

Package ‘mrdrc’

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Title Model-robust concentration-response analysis

LazyLoad yes

LazyData yes

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Description Model-robust, semi-parametric modelling of continuous and quantal concentration/dose-response data.

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Depends R (>= 2.6.0), drc, locfit

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pnsdrm	<i>Parametric, non-parametric or semi-parametric dose-response modelling</i>
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Description

Parametric, non-parametric or semi-parametric dose-response modelling of both continuous and quantal data.

Usage

```
pnsdrm(predictor, response, weights, type = c("continuous", "binomial"),
model = c("semi-parametric", "non-parametric", "parametric"),
fct = NULL, robust = FALSE, respLev = c(10, 20, 50),
reference = NULL, level = 0.95, logex = FALSE)
```

```
pnsdrm.calc(predictor, response, weights, type = c("continuous", "binomial"),
model = c("semi-parametric", "non-parametric", "parametric"),
fct = NULL, robust = FALSE, respLev = c(10, 20, 50),
reference = NULL, level = 0.95, logex = FALSE)
```

Arguments

predictor	numeric vector of concentrations/doses.
response	numeric vector of response values (proportions in case of quantal data).
weights	numeric vector of weights needed for quantal data.
type	character string specifying the type of response.
model	character string specifying the model to be fit.
fct	a built-in function or a list of built-in functions from the package 'drc'.
robust	logical specifying whether or not a robust approach should be used. Only for the semi-parametric approach.
respLev	numeric vector of requested ED level.
reference	optional reference value for the lower limit.
level	numeric specifying the confidence level.
logex	logical indicating whether or not a logarithmic x axis should be used.

Details

The parametric estimation is based on the model fitting function `drm` in the package 'drc'. The non-parametric estimation relies on the 'locfit' package.

The semi-parametric approach is mainly based on the development in Nottingham and Birch (2000), whereas the non-parametric approach uses on the package 'EffectiveDose' which implements the method introduced in Dette *et al* (2004).

plot and print methods are available.

Value

A list containing the requested ED values and additional information about the underlying model fit(s).

Author(s)

Christian Ritz (wrapper functions) Mads Jeppe Tarp-Johansen (internal functions)

References

Dette, H., Neumeier, N. and Pilz, K. F. (2004) A Note on Nonparametric Estimation of the Effective Dose in Quantal Bioassay, *J. Amer. Statist. Assoc.*, **100**, 503–510.

Nottingham, Q. and Birch, J. B. (2000) A Semiparametric Approach to Analysing Dose-Response Data, *Statist. Med.*, **19**, 389–404.

Examples

```
## Analysing deguelin (in the package 'drc')

## Semi-parametric model
deguelin.mrr1 <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
model = "semi-parametric", fct = LL.2())
deguelin.mrr1
plot(deguelin.mrr1)

## The same
gmFct <- getMeanFunctions(fname = "LL.2")
deguelin.mrr1b <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
model = "semi-parametric", fct = gmFct)
deguelin.mrr1b
plot(deguelin.mrr1b)

## The same again
deguelin.mrr1c <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
model = "semi-parametric", fct = list(LL.2()))
deguelin.mrr1c
plot(deguelin.mrr1c)

deguelin.mrr1d <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
model = "semi-parametric", fct = W1.2())
deguelin.mrr1d
plot(deguelin.mrr1d)

## The same
gmFct <- getMeanFunctions(fname = "W1.2")
deguelin.mrr1e <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
model = "semi-parametric", fct = gmFct)
deguelin.mrr1e
plot(deguelin.mrr1e)
```

```
### Parametric models
#deguelin.mrr2 <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
#model = "parametric", fct = list(LL.2(), W1.2(), W2.2()))
#deguelin.mrr2
#plot(deguelin.mrr2)

### The same parametric models
#deguelin.mrr2b <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
#model = "parametric", fct = list(W2.2(), LL.2(), W1.2()))
#deguelin.mrr2b
#plot(deguelin.mrr2b)

## Non-parametric approach -- currently not available
#deguelin.mrr3 <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
#model = "non-parametric")
#deguelin.mrr3
#plot(deguelin.mrr3)

## Semi-parametric model with reference level 0.3
deguelin.mrr4 <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
model = "semi-parametric", fct = LL.2(), reference = 0.3)
deguelin.mrr4
plot(deguelin.mrr4)

## Semi-parametric models
deguelin.mrr5 <- pnsdrm(deguelin$dose, deguelin$r, deguelin$n, type = "binomial",
model = "semi-parametric", fct = list(LL.2(), W1.2(), W2.2()))
deguelin.mrr5
plot(deguelin.mrr5)

## Analysing ryegrass (in the package 'drc')

ryegrass.mrr1 <- pnsdrm(ryegrass$conc, ryegrass$rootl, type = "continuous",
model = "semi-parametric", fct = LL.5())
ryegrass.mrr1
plot(ryegrass.mrr1)
plot(ryegrass.mrr1, log = "x")

ryegrass.mrr2 <- pnsdrm(ryegrass$conc, ryegrass$rootl, type = "continuous",
model = "semi-parametric", fct = list(LL.3(), LL.4(), LL.5()))
ryegrass.mrr2
plot(ryegrass.mrr2)

#ryegrass.mrr3 <- pnsdrm(ryegrass$conc, ryegrass$rootl, type = "continuous",
#model = "parametric", fct = list(LL.3(), LL.4(), LL.5()))
#ryegrass.mrr3
#plot(ryegrass.mrr3)
```

```
ryegrass.mrr4 <- pnsdrm(ryegrass$conc, ryegrass$rootl, type = "continuous",
model = "semi-parametric", fct = list(L.4(), LL.4(), W1.4(), W2.4()))
ryegrass.mrr4
plot(ryegrass.mrr4)
```

```
## Analysing lettuce (in the package 'drc')
```

```
lettuce.mrr1 <- pnsdrm(lettuce$conc, lettuce$weight, type = "continuous",
model = "semi-parametric", fct = LL.3())
lettuce.mrr1
plot(lettuce.mrr1)
```

```
lettuce.mrr2 <- pnsdrm(lettuce$conc, lettuce$weight, type = "continuous",
model = "semi-parametric", fct = BC.4())
lettuce.mrr2
plot(lettuce.mrr2)
```

```
#lettuce.mrr3 <- pnsdrm(lettuce$conc, lettuce$weight, type = "continuous",
#model = "semi-parametric", fct = LL.3(), robust = TRUE)
```

```
#lettuce.mrr3
#plot(lettuce.mrr3)
```

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