrf(fit)
```

Arguments

fit	An object of class `fitTK`

Value

An object of class `data.frame` with two columns: PSRF and parameter

a data frame with Potential Scale Reduction Factors

---

quantile_table   *Quantiles of parameters*

Description

Quantiles of parameters

Usage

```
quantile_table(fit, probs = c(0.025, 0.5, 0.975))
```

Arguments

fit   An object of class `fitTK`

probs   Scalar or Vector of quantiles. Default is 0.025, 0.5 and 0.975 giving median and
                95% credible interval

Value

A data frame with quantiles

---

replace_   *Replace element of a vector*

Description

Replace element of a vector

Usage

```
replace_(x, from, to)
```

Arguments

x   a vector

from   a vector of elements to replace

to   a vector with replacing elements

Value

a vector

Examples

```
replace_(1:10,c(2,4,5,8), c(0,0,0,0))
replace_(c(1,2,2,3,2),c(3,2), c(4,5))
```

---

t95	*Return the time at 95% depuration of the parent component*

Description

Return the time at 95% depuration of the parent component

Usage

```
t95(fit)
```

Arguments

fit   An object of class `fitTK`

Value

a numeric object

---

waic	*Widely Applicable Information Criterion (WAIC)*

Description

Compute WAIC using the `waic()` method of the loo package.

Usage

```
waic(fit)
```

Arguments

fit   An object of class `fitTK`

Value

A numeric containing the WAIC

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