

# Package ‘rbioacc’

July 23, 2025

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

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

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

**License** MIT + file LICENSE

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**RoxygenNote** 7.3.1

**Biarch** true

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**VignetteBuilder** knitr

**NeedsCompilation** yes

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rbioacc-package      *The 'rbioacc' package.*

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## Description

A DESCRIPTION OF THE PACKAGE

## Author(s)

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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**

<code>df</code>	A data frame to pivot.
<code>names_to</code>	A string specifying the name of the column to create from the data stored in the column names of <code>df</code> .
<code>values_to</code>	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**

<code>data_frame</code>	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	<i>Data on Chironomus with several exposure routes.</i>
---------------	---

---

**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

*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  $\mu\text{g.mL}^{-1}$  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 *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. 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, 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	<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, ...)

## 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 original data of the fit object x

**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(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	<i>Prediction function using fitTK object</i>
---------------	---

---

**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.

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

**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	<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

---

replace_	<i>Replace element of a vector</i>
----------	------------------------------------

---

**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	<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

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