

# 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](https://doi.org/10.1101/2021.09.08.459421)>.

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**Author** Virgile Baudrot [aut],  
Sandrine Charles [aut],  
Ohélia Gestin [ctb],  
Mélina Kaag [aut],  
Christelle Lopez [ctb],  
Gauthier Multari [ctb],  
Alain Pavé [ctb],  
Aude Ratier [aut],  
Aurélie Siberchicot [aut, cre]

**Maintainer** Aurélie Siberchicot <aurelie.siberchicot@univ-lyon1.fr>

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## R topics documented:

rbioacc-package . . . . .	3
.fonte . . . . .	3
.index_col_exposure . . . . .	4
.index_col_metabolite . . . . .	4
.is_equal_rmInf . . . . .	5
bioacc_metric . . . . .	5
Chironomus_benzoapyrene . . . . .	6
Chiro_Creuzot . . . . .	6
corrMatrix . . . . .	7
corrPlot . . . . .	7
df_ppc . . . . .	8
df_PriorPost . . . . .	9
equations . . . . .	9
exposure_names . . . . .	10
Exposure_Sialis_lutaria . . . . .	10
fitTK . . . . .	10
Gammarus_azoxistrobine_1d_Rosch2017 . . . . .	11
Internal_Sialis_lutaria . . . . .	11
Male_Gammarus_Merged . . . . .	12
Male_Gammarus_seanine_growth . . . . .	12
Male_Gammarus_Single . . . . .	13
mcmcTraces . . . . .	14
modelData . . . . .	14
modelData_ode . . . . .	15
Oncorhynchus_two . . . . .	16
plot.bioaccMetric . . . . .	16
plot.fitTK . . . . .	17
plot.predictTK . . . . .	17
plot_exposure . . . . .	18
plot_PriorPost . . . . .	18
predict.fitTK . . . . .	19
psrf . . . . .	20
quantile_table . . . . .	20
t95 . . . . .	21
waic . . . . .	21

**Index**

**22**

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rbioacc-package      *The 'rbioacc' package.*

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## Description

A DESCRIPTION OF THE PACKAGE

## References

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

---

.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	<i>Correlations between parameters: colored matrix</i>
------------	--

---

**Description**

Correlations between parameters: colored matrix

**Usage**

```
corrMatrix(fit)
```

**Arguments**

`fit` An object of class `fitTK`

**Value**

A heatmap of class `ggplot`.

---

corrPlot	<i>Correlations between parameters: pairs plot</i>
----------	--

---

**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)

---

df_ppc	<i>PPC data.frame</i>
--------	-----------------------

---

### 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	<i>Data frame of Posterior over Prior</i>
--------------	---

---

**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. Deterministic parameters can be selected by setting "deterministic" and stochastic parameter with "stochastic"

**Value**

An object of class `data.frame`

---

equations	<i>Equations of the mathematical model used for the fit</i>
-----------	---

---

**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	<i>Retrieve exposure routes names from object</i>
----------------	---

---

**Description**

Retrieve exposure routes names from object

**Usage**

```
exposure_names(object)
```

**Arguments**

object            a data frame.

**Value**

A vector of string

---

Exposure_Sialis_lutaria	<i>Data on Sialis lutaria exposure time series</i>
-------------------------	--

---

**Description**

Data on Sialis lutaria exposure time series

**Usage**

```
data(Exposure_Sialis_lutaria)
```

---

fitTK	<i>Posterior predictive check</i>
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---

**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  $\mu\text{g.mL}^{-1}$  exposure concentrations, and 7 days for 0.000141604  $\mu\text{g.mL}^{-1}$  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  $\mu\text{g.mL}^{-1}$  exposure concentrations, and 7 days for 0.000141604  $\mu\text{g.mL}^{-1}$  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  $\mu\text{g.mL}^{-1}$ .

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

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

### 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  $\mu\text{g.mL}^{-1}$ .  
`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  $\mu\text{g.mL}^{-1}$ .  
`replicate` A vector of class `integer` for replicate identification.  
`conc` A vector of class `numeric` with Hg concentration in organism in  $\mu\text{g.mL}^{-1}$ .

**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	<i>Traces of MCMC iterations</i>
------------	----------------------------------

---

**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. Deterministic parameters can be selected by setting "deterministic" and stochastic parameter with "stochastic"

**Value**

A traceplot of class ggplot.

---

modelData	<i>Create a list giving data and parameters to use in the model inference.</i>
-----------	--

---

**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	<i>Create a list giving data and parameters to use in the model inference.</i>
---------------	--

---

**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	<i>Data on Oncorhynchus exposition</i>
------------------	--

---

**Description**

Data on Oncorhynchus exposition

**Usage**

```
data(Oncorhynchus_two)
```

---

plot.bioaccMetric	<i>Plot function for object of class bioaccMetric</i>
-------------------	---

---

**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	<i>Plotting method for fitTK objects</i>
------------	--

---

**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, ...)
```

**Arguments**

x	And object returned by fitTK
...	Additional arguments

**Value**

a plot of class ggplot

---

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

---

**Description**

This is the generic plot S3 method for the predictTK.

**Usage**

```
## 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	<i>Plot exposure profile</i>
---------------	------------------------------

---

**Description**

Plot exposure profile

**Usage**

```
plot_exposure(object)
```

**Arguments**

object            a data frame with exposure column

**Value**

a plot of class ggplot

---

plot_PriorPost	<i>Plot Posterior over Prior</i>
----------------	----------------------------------

---

**Description**

Plot Posterior over Prior

Plot Posterior over Prior

**Usage**

```
plot_PriorPost(fit, ...)
```

```
## S3 method for class 'fitTK'
```

```
plot_PriorPost(fit, select = "all", ...)
```

**Arguments**

fit                An object of class fitTK returned by the function fitTK().

...                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.

---

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_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	<i>Potential Scale Reduction Factors (PSRF) of the parameters</i>
------	---

---

**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	<i>Quantiles of parameters</i>
----------------	--------------------------------

---

**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

---

t95	<i>Return the time at 95% depuration of the parent component</i>
-----	--

---

**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	<i>Widely Applicable Information Criterion (WAIC)</i>
------	---

---

**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

# Index

## \* dataset

Chiro\_Creuzot, [6](#)  
Chironomus\_benzoapyrene, [6](#)  
Exposure\_Sialis\_lutaria, [10](#)  
Gammarus\_azoxistrobine\_1d\_Rosch2017,  
[11](#)  
Internal\_Sialis\_lutaria, [11](#)  
Male\_Gammarus\_Merged, [12](#)  
Male\_Gammarus\_seanine\_growth, [12](#)  
Male\_Gammarus\_Single, [13](#)  
Oncorhynchus\_two, [16](#)  
.fonte, [3](#)  
.index\_col\_exposure, [4](#)  
.index\_col\_metabolite, [4](#)  
.is\_equal\_rmInf, [5](#)  
  
bioacc\_metric, [5](#)  
  
Chiro\_Creuzot, [6](#)  
Chironomus\_benzoapyrene, [6](#)  
corrMatrix, [7](#)  
corrPlot, [7](#)  
  
df\_ppc, [8](#)  
df\_PriorPost, [9](#)  
  
equations, [9](#)  
exposure\_names, [10](#)  
Exposure\_Sialis\_lutaria, [10](#)  
  
fitTK, [10](#)  
  
Gammarus\_azoxistrobine\_1d\_Rosch2017,  
[11](#)  
  
Internal\_Sialis\_lutaria, [11](#)  
  
Male\_Gammarus\_Merged, [12](#)  
Male\_Gammarus\_seanine\_growth, [12](#)  
Male\_Gammarus\_Single, [13](#)  
mcmcTraces, [14](#)  
  
modelData, [14](#)  
modelData\_ode, [15](#)  
  
Oncorhynchus\_two, [16](#)  
  
plot.bioaccMetric, [16](#)  
plot.fitTK, [17](#)  
plot.predictTK, [17](#)  
plot\_exposure, [18](#)  
plot\_PriorPost, [18](#)  
ppc (df\_ppc), [8](#)  
predict.fitTK, [19](#)  
predict\_manual (predict.fitTK), [19](#)  
psrf, [20](#)  
  
quantile\_table, [20](#)  
  
rbioacc (rbioacc-package), [3](#)  
rbioacc-package, [3](#)  
  
t95, [21](#)  
  
waic, [21](#)