

# Package ‘dfpk’

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**Type** Package

**Title** Bayesian Dose-Finding Designs using Pharmacokinetics (PK) for Phase I Clinical Trials

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**Description** Statistical methods involving PK measures are provided, in the dose allocation process during a Phase I clinical trials. These methods, proposed by Ursino et al, (2017) <doi:10.1002/bimj.201600084>, enter pharmacokinetics (PK) in the dose finding designs in different ways, including covariates models, dependent variable or hierarchical models. This package provides functions to generate data from several scenarios and functions to run simulations which their objective is to determine the maximum tolerated dose (MTD).

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**Depends** R (>= 3.4.0), Rcpp (>= 0.12.11), rstan (>= 2.18.1)

**Imports** ggplot2 (>= 2.0.0), dfrmc, methods, stats, graphics, grDevices, PK

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**NeedsCompilation** yes

**SystemRequirements** GNU make

**URL** <http://github.com/artemis-toumazi/dfpk>

**BugReports** <http://github.com/artemis-toumazi/dfpk/issues>

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dfpk-package	<i>Bayesian Dose-Finding Designs using Pharmacokinetics (PK) for Phase I Clinical Trials.</i>
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## Description

Statistical methods involving PK measures are provided, in the dose allocation process during a Phase I clinical trials. These methods, proposed by Ursino et al, (2017) <doi:10.1002/bimj.201600084>, enter pharmacokinetics (PK) in the dose finding designs in different ways, including covariates models, dependent variable or hierarchical models. This package provides functions to generate data from several scenarios and functions to run simulations which their objective is to determine the maximum tolerated dose (MTD).

## Details

The three main functions of the `dfpk` package are `sim.data`, `nsim` and `nextDose`, for generating PK data based on the input settings, simulating "n" clinical trials and determining the next recommended dose for an ongoing phase I clinical trial based on an enrolled patient's data, respectively. Subsequently, six dose-finding methods/models can be applied: `dtox`, `pktox`, `pkcrm`, `pkcov`, `pkpop`, and `pklogit` which each one creates a Bayesian model and fits it using **Stan**.

Since **dfpk** is based on **Stan** models, a C++ compiler is required. The program Rtools (available on <https://cran.r-project.org/bin/windows/Rtools/>) comes with a C++ compiler for Windows while on Mac, you should use Xcode. For further instructions on how to get the compilers running, see the prerequisites section on <https://github.com/stan-dev/rstan/wiki/RStan-Getting-Started>.

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## References

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <[doi:10.1002/bimj.201600084](https://doi.org/10.1002/bimj.201600084)>.

Toumazi, A., et al, (2018) `dfpk`: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <[doi:10.1016/j.cmpb.2018.01.023](https://doi.org/10.1016/j.cmpb.2018.01.023)>.

---

AUC.estim

*Estimation of the area under the curve, AUC.*

---

## Description

The `AUC.estim` function uses a compartmental method or a non-compartmental method to estimate the AUC. In the field of pharmacokinetics, the area under the curve (AUC) is the area under the curve (mathematically known as definite integral) in a plot of concentration of drug in blood plasma against time. AUC is computed as the doses over the second pharmacokinetic's parameter, the clearance (CL).

## Usage

```
AUC.estim(t, conc, dose, method = 2)
```

## Arguments

<code>t</code>	A vector of the sampling time.
<code>conc</code>	The concentration of the drug in blood plasma.
<code>dose</code>	A vector of dose levels assigned to patients.

method A string number specifying the method for calculation of AUC. Possible values are "1" for a compartmental method and "2" for non-compartmental method (default=2).

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### References

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, Biometrical Journal, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, Computer Methods and Programs in Biomedicine, <doi:10.1016/j.cmpb.2018.01.023>.

### See Also

[pk.estim](#), [nsim](#)

### Examples

```
#### A Compartmental method for calculation of AUC ####

dose = c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
conc = c(20, 30, 40, 50, 60, 70)
t = seq(0, 24, length.out=48)
auc_estimation <- AUC.estim(t, conc, dose, method = 1)
auc_estimation
```

---

dose-class	<i>An S4 class to perform parameter estimation at each step during a dose-finding trial.</i>
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### Description

An S4 class to perform parameter estimation at each step during a dose-finding trial.

### Slots

N The total number of enrolled patients.  
y A binary vector of toxicity outcomes from previous patients; 1 indicates a toxicity, 0 otherwise.  
AUCs A vector with the computed AUC values of each patient.  
doses A vector with the doses panel.  
x A vector with the dose level assigned to the patients.  
theta The toxicity threshold.

**options** a list of Stan model's options.  
**newDose** The next recommended dose (RD) level; equals to 0 if the trial has stopped, according to the stopping rules.  
**pstim** The estimated mean probabilities of toxicity.  
**pstimQ1** The 1st quartile of estimated probability of toxicity.  
**pstimQ3** The 3rd quartile of estimated probability of toxicity.  
**parameters** The Stan model's estimated parameters.  
**model** A character string to specify the selected dose-finding model. See for details [dtox](#), [pkcov](#), [pkcrm](#), [pktox](#), [pkpop](#), [pklogit](#).

---

dosefinding-class      *An S4 class to represent a dosefinding results.*

---

## Description

An S4 class to represent a dosefinding results.

## Slots

**pid** The patient's ID provided in the study.  
**N** The total sample size per trial.  
**time** The sampling time points.  
**doses** A vector with the doses panel.  
**conc** The estimated concentration values for each patient at each dose.  
**p0** The skeleton of CRM for [pkcrm](#); defaults to NULL.  
**L** The AUC threshold to be set before starting the trial for [pkcrm](#); defaults to NULL.  
**nchains** The number of chains for the Stan model.  
**niter** The number of iterations for the Stan model.  
**nadapt** The number of warmup iterations for the Stan model.  
**newDose** The next maximum tolerated dose (MTD) if TR=1 otherwise the percentage of MTD selection for each dose level after all trials starting from dose 0; equals to 0 if the trial has stopped before the end, according to the stopping rules.  
**MTD** A vector containing the next maximum tolerated doses (MTD) of each trial (TR); equals to 0 if the trial has stopped before the end, according to the stopping rules.  
**MtD** The final next maximum tolerated (MTD) dose after all the trials.  
**theta** The toxicity target.  
**doseLevels** A vector of dose levels assigned to patients in the trial.  
**toxicity** The estimated toxicity outcome.  
**AUCs** A vector with the computed AUC values of each patient.  
**TR** The total number of trials to be simulated.

preal The prior toxicity probabilities.  
 pstim The estimated mean probabilities of toxicity.  
 pstimQ1 The 1st quartile of estimated probability of toxicity.  
 pstimQ3 The 3rd quartile of estimated probability of toxicity.  
 model A character string to specify the selected dose-finding model. See for details [dtox](#), [pkcov](#), [pkcrm](#), [pktox](#), [pkpop](#), [pklogit](#)..  
 seed The seed of the random number generator that is used at the beginning of each trial.

---

dtox *Dose finding method DTOX.*

---

### Description

The DTOX model enables us to estimate posterior probability of toxicity  $p_T$  versus dose directly. The dose-toxicity model is given by:

$$p_T(d_k, \boldsymbol{\beta}) = \Phi(-\beta_0 + \beta_1 \log(d_k))$$

where  $\beta_q \sim U(l_q, u_q) \forall q = 0, 1$  and

$$beta0mean = c(l_0, u_0),$$

$$beta1mean = c(l_1, u_1)$$

where default choices are  $beta0mean = c(0, 16.71)$  and  $beta1mean = c(0, 6.43)$ . So the default choices for model's priors are given by

$$betapriors = c(l_0 = 0, u_0 = 16.71, l_1 = 0, u_1 = 6.43)$$

Finally, the DTOX model has the following stopping rule in toxicity: if

$$P(p_T(dose) > theta) > prob$$

then, no dose is suggested and the trial is stopped.

### Usage

```

dtox(y, doses, x, theta, prob = 0.9, options=list(nchains = 4, niter = 4000,
nadapt = 0.8), betapriors = c(0, 16.71, 0, 6.43), thetaL = NULL,
auc = NULL, deltaAUC = NULL, p0 = NULL, L = NULL, CI = TRUE)

```

**Arguments**

y	A binary vector of patient's toxicity outcomes; TRUE indicates a toxicity, FALSE otherwise.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity target.
prob	The threshold of the posterior probability of toxicity for the stopping rule; defaults to 0.9.
betapriors	A vector with the value for the prior distribution of the regression parameters in the model; defaults to <code>betapriors = c(beta0mean, beta1mean)</code> , where <code>beta0mean = c(0, 16.71)</code> and <code>beta1mean = c(0, 6.43)</code> .
options	A list with the Stan model's options; the number of chains, how many iterations for each chain and the number of warmup iterations; defaults to <code>options = list(nchains = 4, niter = 4000, nadapt = 0.8)</code> .
auc	A vector with the computed AUC values of each patient for <code>pktox</code> , <code>pkcrm</code> , <code>pklogit</code> and <code>pkpop</code> ; defaults to NULL.
deltaAUC	The difference between computed individual AUC and the AUC of the population at the same dose level (defined as an average); argument for <code>pkcov</code> ; defaults to NULL.
p0	The skeleton of CRM for <code>pkcrm</code> ; defaults to NULL (must be defined only in the PKCRM model).
L	The AUC threshold to be set before starting the trial for <code>pklogit</code> , <code>pkcrm</code> and <code>pktox</code> ; defaults to NULL (must be defined only in the PKCRM model).
thetaL	A second threshold of AUC; must be defined only in the PKCRM model.
CI	A logical constant indicating the estimated 95% credible interval; defaults to TRUE.

**Value**

A list is returned, consisting of determination of the next recommended dose and estimations of the model. Objects generated by `dtox` contain at least the following components:

newDose	The next maximum tolerated dose (MTD); equals to "NA" if the trial has stopped before the end, according to the stopping rules.
pstim	The mean values of estimated probabilities of toxicity.
p_sum	The summary of the estimated probabilities of toxicity if <code>CI = TRUE</code> , otherwise is NULL.
parameters	The estimated model's parameters.

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## References

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

## See Also

[sim.data](#), [nsim](#), [nextDose](#)

## Examples

```
## Not run:
doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
theta <- 0.2
options <- list(nchains = 2, niter = 4000, nadapt = 0.8)
x <- c(1, 2, 3, 4, 5, 6)
y <- c(FALSE, FALSE, FALSE, FALSE, TRUE, FALSE)

res <- dtox(y, doses, x, theta, options = options)

## End(Not run)
```

---

invlogit

*Inverse logistic functions.*

---

## Description

Inverse-logit function, transforms continuous values to the range (0, 1)

## Usage

```
invlogit(x)
```

## Arguments

x                    A vector of continuous values

## Details

The Inverse-logit function defined as:  $\text{logit}^{-1}(x) = e^x / (1 + e^x)$  transforms continuous values to the range (0, 1), which is necessary, since probabilities must be between 0 and 1 and maps from the linear predictor to the probabilities.

## Value

A vector of estimated probabilities



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---

nextDose	<i>Next dose determination of a phase I clinical trial.</i>
----------	---

---

**Description**

nextDose is used to perform parameter estimation at each step during a dose-finding trial. Determines the next or recommended dose level in a phase I clinical trial.

**Usage**

```
nextDose(model, y, AUCs, doses, x, theta, options, prob = 0.9,
  betapriors = NULL, thetaL = NULL, p0 = NULL, L = NULL,
  deltaAUC = NULL, CI = TRUE)
```

**Arguments**

model	A character string to specify the selected dose-finding model. See for details <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pkcrm</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> , <a href="#">pklogit</a> .
y	A binary vector of the toxicity outcomes from previous patients; 1 indicates a toxicity, 0 otherwise.
AUCs	A vector with the computed AUC values of each patient for <a href="#">pktox</a> , <a href="#">pkcrm</a> , <a href="#">pklogit</a> and <a href="#">pkpop</a> ; defaults to NULL.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity threshold.
options	A list with the Stan model's options.
prob	The threshold of the posterior probability of toxicity for the stopping rule in the selected model; defaults to 0.9. See for details <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pkcrm</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> , <a href="#">pklogit</a> .
betapriors	A vector with the value for the prior distribution of the regression parameters in the model; defaults to NULL.
thetaL	A second threshold of AUC in the <a href="#">pkcrm</a> model; defaults to theta in the PKCRM model and NULL for the models <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> and <a href="#">pklogit</a> .
p0	The skeleton of CRM for <a href="#">pkcrm</a> ; defaults to NULL.
L	The AUC threshold to be set before starting the trial for <a href="#">pkcrm</a> ; defaults to NULL.
deltaAUC	A vector of the difference between computed individual AUC and the AUC of the population at the same dose level (defined as an average); argument for <a href="#">pkcov</a> ; defaults to NULL.
CI	A logical constant indicating the estimated 95% credible interval; defaults to TRUE.

**Value**

An object of class "dose" is returned, consisting of determination of the next recommended dose and estimations. Objects generated by nextDose contain at least the following components:

N	The total number of enrolled patients.
y	A binary vector of toxicity outcomes from previous patients; 1 indicates a toxicity, 0 otherwise.
AUCs	A vector with the computed AUC values of each patient.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity threshold.
options	List with the Stan model's options.
newDose	The next recommended dose (RD) level; equals to 0 if the trial has stopped, according to the stopping rules.
pstim	The mean values of the estimated probabilities of toxicity.
pstimQ1	The 1st quartile of the estimated probabilities of toxicity if CI = TRUE, otherwise is NULL.
pstimQ3	The 3rd quartile of the estimated probabilities of toxicity if CI = TRUE, otherwise is NULL.
parameters	The estimated model's parameters.
model	A character string to specify the selected dose-finding model. See for details <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pkcrm</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> , <a href="#">pklogit</a> .

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**References**

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

**See Also**

[nsim](#)

## Examples

```
## Not run:
doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
theta <- 0.2
options <- list(nchains = 4, niter = 4000, nadapt = 0.9)
AUCs <- c(1.208339, 5.506040, 6.879835, 3.307928, 3.642430,
          10.271291, 3.885522, 3.086622, 2.537158, 5.525917,
          8.522176, 4.642741, 11.048531, 10.246976, 5.226807)
x <- c(1, 2, 3, 4, 5, 6, 4, 4, 4, 5, 5, 4, 4, 5, 5)
y <- c(0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0)
nextD <- nextDose(model = "pktox", y=y, AUCs=AUCs, doses=doses,
                  x=x, theta=theta, options=options)

## End(Not run)
```

---

nsim	<i>Simulate a single or n prospective clinical trial(s) using the PK measure in the dose finding designs.</i>
------	---

---

## Description

nsim is used to simulate a single or "n" prospective clinical trial(s) using the PK data and then link them to toxicity under a specified dose-toxicity configuration. The objective is to determine the maximum tolerated dose (MTD).

## Usage

```
nsim(doses, N, cohort, icon, theta, model, simulatedData, TR, prob = 0.9, AUCmethod = 2,
     options = list(nchains = 4, niter = 4000, nadapt = 0.8), betapriors = NULL,
     thetaL=NULL, p0 = 0, L = 0, CI = FALSE, seed = 190591)
```

## Arguments

doses	A vector with the doses panel.
N	The total sample size per trial.
cohort	The cohort size in the trial.
icon	A vector containing the index of real blood sampling.
theta	The toxicity threshold.
model	A character string to specify the selected dose-finding model. See for details <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pkcrm</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> , <a href="#">pklogit</a> .
simulatedData	A list for each trial containing the simulated datasets; a "scen" object. See for details <a href="#">sim.data</a> .
TR	The total number of trials to be simulated.

prob	The threshold of the posterior probability of toxicity for the stopping rule in the selected model; defaults to 0.9. See for details <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pkcrm</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> , <a href="#">pklogit</a> .
AUCmethod	A string number specifying the estimation method for AUC. Valid choices are "1" for a "compartmental method" and "2" for non-compartmental method; defaults to 2.
options	A list with the Stan model's options; the number of chains, how many iterations for each chain and the number of warmup iterations; defaults to options = list(nchains = 4, niter = 4000, nadapt = 0.8)
betapriors	A vector with the value for the prior distribution of the regression parameters in the selected model; defaults to NULL.
thetaL	A second threshold of AUC in the <a href="#">pkcrm</a> model; defaults to theta in the PKCRM model and NULL for the models <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> and <a href="#">pklogit</a> .
p0	The skeleton of CRM for <a href="#">pkcrm</a> ; defaults to NULL.
L	The AUC threshold to be set before starting the trial for <a href="#">pkcrm</a> ; defaults to NULL.
CI	A logical constant indicating the estimated 95% credible interval; defaults to FALSE.
seed	The seed of the random number generator that is used at the beginning of each trial; defaults to 190591.

### Value

An object of class "dosefinding" is returned, consisting of determination of the next recommended dose and estimations. Objects generated by nsim contain at least the following components:

pid	The patient's ID during the trial.
N	The total sample size per trial.
time	The sampling time points.
doses	A vector with the doses panel.
conc	The estimated concentration values for each patient at each dose.
nchains	The number of chains in the Stan model.
niter	The number of iterations for each chain in the Stan model.
nadapt	The number of warmup iterations.
newDose	The next maximum tolerated dose (MTD) if TR=1 otherwise the percentage of MTD selection for each dose level after all trials starting from dose 0; equals to 0 if the TR=1 has stopped before the end, according to the stopping rules.
MTD	A vector containing the next maximum tolerated doses (MTD) of each trial (TR); equals to 0 if the trial has stopped before the end, according to the stopping rules.
theta	The toxicity threshold.
doseLevels	A vector of dose levels assigned to patients in the trial.
toxicity	The estimated toxicity outcome.

AUCs	A vector with the computed AUC values of each patient.
TR	The total number of trials to be simulated.
preal	The prior toxicity probabilities.
pstim	The mean values of the estimated probabilities of toxicity.
pstimQ1	The 1st quartile of the estimated probabilities of toxicity if CI = TRUE, otherwise is NULL.
pstimQ3	The 3rd quartile of the estimated probabilities of toxicity if CI = TRUE, otherwise is NULL.
model	A character string to specify the selected dose-finding model. See for details <a href="#">dtox</a> , <a href="#">pkcov</a> , <a href="#">pkcrm</a> , <a href="#">pktox</a> , <a href="#">pkpop</a> , <a href="#">pklogit</a> .
seed	The seed of the random number generator that is used at the beginning of each trial.

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### References

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

### See Also

[sim.data](#)

### Examples

```
## Not run:
  TR = 10                                # Total number of simulations
  N = 30
  limitTox <- 10.96
  PKparameters <- c(2, 10, 100)          # PK parameters ka,CL,V
  omegaIIV <- 0.7
  omegaAlpha <- 0
  doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
  timeSampling <- seq(0, 24, length.out=48)
  sigma <- rep(0.2, length(timeSampling))

  gen.scen <- sim.data(PKparameters,omegaIIV,omegaAlpha,sigma,doses,
                      limitTox,timeSampling, N, TR)

  cohort = 1
  simulatedData <- gen.scen
```

```

icon <- c(2:6, round(seq(9, 48, ((48-9)/4))))
theta <- 0.2

#####
##### Select a model #####
#####

model = "pktox"

#####
##### Run the simulation(s) #####
#####

results_sim <- nsim(doses, N, cohort, icon, theta, model, simulatedData, TR,
                    AUCmethod = 1)
results_sim

## End(Not run)

```

---

pk.estim

*The pharmacokinetic's (PK) measure of exposure.*

---

## Description

Estimation of the pharmacokinetic's (PK) measure of exposure.

## Usage

```
pk.estim(par, t, dose, conc)
```

## Arguments

par	The pharmacokinetic's parameters.
t	The time sampling.
dose	The doses levels of the drug.
conc	The concentration of the drug in blood plasma.

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## References

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

**See Also**[AUC.estim, nsim](#)**Examples**

```

par <- c(2,10,100)
conc <- c(20,30,40,50,60,70)
t <- seq(0,24,length.out=48)
dose <- c(12.59972,34.65492,44.69007,60.80685,83.68946,100.37111)
pk.estim(par,t,dose,conc)

```

pkcov

*Dose finding method PKCOV.***Description**

The PKCOV model is a modification of the method proposed by Piantadosi and Liu (1996) who suggested to use the AUC as covariate for  $p_T$ , probability of toxicity, through the logit link. Therefore, the dose-toxicity model is:

$$\text{logit}(p_T(d_k, \Delta z_{d_k}, \boldsymbol{\beta})) = -\beta_0 + \beta_1 \log(d_k) + \beta_2 \Delta z_{d_k}$$

where  $\boldsymbol{\beta} = (\beta_1, \beta_2)$ ,  $\beta_0$  is a constant with  $\beta_0 = -\text{beta0mean}$ ,

$$\beta_1 \sim U(l_1, u_1),$$

$$\beta_2 \sim U(0, 5),$$

$$\text{beta1mean} = c(l_1, u_1)$$

where default choices are  $\text{beta0mean} = -14.76$ ,  $\text{beta1mean} = c(0, 8.23)$  and  $\Delta z_{d_k}$  is the difference between the logarithm of population AUC at dose  $d_k$  and  $z$ , the logarithm of AUC of the subject at the same dose. Therefore, the default choices for model's priors are given by

$$\text{betapriors} = c(\text{beta0mean} = -14.76, l_1 = 0, u_1 = 8.23)$$

Finally, the PKCOV model has the following stopping rule in toxicity: if

$$P(p_T(\text{dose}) > \text{theta}) > \text{prob}$$

then, no dose is suggested and the trial is stopped.

**Usage**

```

pkcov(y, auc, doses, x, theta, deltaAUC, prob = 0.9, options=list(nchains = 4,
  niter = 4000, nadapt = 0.8), betapriors = c(-14.76, 0, 3.23+5),
  thetaL = NULL, p0 = NULL, L = NULL, CI =TRUE)

```

**Arguments**

y	A binary vector of patient's toxicity outcomes; TRUE indicates a toxicity, FALSE otherwise.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity target.
prob	The threshold of the posterior probability of toxicity for the stopping rule; defaults to 0.9.
betapriors	A vector with the value for the prior distribution of the regression parameters in the model; defaults to <code>betapriors = c(beta0mean, beta1mean)</code> , where <code>beta0mean = -14.76</code> and <code>beta1mean = c(0, 8.23)</code> .
options	A list with the Stan model's options; the number of chains, how many iterations for each chain and the number of warmup iterations; defaults to <code>options = list(nchains = 4, niter = 4000, nadapt = 0.8)</code> .
auc	A vector with the computed AUC values of each patient for <code>pktox</code> , <code>pkcrm</code> , <code>pklogit</code> and <code>pkpop</code> ; defaults to NULL.
deltaAUC	The difference between computed individual AUC and the AUC of the population at the same dose level (defined as an average); argument for <code>pkcov</code> ; defaults to NULL.
p0	The skeleton of CRM for <code>pkcrm</code> ; defaults to NULL (must be defined only in the PKCRM model).
L	The AUC threshold to be set before starting the trial for <code>pklogit</code> , <code>pkcrm</code> and <code>pktox</code> ; defaults to NULL (must be defined only in the PKCRM model).
thetaL	A second threshold of AUC; must be defined only in the PKCRM model.
CI	A logical constant indicating the estimated 95% credible interval; defaults to TRUE.

**Value**

A list is returned, consisting of determination of the next recommended dose and estimations of the model. Objects generated by `pkcov` contain at least the following components:

newDose	The next maximum tolerated dose (MTD); equals to "NA" if the trial has stopped before the end, according to the stopping rules.
pstim	The mean values of estimated probabilities of toxicity.
p_sum	The summary of the estimated probabilities of toxicity if <code>CI = TRUE</code> , otherwise is NULL.
parameters	The estimated model's parameters.

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## References

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Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

Piantadosi, S. and Liu, G. (1996) Improved designs for dose escalation studies using pharmacokinetic measurements. *Statistics in Medicine*, 15 (15), 1605-1618.

## See Also

[sim.data](#), [nsim](#), [nextDose](#)

## Examples

```
## Not run:
doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
theta <- 0.2
AUCs <- c(0.43, 1.4, 5.98, 7.98, 11.90, 3.45)
x <- c(1,2,3,4,5,6)
y <- c(FALSE, FALSE, FALSE, FALSE, TRUE, FALSE)
deltaAUC <- c(0, 1.3, -0.34, -2.7, 0.39, -2.45)
options <- list(nchains = 2, niter = 4000, nadapt = 0.8)
res <- pkcov(y, AUCs, doses, x, theta, deltaAUC, options=options)

## End(Not run)
```

---

pkcrm

*Dose finding method PKCRM.*

---

## Description

The PKCRM model is a combination of PKLIM as given below:

$$z_i | \beta, \nu \sim N(\beta_0 + \beta_1 \log d_i, \nu^2)$$

where  $\beta = (\beta_0, \beta_1)$  are the regression parameters and  $\nu$  is the standard deviation, and the Continual Reassessment Method's (CRM) model:

$$p_T(d_k, \beta) = d_k^\beta(CRM)$$

The default choices of the priors are:

$$\beta | \nu \sim N(m, \nu * beta0),$$

$$\nu \sim Beta(1, 1),$$

$$m = (-\log(CL_{pop}), 1)$$

where  $Cl_{pop}$  is the population clearance. where default choices are  $Cl_{pop} = 10$  and  $\beta_0 = 10000$ . Therefore, the default choices for model's priors are given by

$$betapriors = c(Cl_{pop} = 10, \beta_0 = 10000)$$

For the CRM model:

Skeleton CRM = (0.01, 0.05, 0.1, 0.2, 0.35, 0.45) and

$$\beta \sim N(0, 1.34)$$

Finally, the PKCRM model has the following stopping rule in toxicity: if

$$P(p_T(dose) > \theta) > prob$$

then, no dose is suggested and the trial is stopped.

### Usage

```
pkcrm(y, auc, doses, x, theta, p0, L, prob = 0.9, options = list(nchains = 4,
  niter = 4000, nadapt = 0.8), betapriors = c(10, 10000), thetaL=NULL,
  deltaAUC = NULL, CI = TRUE)
```

### Arguments

y	A binary vector of patient's toxicity outcomes; TRUE indicates a toxicity, FALSE otherwise.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity target.
prob	The threshold of the posterior probability of toxicity for the stopping rule; defaults to 0.9.
betapriors	A vector with the value for the prior distribution of the regression parameters in the model; defaults to $betapriors = c(Cl_{pop}, \beta_0)$ , where $Cl_{pop} = 10$ and $\beta_0 = 10000$ .
options	A list with the Stan model's options; the number of chains, how many iterations for each chain and the number of warmup iterations; defaults to $options = list(nchains = 4, niter = 4000, nadapt = 0.8)$ .
auc	A vector with the computed AUC values of each patient for pktox, pkcrm, pklogit and pkpop; defaults to NULL.
deltaAUC	The difference between computed individual AUC and the AUC of the population at the same dose level (defined as an average); argument for pkcov; defaults to NULL.
p0	The skeleton of CRM for pkcrm; defaults to NULL (must be defined only in the PKCRM model).
L	The AUC threshold to be set before starting the trial for pklogit, pkcrm and pktox; defaults to NULL (must be defined only in the PKCRM model).
thetaL	A second threshold of AUC; must be defined only in the PKCRM model.
CI	A logical constant indicating the estimated 95% credible interval; defaults to TRUE.

**Value**

A list is returned, consisting of determination of the next recommended dose and estimations of the model. Objects generated by pkcrm contain at least the following components:

newDose	The next maximum tolerated dose (MTD); equals to "NA" if the trial has stopped before the end, according to the stopping rules.
pstim	The mean values of estimated probabilities of toxicity.
p_sum	The summary of the estimated probabilities of toxicity if CI = TRUE, otherwise is NULL.
parameters	The estimated model's parameters.

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Patterson, S., Francis, S., Ireson, M., Webber, D., and Whitehead, J. (1999) A novel bayesian decision procedure for early-phase dose-finding studies. *Journal of Biopharmaceutical Statistics*, 9 (4), 583-597.

Whitehead, J., Patterson, S., Webber, D., Francis, S., and Zhou, Y. (2001) Easy-to-implement bayesian methods for dose-escalation studies in healthy volunteers. *Biostatistics*, 2 (1), 47-61.

**See Also**

[sim.data](#), [nsim](#), [nextDose](#)

**Examples**

```
## Not run:
p0 <- c(.01, .05, .1, .2, .35, 0.45)      # Skeleton of CRM
L <- log(15.09)                          # Threshold set
doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
theta <- 0.2
options <- list(nchains = 2, niter = 4000, nadapt = 0.8)
AUCs <- c(0.43, 1.4, 5.98, 7.98, 11.90, 3.45)
x <- c(1,2,3,4,5,6)
y <- c(FALSE, FALSE, FALSE, FALSE, TRUE, FALSE)

res <- pkcrm(y, AUCs, doses, x, theta, p0, L, options = options)

## End(Not run)
```

---

 pklogit

*Dose finding method PKLOGIT.*


---

### Description

The PKLOGIT model, inspired by Whitehead et al. (2007), uses  $z_i$  instead of dose  $d_i$  as a covariate in a logistic regression model for  $p_T$ . Therefore, we have that:

$$\text{logit}(p_T(z, \boldsymbol{\beta})) = -\beta_2 + \beta_3 z$$

with a bivariate Uniform distribution as prior distribution for  $\boldsymbol{\beta} = (\beta_2, \beta_3)$  and the hierarchical model of PK-toxicity for  $z_i$  given as:

$$z_i | \boldsymbol{\beta}, \nu \sim N(\beta_0 + \beta_1 \log d_i, \nu^2)$$

where  $\boldsymbol{\beta} = (\beta_0, \beta_1)$  are the regression parameters and  $\nu$  is the standard deviation.

The default choices of the priors are:

$$\boldsymbol{\beta} | \nu \sim N(m, \nu * \text{beta0}),$$

$$\nu \sim \text{Beta}(1, 1),$$

$$m = (-\log(CL_{pop}), 1),$$

where  $CL_{pop}$  is the population clearance.

$$\beta_2 \sim U(0, \text{beta2mean}),$$

$$\beta_3 \sim U(0, \text{beta3mean})$$

where default choices are  $CL_{pop} = 10$ ,  $\text{beta0} = 10000$ ,  $\text{beta2mean} = 20$  and  $\text{beta3mean} = 10$ . Therefore, the default choices for model's priors are given by

$$\text{betapriors} = c(CL_{pop} = 10, \text{beta0} = 10000, \text{beta2mean} = 20, \text{beta3mean} = 10)$$

Finally, the PKLOGIT model has the following stopping rule in toxicity: if

$$P(p_T(\text{dose}) > \text{theta}) > \text{prob}$$

then, no dose is suggested and the trial is stopped.

### Usage

```
pklogit(y, auc, doses, x, theta, prob = 0.9, options = list(nchains = 4, niter = 4000,
  nadapt = 0.8), betapriors = c(10, 10000, 20, 10), thetaL = NULL,
  p0=NULL, L=NULL, deltaAUC=NULL, CI = TRUE)
```

**Arguments**

y	A binary vector of patient's toxicity outcomes; TRUE indicates a toxicity, FALSE otherwise.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity target.
prob	The threshold of the posterior probability of toxicity for the stopping rule; defaults to 0.9.
betapriors	A vector with the values for the prior distribution of the regression parameters in the model; defaults to betapriors = c( $Cl_{pop}$ , beta0, beta2mean, beta3mean), where $Cl_{pop} = 10$ , beta0 = 10000, beta2mean = 20 and beta3mean = 10.
options	A list with the Stan model's options; the number of chains, how many iterations for each chain and the number of warmup iterations; defaults to options = list(nchains = 4, niter = 4000, nadapt = 0.8).
auc	A vector with the computed AUC values of each patient for pktox, pkcrm, pklogit and pkpop; defaults to NULL.
deltaAUC	The difference between computed individual AUC and the AUC of the population at the same dose level (defined as an average); argument for pkcov; defaults to NULL.
p0	The skeleton of CRM for pkcrm; defaults to NULL (must be defined only in the PKCRM model).
L	The AUC threshold to be set before starting the trial for pklogit, pkcrm and pktox; defaults to NULL (must be defined only in the PKCRM model).
thetaL	A second threshold of AUC; must be defined only in the PKCRM model.
CI	A logical constant indicating the estimated 95% credible interval; defaults to TRUE.

**Value**

A list is returned, consisting of determination of the next recommended dose and estimations of the model. Objects generated by pklogit contain at least the following components:

newDose	The next maximum tolerated dose (MTD); equals to "NA" if the trial has stopped before the end, according to the stopping rules.
pstim	The mean values of estimated probabilities of toxicity.
p_sum	The summary of the estimated probabilities of toxicity if CI = TRUE, otherwise is NULL.
parameters	The estimated model's parameters.

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## References

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Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

Whitehead, J., Zhou, Y., Hampson, L., Ledent, E., and Pereira, A. (2007) A bayesian approach for dose-escalation in a phase i clinical trial incorporating pharmacodynamic endpoints. *Journal of Biopharmaceutical Statistics*, 17 (6), 1117-1129.

## See Also

[sim.data](#), [nsim](#), [nextDose](#)

## Examples

```
## Not run:
doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
theta <- 0.2
options <- list(nchains = 2, niter = 4000, nadapt = 0.8)
AUCs <- c(0.43, 1.4, 5.98, 7.98, 11.90, 3.45)
x <- c(1, 2, 3, 4, 5, 6)
y <- c(FALSE, FALSE, FALSE, FALSE, TRUE, FALSE)

res <- pklogit(y, AUCs, doses, x, theta, options = options)

## End(Not run)
```

---

pkpop

*Dose finding method PKPOP.*

---

## Description

The PKPOP model is a variation of the PKLOGIT model which replaced AUCs ( $z_j$ ) with AUC of the population ( $z_{k,pop}$ ), where  $z_{k,pop}$  is the mean value of the logarithm of AUC at dose k, predicted by the hierarchical model:

$$z_i | \boldsymbol{\beta}, \nu \sim N(\beta_0 + \beta_1 \log d_i, \nu^2)$$

where  $\boldsymbol{\beta} = (\beta_0, \beta_1)$  are the regression parameters and  $\nu$  is the standard deviation. and the logistic regression model:

$$\text{logit}(p_T(z_{k,pop}, \boldsymbol{\beta})) = -\beta_3 + \beta_4 z_{k,pop}$$

with a bivariate Uniform distribution as prior distribution for the parameters  $\boldsymbol{\beta} = (\beta_3, \beta_4)$ .

The default choices of the priors are:

$$\boldsymbol{\beta} | \nu \sim N(m, \nu * \text{beta0}),$$

$$\nu \sim \text{Beta}(1, 1),$$

$$m = (-\log(CL_{pop}), 1),$$

where  $Cl_{pop}$  is the population clearance.

$$\beta_3 \sim U(0, beta3mean),$$

$$\beta_4 \sim U(0, beta4mean)$$

where default choices are  $Cl_{pop} = 10$ ,  $beta0 = 10000$ ,  $beta3mean = 10$  and  $beta4mean = 5$ . Therefore, the default choices for model's priors are given by

$$betapriors = c(Cl_{pop} = 10, beta0 = 10000, beta3mean = 10, beta4mean = 5)$$

Finally, the PKPOP model has the following stopping rule in toxicity: if

$$P(p_T(dose) > theta) > prob$$

then, no dose is suggested and the trial is stopped.

### Usage

```
pkpop(y, auc, doses, x, theta, prob = 0.9, options = list(nchains = 4, niter = 4000,
  nadapt = 0.8), betapriors = c(10, 10000, 10, 5), thetaL = NULL, p0=NULL,
  L=NULL, deltaAUC=NULL, CI = TRUE)
```

### Arguments

y	A binary vector of patient's toxicity outcomes; TRUE indicates a toxicity, FALSE otherwise.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity target.
prob	The threshold of the posterior probability of toxicity for the stopping rule; defaults to 0.9.
betapriors	A vector with the value for the prior distribution of the regression parameters in the model; defaults to $betapriors = c(Cl_{pop}, beta0, beta3mean, beta4mean)$ , where $Cl_{pop} = 10$ , $beta0 = 10000$ , $beta3mean = 10$ and $beta4mean = 5$ .
options	A list with the Stan model's options; the number of chains, how many iterations for each chain and the number of warmup iterations; defaults to $options = list(nchains = 4, niter = 4000, nadapt = 0.8)$ .
auc	A vector with the computed AUC values of each patient for pktox, pkcrm, pklogit and pkpop; defaults to NULL.
deltaAUC	The difference between computed individual AUC and the AUC of the population at the same dose level (defined as an average); argument for pkcov; defaults to NULL.
p0	The skeleton of CRM for pkcrm; defaults to NULL (must be defined only in the PKCRM model).
L	The AUC threshold to be set before starting the trial for pklogit, pkcrm and pktox; defaults to NULL (must be defined only in the PKCRM model).
thetaL	A second threshold of AUC; must be defined only in the PKCRM model.
CI	A logical constant indicating the estimated 95% credible interval; defaults to TRUE.

**Value**

A list is returned, consisting of determination of the next recommended dose and estimations of the model. Objects generated by `pkpop` contain at least the following components:

<code>newDose</code>	The next maximum tolerated dose (MTD); equals to "NA" if the trial has stopped before the end, according to the stopping rules.
<code>pstim</code>	The mean values of estimated probabilities of toxicity.
<code>p_sum</code>	The summary of the estimated probabilities of toxicity if <code>CI = TRUE</code> , otherwise is <code>NULL</code> .
<code>parameters</code>	The estimated model's parameters.

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Toumazi, A., et al, (2018) `dfpk`: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

Patterson, S., Francis, S., Ireson, M., Webber, D., and Whitehead, J. (1999) A novel bayesian decision procedure for early-phase dose-finding studies. *Journal of Biopharmaceutical Statistics*, 9 (4), 583-597.

Whitehead, J., Patterson, S., Webber, D., Francis, S., and Zhou, Y. (2001) Easy-to-implement bayesian methods for dose-escalation studies in healthy volunteers. *Biostatistics*, 2 (1), 47-61.

Whitehead, J., Zhou, Y., Hampson, L., Ledent, E., and Pereira, A. (2007) A bayesian approach for dose-escalation in a phase i clinical trial incorporating pharmacodynamic endpoints. *Journal of Biopharmaceutical Statistics*, 17 (6), 1117-1129.

**See Also**

[pklogit](#), [sim.data](#), [nsim](#), [nextDose](#)

**Examples**

```
## Not run:
doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
theta <- 0.2      # choice
options <- list(nchains = 2, niter = 4000, nadapt = 0.8)
AUCs <- c(0.43, 1.4, 5.98, 7.98, 11.90, 3.45)
x <- c(1, 2, 3, 4, 5, 6)
y <- c(FALSE, FALSE, FALSE, FALSE, TRUE, FALSE)

res <- pkpop(y, AUCs, doses, x, theta, options = options)

## End(Not run)
```



pktox

*Dose finding method PKTOX.***Description**

The PKTOX model is essentially the PKLOGIT model with a probit regression model replacing the logistic regression, that is given by:

$$p_T(z, \beta) = \Phi(-\beta_2 + \beta_3 z)$$

with a bivariate Uniform distribution as prior distribution for the parameters  $\beta = (\beta_2, \beta_3)$  and the hierarchical model of PK-toxicity for  $z_i$  given as:

$$z_i | \beta, \nu \sim N(\beta_0 + \beta_1 \log d_i, \nu^2)$$

where  $\beta = (\beta_0, \beta_1)$  are the regression parameters and  $\nu$  is the standard deviation.

The default choices of the priors are:

$$\beta | \nu \sim N(m, \nu * \text{beta0}),$$

$$\nu \sim \text{Beta}(1, 1),$$

$$m = (-\log(CL_{pop}), 1),$$

where  $CL_{pop}$  is the population clearance.

$$\beta_2 \sim U(0, \text{beta2mean}),$$

$$\beta_3 \sim U(0, \text{beta3mean})$$

where default choices are  $CL_{pop} = 10$ ,  $\text{beta0} = 10000$ ,  $\text{beta2mean} = 20$  and  $\text{beta3mean} = 10$ . Therefore, the default choices for model's priors are given by

$$\text{betapriors} = c(CL_{pop} = 10, \text{beta0} = 10000, \text{beta2mean} = 20, \text{beta3mean} = 10)$$

Finally, the PKTOX model has the following stopping rule in toxicity: if

$$P(p_T(\text{dose}) > \text{theta}) > \text{prob}$$

then, no dose is suggested and the trial is stopped.

**Usage**

```
pktox(y, auc, doses, x, theta, prob = 0.9, options = list(nchains = 4, niter = 4000,
  nadapt = 0.8), betapriors = c(10, 10000, 20, 10), thetaL = NULL,
  p0=NULL, L=NULL, deltaAUC=NULL, CI = TRUE)
```

**Arguments**

y	A binary vector of patient's toxicity outcomes; TRUE indicates a toxicity, FALSE otherwise.
doses	A vector with the doses panel.
x	A vector with the dose level assigned to the patients.
theta	The toxicity target.
prob	The threshold of the posterior probability of toxicity for the stopping rule; defaults to 0.9.
betapriors	A vector with the value for the prior distribution of the regression parameters in the model; defaults to <code>betapriors = c(Cl<sub>pop</sub>, beta0, beta2mean, beta3mean)</code> , where $Cl_{pop} = 10$ , $\beta_0 = 10000$ , $\beta_{2mean} = 20$ and $\beta_{3mean} = 10$ .
options	A list with the Stan model's options; the number of chains, how many iterations for each chain and the number of warmup iterations; defaults to <code>options = list(nchains = 4, niter = 4000, nadapt = 0.8)</code> .
auc	A vector with the computed AUC values of each patient for <code>pktox</code> , <code>pkcrm</code> , <code>pklogit</code> and <code>pkpop</code> ; defaults to NULL.
deltaAUC	The difference between computed individual AUC and the AUC of the population at the same dose level (defined as an average); argument for <code>pkcov</code> ; defaults to NULL.
p0	The skeleton of CRM for <code>pkcrm</code> ; defaults to NULL (must be defined only in the PKCRM model).
L	The AUC threshold to be set before starting the trial for <code>pklogit</code> , <code>pkcrm</code> and <code>pktox</code> ; defaults to NULL (must be defined only in the PKCRM model).
thetaL	A second threshold of AUC; must be defined only in the PKCRM model.
CI	A logical constant indicating the estimated 95% credible interval; defaults to TRUE.

**Value**

A list is returned, consisting of determination of the next recommended dose and estimations of the model. Objects generated by `pktox` contain at least the following components:

newDose	The next maximum tolerated dose (MTD); equals to "NA" if the trial has stopped before the end, according to the stopping rules.
pstim	The mean values of estimated probabilities of toxicity.
p_sum	The summary of the estimated probabilities of toxicity if <code>CI = TRUE</code> , otherwise is NULL.
parameters	The estimated model's parameters.

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Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

Whitehead, J., Zhou, Y., Hampson, L., Ledent, E., and Pereira, A. (2007) A bayesian approach for dose-escalation in a phase i clinical trial incorporating pharmacodynamic endpoints. *Journal of Biopharmaceutical Statistics*, 17 (6), 1117-1129.

**See Also**

[pklogit](#), [sim.data](#), [nsim](#), [nextDose](#)

**Examples**

```
## Not run:
doses <- c(12.59972, 34.65492, 44.69007, 60.80685, 83.68946, 100.37111)
theta <- 0.2
options <- list(nchains = 2, niter = 4000, nadapt = 0.8)
AUCs <- c(0.43, 1.4, 5.98, 7.98, 11.90, 3.45)
x <- c(1,2,3,4,5,6)
y <- c(FALSE, FALSE, FALSE, FALSE, TRUE, FALSE)

res <- pktox(y, AUCs, doses, x, theta, options = options)

## End(Not run)
```

---

plot,dose,missing-method

*The graphical representation of dose escalation for each patient in the trial.*

---

**Description**

The graphical representation of dose escalation for each patient in the trial.

**Usage**

```
## S4 method for signature 'dose,missing'
plot(x, y = NA, ask = TRUE, CI = TRUE, ...)
```

**Arguments**

x                    a "dose" object.  
y                    the "y" argument is not used in the plot-method for "dose" object.  
ask                  Choose plot or not; defaults to TRUE.

CI            Indicate if the "dose" object includes the 95% credible interval for the posterior dose response plot; defaults to TRUE.

...           other arguments to the `plot.default` function can be passed here.

**Author(s)**

Artemis Toumazi <artemis.toumazi@gmail.com>, Moreno Ursino <moreno.ursino@inserm.fr>, Sarah Zohar <sarah.zohar@inserm.fr>

**References**

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) *dfpk*: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

---

`plot,dosefinding,missing-method`

*The graphical representation of dose-finding results.*

---

**Description**

A plot selection showing either the dose escalation allocation of the selected trial or the plot of the final posterior distributions of the probability of toxicity at each dose or the boxplot of the sampling distribution of the probability of toxicity at each dose in the end of the trial over the total number of trials.

**Usage**

```
## S4 method for signature 'dosefinding,missing'
plot(x, y = NA, TR = 1, ask = TRUE,
     CI = TRUE, ...)
```

**Arguments**

x            a "dosefinding" object.

y            the "y" argument is not used in the plot-method for "dosefinding" object.

TR           The number of the selected trial that user wants to plot; defaults to 1.

ask          Choose plot or not; defaults to TRUE.

CI           Indicate if the "dosefinding" object includes the 95% credible interval for the posterior dose response plot; defaults to TRUE.

...          other arguments to the `plot.default` function can be passed here.

**Author(s)**

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**References**

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, Biometrical Journal, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, Computer Methods and Programs in Biomedicine, <doi:10.1016/j.cmpb.2018.01.023>.

---

plot,scen,missing-method

*The graphical representation of the drug's concentration in the plasma at time t after the drug administration.*

---

**Description**

The graphical representation of the drug's concentration in the plasma at time t after the drug administration.

**Usage**

```
## S4 method for signature 'scen,missing'  
plot(x, y = NA, col = rainbow(length(x@doses)),  
     xlab = "Time (hours)", ylab = "Concentration (mg/L)",  
     main = "Pharmacokinetics: Concentration vs Time", ...)
```

**Arguments**

x	a "scen" object or a list of the selected trial from a "scen" object.
y	the "y" argument is not used in the plot-method for "scen" object.
col	the color argument to the <code>plot.default</code> function.
xlab	the label of x-axis.
ylab	the label of y-axis.
main	the title of the graph.
...	other arguments to the <code>plot.default</code> function can be passed here.

**Author(s)**

Artemis Toumazi <artemis.toumazi@gmail.com>, Moreno Ursino <moreno.ursino@inserm.fr>, Sarah Zohar <sarah.zohar@inserm.fr>

## References

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

---

scen-class

*An S4 class to represent a simulated scenarios.*

---

## Description

An S4 class to represent a simulated scenarios.

## Slots

`PKparameters` Subject's pharmacokinetic's (PK) parameters from the population distributions defined by the population mean.

`nPK` The length of the time points.

`time` The sampling time points.

`idtr` The id number of the corresponding simulated dataset.

`N` The total sample size per trial.

`doses` A vector with the doses panel.

`preal` The prior toxicity probabilities.

`limitTox` The toxicity threshold.

`omegaIIV` The inter-individual variability for the clearance and the volume of distribution.

`omegaAlpha` The patient's sensitivity parameter.

`conc` The concentration computed at the PK population values.

`concPred` The concentration values with proportional errors for each patient at each dose.

`tox` The toxicity outcome.

`tab` A summary matrix containing the sampling time points at the first row followed by `concPred`, parameters and `alphaAUC`. It used by the simulation function `nsim`.

`parameters` The simulated PK parameters of each patient.

`alphaAUC` A vector with the computed AUC values of each patient.

---

show-methods	<i>S4 Methods for Function show</i>
--------------	-------------------------------------

---

**Description**

S4 Methods for function show.

**Methods**

signature(object = "dosefinding") S4 method to store and present the dose-finding results.

signature(object = "scen") S4 method to store and present the simulated datasets.

signature(object = "dose") S4 method to store and present the next recommended dose level in an ongoing trial.

---

sim.data	<i>Generate and store PK and toxicity data.</i>
----------	---

---

**Description**

This function can be used to generate and store PK and toxicity data in order to be used for simulation according to the dose-finding model.

**Usage**

```
sim.data(PKparameters, omegaIIV, omegaAlpha, sigma, doses, limitTox,
         timeSampling, N, TR, seed=190591)
```

**Arguments**

PKparameters	Subject's pharmacokinetic's (PK) parameters from the population distributions defined by the population mean.
omegaIIV	The inter-individual variability for the clearance and the volume of distribution; possible values may be 70% or 30% in different simulated data.
omegaAlpha	The patient's sensitivity parameter.
sigma	The additive or proportional error.
doses	A vector with the doses panel.
limitTox	The toxicity threshold.
timeSampling	The sampling time points.
N	The total sample size per trial.
TR	The total number of simulated datasets.
seed	The seed of the random number generator that is used at the beginning of each trial; defaults to 190591.

**Value**

An object of class "scen" is returned, consisting of simulated PK and toxicity data. Objects generated by sim.data contain at least the following components:

PKparameters	Subject's pharmacokinetic's (PK) parameters from the population distributions defined by the population mean.
nPK	The length of the time points.
time	The sampling time points.
idtr	The id number of the corresponding simulated dataset.
N	The total sample size per trial.
doses	A vector with the doses panel.
preal	The prior toxicity probabilities.
limitTox	The toxicity threshold.
omegaIIV	The inter-individual variability for the clearance and the volume of distribution.
omegaAlpha	The patient's sensitivity parameter.
conc	The concentration computed at the PK population values.
concPred	The concentration values with proportional errors for each patient at each dose.
tox	The toxicity outcome.
parameters	The simulated PK parameters of each patient.
alphaAUC	A vector with the computed AUC values of each patient.
tab	A summary matrix containing the sampling time points at the first row followed by concPred, parameters and alphaAUC. It used by the simulation function <a href="#">nsim</a> .

**Author(s)**

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**References**

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, Biometrical Journal, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, Computer Methods and Programs in Biomedicine, <doi:10.1016/j.cmpb.2018.01.023>.

**See Also**

[nsim](#)



**Examples**

```

TR = 10
N = 30
limitTox <- 10.96
PKparameters <- c(2,10,100)      # PK parameters ka,CL,V
omegaIIV <- 0.7                  # Inter-individual
omegaAlpha <- 0
doses <- c(12.59972,34.65492,44.69007,60.80685,83.68946,100.37111)
timeSampling <- seq(0,24,length.out=48)
sigma <- rep(0.2,length(timeSampling)) # sigma: Additive or proportional error

gen.scen <- sim.data(PKparameters,omegaIIV,omegaAlpha,sigma,doses,
                    limitTox,timeSampling, N, TR, seed=190591)
gen.scen[[1]]      # returns the first simulated dataset.

#### Graphical representation of the first simulated data
# plot(gen.scen[[1]])

```

---

stan\_f

---

*The data stan\_f includes all the Stan models that dfpk package uses.*


---

**Description**

A character vector with paths to .stan files to include in the package.

**Usage**

```
data("stan_f")
```

**References**

Ursino, M., et al, (2017) Dose-finding methods for Phase I clinical trials using pharmacokinetics in small populations, *Biometrical Journal*, <doi:10.1002/bimj.201600084>.

Toumazi, A., et al, (2018) dfpk: An R-package for Bayesian dose-finding designs using pharmacokinetics (PK) for phase I clinical trials, *Computer Methods and Programs in Biomedicine*, <doi:10.1016/j.cmpb.2018.01.023>.

**Examples**

```

data(stan_f)
## maybe str(stan_f) ; plot(stan_f) ...

```

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