Package ‘ToxicR’

August 8, 2022

Type Package
Title Analyzing Toxicology Dose-Response Data
Version 22.8.1.0.2
Date 2022-08-31
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Depends R (>= 4.1.0)
License LGPL (>= 3)
URL https://github.com/NIEHS/ToxicR
LazyData true
Imports Rcpp (>= 1.0.0), ggplot2 (>= 3.3.2), shiny (>= 1.5.0), coda (>= 0.19-4), scales (>= 1.1.1), tidyverse (>= 1.3.0), forcats, ggridges (>= 0.5.3), doBy (>= 4.6.11), multcomp (>= 1.4), dplyr (>= 1.0.7)
LinkingTo Rcpp, RcppEigen, RcppGSL
RoxygenNote 7.1.2
VignetteBuilder knitr
Suggests rmarkdown, actuar (>= 3.2-0), ggpubr (>= 0.4.0), testthat (>= 3.1.0), gridExtra (>= 2.3), VIM (>= 6.1.1), knitr (>= 1.36), modules, plotly (>= 4.9.2.1)
NeedsCompilation: yes

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Repository: CRAN

Date/Publication: 2022-08-08 15:30:02 UTC

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cleveland_plot  

Description
Create a Cleveland plot from a model averaged model.

Usage

cleveland_plot(A)

Arguments
A  the model averaged model to plot

Value
Returns a ggplot2 graphics object.

Examples

mData <- matrix(c(0, 2,50,
                  1, 2,50,
                  3, 10, 50,
                  16, 18,50,
                  32, 18,50,
                  33, 17,50),nrow=6,ncol=3,byrow=TRUE)
D <- mData[,1]
Y <- mData[,2]
N <- mData[,3]

model = ma_dichotomous_fit(D,Y,N)
cleveland_plot(model)

create_continuous_prior  

create_continuous_prior Given priorlist, a model, and a distribution. Create a prior for a given analysis.

Description
create_continuous_prior Given priorlist, a model, and a distribution. Create a prior for a given analysis.
create_dichotomous_prior

Usage
create_dichotomous_prior(prior, model)

Arguments
prior First Prior
model Model to be used should be one of "hill", "gamma", "logistic", "log-logistic", "log-probit", "multistage", "probit", "qlinear", or "weibull"
**create_prior_list**

Create a list of priors for a model.

**Description**

Given priors created using the ToxicR prior functions, create a list of priors for a model.

**Usage**

```r
create_prior_list(x1, x2, ...)
```

**Arguments**

- `x1`: First Prior
- `x2`: Second Prior
- `...`: Additional arguments

**Value**

new BMDprior list. This object is essentially a matrix where each row is an element defined by a prior object (e.g., `normprior` or `lnormprior`).

**Examples**

```r
plist<- create_prior_list(normprior(0,0.1,-100,100), # a
lnormprior(1,0.2,0,18))

power_normal <- create_dichotomous_prior(plist,"logistic")
```
### DichotomousDR

**Description**

A dataset containing 733 dichotomous dose-response studies that were involved in regulatory risk assessment.

**Usage**

```r
dichotomousDR
```

**Format**

A data frame with 2727 rows and 11 variables:

- **ID** - The study ID in the database.
- **chemical** - Name of the Chemical in the study.
- **data.source** - Source of the risk assessment data.
- **CASRN** - Chemical’s CASRN
- **dose** - Dose spacing of the study using the original study.
- **r.dose** - Doses of the experiment relative to 1 being the maximum dose tested.
- **n** - Number of animals on test.
- **obs** - Number of adverse events.
- **organ** - Organ impacted.
- **effect** - Type of adverse effect.
- **study.source** - Publication related to the experiment.


### lnormprior

**Description**

Specify a log-normal prior for a ToxicR Bayesian model fit.

**Usage**

```r
lnormprior(mean = 0, sd = 1, lb = -100, ub = 100)
```
**Arguments**

- **mean**: log-mean of the prior distribution.
- **sd**: log-sd of the prior distribution.
- **lb**: lower bound on the distribution. Necessary for the optimization algorithms. To make sure it is a fully normal prior, make lb small relative to the mean/sd.
- **ub**: upper bound on the distribution. Necessary for the optimization algorithms. To make sure it is a fully normal prior, make ub large relative to the mean/sd.

**Value**

A normal prior model object. This object essentially a vector with the first element as 2 (for log-normal), the second element the mean, the third element the log-variance, the fourth and fifth elements the lower and upper bounds, respectively.

**Examples**

```r
# Log-Normal Prior with mean 0, sd=1
lnormprior(mean = 0, sd = 1, lb = -1e4, ub=1e4)

# Truncated Log-Normal prior, Truncated below at 1
lnormprior(mean = 0, sd = 1, lb = 1, ub=1e4)
```

---

**MA density plot**

*MA density plot - Create a density plot from a model averaged model.*

**Description**

Create a density plot from a model averaged model fit with MCMC.

**Usage**

`MA density_plot(A)`

**Arguments**

- **A**: the model averaged model to plot

**Value**

Returns a ggplot2 graphics object.
Examples

doses <- cbind(c(0,25,50,100,200))
y <- cbind(c(6,5.2,2.4,1.1,0.75),
          c(20,20,19,20,20),
          c(1.2,1.1,0.81,0.74,0.66))
model <- ma_continuous_fit(doses,y,
                           fit_type = "mcmc",BMD_TYPE = 'sd',BMR = 1)
MAdensity_plot(model)

ma_continuous_fit - Fit a model averaged continuous BMD model.

Description

Fit a model averaged continuous BMD model.

Usage

ma_continuous_fit(
  D,
  Y,
  model_list = NA,
  fit_type = "laplace",
  BMD_TYPE = "sd",
  BMR = 0.1,
  point.p = 0.01,
  alpha = 0.05,
  samples = 21000,
  burnin = 1000
)

Arguments

D                doses matrix
Y                response matrix
model_list       a list of configurations for the single models (priors, model type). To create a
                 model list, one creates a list of continuous model priors using create_continuous_prior.
fit_type         the method used to fit ("laplace", "mle", or "mcmc")
BMD_TYPE         BMD_TYPE specifies the type of benchmark dose analysis to be performed. For
                 continuous models, there are four types of BMD definitions that are commonly used.
                 - Standard deviation is the default option, but it can be explicitly specified
                   with 'BMD_TYPE = "sd"'. This definition defines the BMD as the dose associated
                   with the mean/median changing a specified number of standard deviations
                   from the mean at the control dose., i.e., it is the dose, BMD, that solves
\[ |f(dose) - f(0)| = BMR \times \sigma \]

Relative deviation can be specified with 'BMR_TYPE = "rel"'. This defines the BMD as the dose that changes the control mean/median a certain percentage from the background dose, i.e. it is the dose, BMD that solves \[ |f(dose) - f(0)| = (1 \pm BMR)f(0) \]

Hybrid deviation can be specified with 'BMR_TYPE = "hybrid"'. This defines the BMD that changes the probability of an adverse event by a stated amount relative to no exposure (i.e. 0). That is, it is the dose, BMD, that solves \[ \frac{Pr(X > x|dose) - Pr(X > x|0)}{Pr(X < x|0)} = BMR. \]

For this definition, \[ Pr(X < x|0) = 1 - Pr(X > X|0) = \pi_0, \]
where \( 0 \leq \pi_0 < 1 \) is defined by the user as "point_p," and it defaults to 0.01. Note: this discussion assumed increasing data. The fitter determines the direction of the data and inverts the probability statements for decreasing data.

Absolute deviation can be specified with 'BMR_TYPE = "abs"'. This defines the BMD as an absolute change from the control dose of zero by a specified amount. That is the BMD is the dose that solves the equation \[ |f(dose) - f(0)| = BMR \]

BMR
This option specifies the benchmark response BMR. The BMR is defined in relation to the BMD calculation requested (see BMD). By default, the "BMR = 0.1."

point_p
This option is only used for hybrid BMD calculations. It defines a probability that is the cutpoint for observations. It is the probability that observations have this probability, or less, of being observed at the background dose.

alpha
Alpha is the specified nominal coverage rate for computation of the lower bound on the BMDL and BMDU, i.e., one computes a \( 100 \times (1 - \alpha)\% \) confidence interval. For the interval (BMDL,BMDU) this is a \( 100 \times (1 - 2\alpha)\% \). By default, it is set to 0.05.

samples
the number of samples to take (MCMC only)

burnin
the number of burnin samples to take (MCMC only)

Value
This function model object containing a list of individual fits and model averaging fits

- Individual_Model_X: Here \( X \) is a number \( 1 \leq X \leq n \), where \( n \) is the number of models in the model average. For each \( X \), this is an individual model fit identical to what is returned in ‘single_continuous_fit’.

- ma_bmd: The CDF of the model averaged BMD distribution.

- posterior_probs: The posterior model probabilities used in the MA.

- bmd: The BMD and the \( 100 \times (1 - 2\alpha)\% \) confidence intervals.

Examples

```r
hill_m <- function(doses){
  returnV <- 481 -250.3*doses^1.3/(40^1.3 + doses^1.3)
  return(returnV)
}```
```r
}

ma_dichotomous_fit

\{ 

\text{doses} \leftarrow \text{rep(c(0,6.25,12.5,25,50,100), each=10)}
\text{mean} \leftarrow \text{hill_m(doses)}
\text{y} \leftarrow \text{rnorm(length(mean), mean, 20.14)}
\text{model} \leftarrow \text{ma_continuous_fit(doses, y, fit_type = "laplace", BMD_TYPE = 'sd', BMR = 1)}
\text{summary(model)}

\}

\text{ma_dichotomous_fit} \quad \text{ma_dichotomous_fit} - \text{Fit a model averaged dichotomous BMD model.}

\section*{Description}

\text{Fit a model averaged dichotomous BMD model.}

\section*{Usage}

\text{ma_dichotomous_fit(}

\hspace{1em} \text{D,}
\hspace{1em} \text{Y,}
\hspace{1em} \text{N,}
\hspace{1em} \text{model_list = integer(0),}
\hspace{1em} \text{fit_type = "laplace",}
\hspace{1em} \text{BMD_TYPE = "extra",}
\hspace{1em} \text{BMR = 0.1,}
\hspace{1em} \text{point_p = 0.01,}
\hspace{1em} \text{alpha = 0.05,}
\hspace{1em} \text{samples = 21000,}
\hspace{1em} \text{burnin = 1000}

\text{)}

\section*{Arguments}

\begin{description}
\item[D] \text{doses matrix}
\item[Y] \text{response matrix}
\item[N] \text{number of replicates matrix}
\item[model_list] \text{a list of configurations for the single models (priors, model type)}
\item[fit_type] \text{the method used to fit (laplace, mle, or mcmc)}
\item[BMD_TYPE] \text{BMD_TYPE specifies the type of benchmark dose analysis to be performed. For continuous models, there are four types of BMD definitions that are commonly used.}
\hspace{1em} \text{- Standard deviation is the default option, but it can be explicitly specified with 'BMR_TYPE = "sd"'. This definition defines the BMD as the dose associated with the mean/median changing a specified number of standard deviations from the mean at the control dose, i.e., it is the dose, BMD, that solves } | f(dose) - f(0) | = BMR \times \sigma
\end{description}
```
- Relative deviation can be specified with `BMR_TYPE = "rel"`. This defines the BMD as the dose that changes the control mean/median a certain percentage from the background dose, i.e. it is the dose, BMD that solves $|f(dose) - f(0)| = (1 \pm BMR)f(0)$.

- Hybrid deviation can be specified with `BMR_TYPE = "hybrid"`. This defines the BMD that changes the probability of an adverse event by a stated amount relative to no exposure (i.e. 0). That is, it is the dose, BMD, that solves $rac{Pr(X > x|dose) - Pr(X > x|0)}{Pr(X < x|0)} = BMR$. For this definition, $Pr(X < x|0) = 1 - Pr(X > X|0) = \pi_0$, where $0 \leq \pi_0 < 1$ is defined by the user as "point_p," and it defaults to 0.01. Note: this discussion assumed increasing data. The fitter determines the direction of the data and inverts the probability statements for decreasing data.

- Absolute deviation can be specified with `BMR_TYPE="abs"`. This defines the BMD as an absolute change from the control dose of zero by a specified amount. That is the BMD is the dose that solves the equation $|f(dose) - f(0)| = BMR$

**BMR**

This option specifies the benchmark response BMR. The BMR is defined in relation to the BMD calculation requested (see BMD). By default, the "BMR = 0.1."

**point_p**

This option is only used for hybrid BMD calculations. It defines a probability that is the cutoff point for observations. It is the probability that observations have this probability, or less, of being observed at the background dose.

**alpha**

Alpha is the specified nominal coverage rate for computation of the lower bound on the BMDL and BMDU, i.e., one computes a $100 \times (1 - \alpha)\%$. For the interval (BMDL,BMDU) this is a $100 \times (1 - 2\alpha)\%$. By default, it is set to 0.05.

**samples**

the number of samples to take (MCMC only)

**burnin**

the number of burnin samples to take (MCMC only)

**Value**

a model object containing a list of single models

- **Individual_Model_X**: Here X is a number $1 \leq X \leq n$, where n is the number of models in the model average. For each X, this is an individual model fit identical to what is returned in 'single_continuous_fit'.

- **ma_bmd**: The CDF of the model averaged BMD distribution.

- **posterior_probs**: The posterior model probabilities used in the MA.

- **bmd**: The BMD and the $100 \times (1 - 2\alpha)\%$ confidence intervals.

**Examples**

```r
mData <- matrix(c(0, 2, 50, 1, 2, 50, 3, 10, 50, 16, 18, 50, 32, 18, 50, 33, 17, 50), nrow=6, ncol=3, byrow=TRUE)
```
D <- mData[,1]
Y <- mData[,2]
N <- mData[,3]
model = ma_dichotomous_fit(D,Y,N)
summary(model)

---

### normprior

Create a normal prior object.

#### Description

Specify a normal prior for a ToxicR Bayesian model fit.

#### Usage

```r
normprior(mean = 0, sd = 1, lb = -100, ub = 100)
```

#### Arguments

- `mean`: mean of the prior
- `sd`: sd of the prior distribution.
- `lb`: lower bound on the distribution. Necessary for the optimization algorithms. To make sure it is a fully normal prior, make `lb` small relative to the mean/sd.
- `ub`: Upper bound on the distribution. Necessary for the optimization algorithms. To make sure it is a fully normal prior, make `ub` large relative to the mean/sd.

#### Value

A normal prior model object. This object essentially a vector with the first element as 1 (for normal), the second element the mean, the third element the variance, the fourth and fifth elements the lower and upper bounds, respectively.

#### Examples

```r
# Normal Prior with mean 0, sd -1
normprior(mean = 0, sd = 1, lb = -1e4, ub = 1e4)

# Truncated Normal prior, Truncated below at 0
normprior(mean = 0, sd = 1, lb = 0, ub = 1e4)
```
ntp_599_female

Long term Thyroid Adenoma data from NTP Report 599

Description
This dataset contains Thyroid Adenoma data for female rats for the technical report TR-599: Sodium Tungstate Dihydrate.

Usage
ntp_599_female

Format
A data frame with 200 rows and 4 variables:

- **treatment** - The dose group for the observation.
- **days_on_study** - Number of days on the study, 730 is the max.
- **adenoma** - Thyroid Adenoma (Yes/No) (1/0).
- **dose** - The dose in mg/L

For more information see: doi:10.22427/NTPDATATR599

ntp_599_hemotology

Clinical Chemistry data from NTP Report 599

Description
This dataset contains clinical chemistry data for all rats in the short term 90-day study.

Usage
ntp_599_hemotology

Format
A data frame with 200 rows and 4 variables:

- **concentration** - The dose group for the observation.
- **sex** - Male/Female.
- **response** - Response variable
- **response_type** - The type of response measured

For more information see: doi:10.22427/NTPDATATR599
Description

ntp_dunnett Dunn’s test

Usage

ntp_dunnett(formula, data, dose_name = "dose")

Arguments

formula An equation of the form $Y \sim X$. Here the variable $Y$ is the response of interest, and $X$ represents discrete experimental conditions. For example, if weight is the dependent variable, and you are interested in looking at the trend across sex one would have 'weight ~ sex'.
data A data frame with column names in the formula.
dose_name The name of the variable containing the doses in the data frame data. It is expected multiple doses for each of the experimental conditions $X$.

Value

The results of a Dunn’s test for each level in dose_name.

Examples

```r
a = ntp_dunnett(response ~ sex + response_type, data=ntp_599_hemotology, dose_name="concentration")
summary(a)
```

Description

ntp_dunnett Dunnett’s test

Usage

ntp_dunnett(formula, data, dose_name = "dose")
Arguments

- **formula**: An equation of the form $Y \sim X$. Here the variable $Y$ is the response of interest, and $X$ represents discrete experimental conditions. For example, if weight is the dependent variable, and you are interested in looking at the trend across sex one would have 'weight ~ sex'.
- **data**: A data frame with column names in the formula.
- **dose_name**: The name of the variable containing the doses in the data frame `data`. It is expected multiple doses for each of the experimental conditions $X$.

Value

The results of Dunnet's test for each level in `dose_name`.

Examples

```r
a = ntp_dunnett(response ~ sex + response_type, data=ntp_599_hematology, dose_name="concentration")
summary(a)
```

ntp_jonckeere

**ntp_jonckeere** Jonckheere’s test for significant differences from background dose

Description

**ntp_jonckeere** Jonckheere’s test for significant differences from background dose

Usage

```r
ntp_jonckeere(formula, data, dose_name = "dose", pair = "Williams")
```

Arguments

- **formula**: An equation of the form $Y \sim X$. Here the variable $Y$ is the response of interest, and $X$ represents discrete experimental conditions. For example, if weight is the dependent variable, and you are interested in looking at the trend across sex one would have 'weight ~ sex'.
- **data**: A data frame with column names in the formula.
- **dose_name**: The name of the variable containing the doses in the data frame `data`. It is expected multiple doses for each of the experimental conditions $X$.
- **pair**: The type of test used for pairwise comparison. It can either be "Williams" or "Shirley".

Value

The results of a global test for difference from background.
\textit{ntp_polyk}  

\textbf{Examples}  

\begin{verbatim}
ntp_jonckeere(response ~ sex + response_type, data=ntp_599_hemotology, dose_name="concentration")
\end{verbatim}  

\begin{verbatim}
ntp_polyk(dose, tumor, daysOnStudy)
\end{verbatim}  

\textbf{Description}  

Poly-k test This function implements the NTP's polyK trend test.

\textbf{Usage}  

\begin{verbatim}
ntp_polyk(dose, tumor, daysOnStudy)
\end{verbatim}  

\textbf{Arguments}  

dose An equation of the form $Y \sim X$. Here the variable $Y$ is the response of interest, and $X$ represents discrete experimental conditions. For example, if weight is the dependent variable, and you are interested in looking at the trend across sex one would have 'weight ~ sex'.

tumor A data frame with column names in the formula.

daysOnStudy The name of the variable containing the doses in the data frame \textit{data}. It is expected multiple doses for each of the experimental conditions \textit{X}.

\textbf{Value}  

The results of a Williams trend test for each level in dose\textunderscore name. More information on this procedure at: doi:10.2307/2531856 and doi:10.2307/2532200 This procedure returns a vector of three p-values for the poly-1.5, poly-3, and poly-6 test respectively.

\textbf{Examples}  

\begin{verbatim}
ntp_polyk(ntp_599_female$dose, ntp_599_female$adenoma, ntp_599_female$days_on_study)
\end{verbatim}
ntp_shirley Shirley's test as programmed at the NTP

Description
ntp_shirley Shirley’s test as programmed at the NTP

Usage
ntp_shirley(formula, data, dose_name = "dose")

Arguments
formula An equation of the form \( Y \sim X \). Here the variable \( Y \) is the response of interest, and \( X \) represents discrete experimental conditions. For example, if weight is the dependent variable, and you are interested in looking at the trend across sex one would have \( \text{weight} \sim \text{sex} \).
data A data frame with column names in the formula.
dose_name The name of the variable containing the doses in the data frame \( data \). It is expected multiple doses for each of the experimental conditions \( X \).

Value
The results of a non-parametric Shirley’s isotone test for trend on each level in \( dose\_name \). For more information see: doi:10.2307/2529789 The returned list contains:

- \( X \): this represents all the class objects on the right hand side of \( Y \sim X \) above.
- \( dose \): the dose groups relative to control.
- testStats: Value of the Shirley test statistic.
- mult_comp_signif: Test's significance as 0, 1, or 2 which is not-significant, significant at the 0.05
- mult_comp_test: The type of test, i.e. "SHIRLEY"

Examples
a = ntp_shirley(weight ~ sex, data=ntp_weight_data)
summary(a)
ntp_weight_data

**Description**

This dataset contains terminal body-weight data for male and female rats for the technical report TR-599: Sodium Tungstate Dihydrate.

**Usage**

ntp_weight_data

**Format**

A data frame with 120 rows and 4 variables:

- **Dose_Group** - The dose group for the observation.
- **dose** - The dose in mg/L
- **sex** - Animal’s Sex
- **weight** - Terminal body-weight

For more information see: doi:10.22427/NTPDATATR599

---

ntp_williams

**William’s trend test**

**Description**

Williams Trend test for

**Usage**

ntp_williams(formula, data, dose_name = "dose")

**Arguments**

- **formula** - An equation of the form \( Y \sim X \). Here the variable \( Y \) is the response of interest, and \( X \) represents discrete experimental conditions. For example, if weight is the dependent variable, and you are interested in looking at the trend across sex one would have \( \text{weight} \sim \text{sex} \).
- **data** - A data frame with column names in the formula.
- **dose_name** - The name of the variable containing the doses in the data frame \( data \). It is expected multiple doses for each of the experimental conditions \( X \).
Value
The results of a Williams trend test for each level in dose,ame. For more information on the Williams trend test: doi:10.2307/2528930

• X: this represents all the class objects on the right hand side of Y ∼ X above.
• dose: the dose groups relative to control.
• willStat: Value of the Shirley test statistic.
• mult_comp_signif: Test’s significance as 0, 1, or 2 which is not-significant, significant at the 0.05
• mult_comp_test: The type of test, i.e. "William"

Examples

```r
a = ntp_williams(weight ~ sex, data=ntp_weight_data)
summary(a)
```

Description

Fit a single continuous BMD model.

Usage

```r
single_continuous_fit(D, Y, model_type = "hill", fit_type = "laplace", prior = NA, BMD_TYPE = "sd", BMR = 0.1, point_p = 0.01, distribution = "normal-ncv", alpha = 0.05, samples = 25000, degree = 2, burnin = 1000, ewald = FALSE, transform = FALSE)
```
Arguments

- **D**: doses matrix
- **Y**: response matrix
- **model_type**: Mean model. It should be one of "hill", "exp-3", "exp-5", "power", "polynomial"
- **fit_type**: the method used to fit (laplace, mle, or mcmc)
- **prior**: Prior / model for the continuous fit. If this is specified, it overrides the parameters 'model_type' and 'distribution.'
- **BMD_TYPE**: BMD_TYPE specifies the type of benchmark dose analysis to be performed. For continuous models, there are four types of BMD definitions that are commonly used.
  - Standard deviation is the default option, but it can be explicitly specified with 'BMR_TYPE = "sd"'. This definition defines the BMD as the dose associated with the mean/median changing a specified number of standard deviations from the mean at the control dose, i.e., it is the dose, BMD, that solves $|f(dose) - f(0)| = BMR \times \sigma$
  - Relative deviation can be specified with 'BMR_TYPE = "rel"'. This defines the BMD as the dose that changes the control mean/median a certain percentage from the background dose, i.e. it is the dose, BMD that solves $|f(dose) - f(0)| = (1 \pm BMR)f(0)$
  - Hybrid deviation can be specified with 'BMR_TYPE = "hybrid"'. This defines the BMD that changes the probability of an adverse event by a stated amount relative to no exposure (i.e. $0$). That is, it is the dose, BMD, that solves $Pr(X > x|dose) - Pr(X > x|0) = BMR$. For this definition, $Pr(X < x|0) = 1 - Pr(X > X|0) = \pi_0$, where $0 \leq \pi_0 < 1$ is defined by the user as "point_p," and it defaults to $0.01$. Note: this discussion assumed increasing data. The fitter determines the direction of the data and inverts the probability statements for decreasing data.
  - Absolute deviation can be specified with 'BMR_TYPE="abs"'. This defines the BMD as an absolute change from the control dose of zero by a specified amount. That is the BMD is the dose that solves the equation $|f(dose) - f(0)| = BMR$.
- **BMR**: This option specifies the benchmark response BMR. The BMR is defined in relation to the BMD calculation requested (see BMD). By default, the "BMR = 0.1."
- **point_p**: This option is only used for hybrid BMD calculations. It defines a probability that is the cutpoint for observations. It is the probability that observations have this probability, or less, of being observed at the background dose.
- **distribution**: The underlying distribution used as the data distribution.
- **alpha**: Alpha is the specified nominal coverage rate for computation of the lower bound on the BMDL and BMDU, i.e., one computes a $100 \times (1 - \alpha)\%$ confidence interval. For the interval (BMDL,BMDU) this is a $100 \times (1 - 2\alpha)\%$ confidence interval. By default, it is set to 0.05.
- **samples**: the number of samples to take (MCMC only)
degree  
the number of degrees of a polynomial model. Only used for polynomial models.

burnin  
the number of burnin samples to take (MCMC only)

ewald  
perform Wald CI computation instead of the default profile likelihood computation. This is the the ‘FAST BMD’ method of Ewald et al (2021)

transform  
Transforms doses using $\log(dose + \sqrt{dose^2 + 1})$. Note: this is a log transform that has a derivative defined when dose = 0.

Value

Returns a model object class with the following structure:

- **full_model**: The model along with the likelihood distribution.
- **bmd**: A vector containing the benchmark dose (BMD) and $100 \times (1 - 2\alpha)$ confidence intervals.
- **parameters**: The parameter estimates produced by the procedure, which are relative to the model given in full_model. The last parameter is always the estimate for $\log(\sigma^2)$.
- **covariance**: The variance-covariance matrix for the parameters.
- **bmd_dis**: Quantiles for the BMD distribution.
- **maximum**: The maximum value of the likelihood/posterior.
- **Deviance**: An array used to compute the analysis of deviance table.
- **prior**: This value gives the prior for the Bayesian analysis.
- **model**: Parameter specifies t mean model used.
- **options**: Options used in the fitting procedure.
- **data**: The data used in the fit.
- **transformed**: Are the data $\log(x + \sqrt{x^2 + 1})$ transformed?

  When MCMC is specified, an additional variable mcmc_result has the following two variables:
  - **PARM_samples**: matrix of parameter samples.
  - **BMD_samples**: vector of BMD sampled values.

Examples

```r
M2 <- matrix(0,nrow=5,ncol=4)
colnames(M2) <- c("Dose","Resp","N","StDev")
M2[,1] <- c(0,25,50,100,200)
M2[,2] <- c(6.5,2.4,4,1.1,0.75)
M2[,3] <- c(20,20,19,20,20)
M2[,4] <- c(1.2,1.1,0.81,0.74,0.66)
model = single_continuous_fit(M2[,1,drop=FALSE], M2[,2:4], BMD_TYPE="sd", BMR=1, ewald = TRUE, distribution = "normal",fit_type="laplace",model_type = "hill")
summary(model)
```
**single_dichotomous_fit**

*Fit a single dichotomous dose-response model to data.*

**Description**

Fit a single dichotomous dose-response model to data.

**Usage**

```r
single_dichotomous_fit(
  D,
  Y,
  N,
  model_type,
  fit_type = "laplace",
  prior = NULL,
  BMR = 0.1,
  alpha = 0.05,
  degree = 2,
  samples = 21000,
  burnin = 1000
)
```

**Arguments**

- **D**
  A numeric vector or matrix of doses.

- **Y**
  A numeric vector or matrix of responses.

- **N**
  A numeric vector or matrix of the number of replicates at a dose.

- **model_type**
  The mean model for the dichotomous model fit. It can be one of the following: "hill", "gamma", "logistic", "log-logistic", "log-probit", "multistage", "probit", "qlinear", "weibull"

- **fit_type**
  the method used to fit (laplace, mle, or mcmc)

- **prior**
  Used if you want to specify a prior for the data.

- **BMR**
  This option specifies the benchmark response BMR. The BMR is defined in relation to the BMD calculation requested (see BMD). By default, the "BMR = 0.1."

- **alpha**
  Alpha is the specified nominal coverage rate for computation of the lower bound on the BMDL and BMDU, i.e., one computes a $100 \times (1 - \alpha)\%$. For the interval (BMDL,BMDU) this is a $100 \times (1 - 2\alpha)\%$ confidence interval. By default, it is set to 0.05.

- **degree**
  the number of degrees of a polynomial model. Only used for polynomial models.

- **samples**
  the number of samples to take (MCMC only)

- **burnin**
  the number of burnin samples to take (MCMC only)
single_dichotomous_fit

Value

Returns a model object class with the following structure:

- **full_model**: The model along with the likelihood distribution.
- **parameters**: The parameter estimates produced by the procedure, which are relative to the model given in full_model. The last parameter is always the estimate for $\log(\sigma^2)$.
- **covariance**: The variance-covariance matrix for the parameters.
- **bmd_dist**: Quantiles for the BMD distribution.
- **bmd**: A vector containing the benchmark dose (BMD) and $100 \times (1 - 2\alpha)$ confidence intervals.
- **maximum**: The maximum value of the likelihood/posterior.
- **gof_p_value**: GOF p-value for the Pearson $\chi^2$ GOF test.
- **gof_chi_sqr_statistic**: The GOF statistic.
- **prior**: This value gives the prior for the Bayesian analysis.
- **model**: Parameter specifies the mean model used.
- **data**: The data used in the fit.
  When MCMC is specified, an additional variable mcmc_result has the following two variables:
  - **PARM_samples**: matrix of parameter samples.
  - **BMD_samples**: vector of BMD sampled values.

Examples

```r
mData <- matrix(c(0, 2, 50,
                  1, 2, 50,
                  3, 10, 50,
                  16, 18, 50,
                  32, 18, 50,
                  33, 17, 50), nrow=6, ncol=3, byrow=TRUE)
D <- mData[,1]
Y <- mData[,2]
N <- mData[,3]
model = single_dichotomous_fit(D, Y, N, model_type = "hill", fit_type = "laplace")
summary(model)
```
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