Package ‘rbioacc’

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Title Inference and Prediction of ToxicoKinetic (TK) Models

Version 1.0.2

Description The MOSAICbioacc application is a turn-key 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>.

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Config/testthat/edition 3

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The 'rbioacc' package.

A simple implementation of `pivot_longer` of `tidyr`

Description

A simple implementation of `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

References

.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. Deterministic 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)
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

**Usage**

```r
df_PriorPost(fit, ...)```

---

### S3 method for class 'fitTK'

```r
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. Deterministic 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**

```r
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)
Gammarus_azoxistrobine_1d_Rosch2017

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_seanine_growth**

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 µg.mL\(^{-1}\) exposure concentrations, and 7 days for 0.000141604 µg.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 µg.mL\(^{-1}\).
- **replicate**: A vector of class integer for replicate identification.
- **conc**: A vector of class numeric with Hg concentration in organism in µg.mL\(^{-1}\).

**References**


---

**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**

```r
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**


---

**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**

```r
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**

mcmcTraces

Traces of MCMC iterations

Description
Traces of MCMC iterations

Usage
mcmcTraces(fit, plots = "all")

Arguments

<table>
<thead>
<tr>
<th>fit</th>
<th>An object of class fitTK</th>
</tr>
</thead>
<tbody>
<tr>
<td>plots</td>
<td>A string selecting the parameters. Defaults is &quot;all&quot; and select all parameters. Deterministic parameters can be selected by setting &quot;deterministic&quot; and stochastic parameter with &quot;stochastic&quot;</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>object</th>
<th>An object of class data.frame</th>
</tr>
</thead>
<tbody>
<tr>
<td>...</td>
<td>Further arguments to be passed to generic methods</td>
</tr>
<tr>
<td>time_accumulation</td>
<td>A scalar giving accumulation time</td>
</tr>
<tr>
<td>elimination_rate</td>
<td>A scalar for the elimination rate. Default is NA. To remove elimination rate, set elimination_rate = 0.</td>
</tr>
</tbody>
</table>
Value

A list with data and parameters required 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

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

```r
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**

```r
data(Oncorhynchus_two)
```

---

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

---

**Description**

Plot function for object of class bioaccMetric

**Usage**

```r
## 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**

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

**Arguments**

- `x`  
  And object returned by `fitTK`
- `...`  
  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**

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

**Arguments**

- `x`  
  An object of class `predictTK` returned by `predict`
- `...`  
  Additional arguments

**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

**Usage**
plot_PriorPost(fit, ...)

```r
## S3 method for class 'fitTK'
plot_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. Deterministic parameters can be selected by setting "deterministic" and stochastic parameter with "stochastic".

**Value**
A plot of class ggplot.
predict.fitTK

**Description**

Use when parameter are manually given by the user.

**Usage**

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

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
- `param`: A dataframe with name of parameters kee, keg, ku1, ku2, ..., km1, km2, ... and kem1, kem2, ..., sigmaConc, sigmaCmet (if metabolites) and sigmaGrowth (if growth).
- `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**  
```r  
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**  
```r  
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
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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