

Package ‘ecotox’

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Type Package

Title Analysis of Ecotoxicology

Version 1.4.4

Description A simple approach to using a probit or logit analysis to calculate lethal concentration (LC) or time (LT) and the appropriate fiducial confidence limits desired for selected LC or LT for ecotoxicology studies (Finney 1971; Wheeler et al. 2006; Robertson et al. 2007). The simplicity of 'ecotox' comes from the syntax it implies within its functions which are similar to functions like `glm()` and `lm()`. In addition to the simplicity of the syntax, a comprehensive data frame is produced which gives the user a predicted LC or LT value for the desired level and a suite of important parameters such as fiducial confidence limits and slope.
Finney, D.J. (1971, ISBN: 052108041X);
Wheeler, M.W., Park, R.M., and Bailer, A.J. (2006) <[doi:10.1897/05-320R.1](https://doi.org/10.1897/05-320R.1)>;
Robertson, J.L., Savin, N.E., Russell, R.M., and Preisler, H.K. (2007, ISBN: 0849323312).

Depends R (>= 3.3.0)

Imports stats, tibble

Suggests covr, data.table, dplyr, ggplot2, Hmisc, openxlsx, readr, testthat, tidyr

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| | |
|--------------|---|
| lamprey_time | <i>Lethal time data for seasonal exposure to TFM for larval sea lamprey</i> |
|--------------|---|

Description

This dataset contains the amount of responding/dead lamprey from 1 to 12 h of exposure to the piscicide, 3-trifluoromethyl-4-nitrophenol (TFM), for the calculated LC50s at each month for the 2011 seasonal larval sea lamprey TFM toxicity data.

Usage

```
lamprey_time
```

Format

A tibble containing 44 rows and 7 columns.

nominal.dose nominal TFM dose(mg/L)

dose averaged measured TFM dose (mg/L) over 12 h of exposures

month month in which toxicity test occurred

hour duration of exposure in hours

response number of lamprey that responded over 12 h exposure to TFM

survive number of lamprey that survived over 12 h exposure to TFM

total total number of lamprey that were exposed to TFM over 12 h

Details

For each month, new lamprey were collected from the deer creek, MI, and were randomly assigned to a tank for exposure to the piscicide, 3-trifluoromethyl-4-nitrophenol (TFM). The LC50 at each month was then calculated and the amount of responding/dead lamprey from 1 to 12 h was recorded.

Source

Hlina, B.L., Birceanu, O., Robinson, C.S., Dhiyebi, H., Wilkie, M.P. *In Reivew*. Seasonal Variation in the Sensitivity of Invasive Sea Lampreys to the Lampricide TFM: Importance of Energy Reserves and Temperature. North American Journal of Fisheries Management

| | |
|-------------|--|
| lamprey_tox | <i>Lethal concentration data for seasonal exposure to TFM for larval sea lamprey</i> |
|-------------|--|

Description

This dataset contains 2011 seasonal larval sea lamprey exposed to the piscicide, 3-trifluoromethyl-4-nitrophenol (TFM) toxicity data.

Usage

lamprey_tox

Format

A tibble containing 64 rows and 7 columns.

nominal_dose nominal TFM dose (mg/L)

tank tank assignment

month month in which toxicity test occurred

dose averaged measured TFM dose (mg/L) over 12 h of exposure

response number of lamprey that responded over 12 h exposure to TFM

survive number of lamprey that survived over 12 h exposure to TFM

total total number of lamprey that were exposed to TFM over 12 h

Details

For each month, new lamprey were collected from the Deer Creek, MI, and were randomly assigned to a tank for exposure to varying doses of the piscicide, 3-trifluoromethyl-4-nitrophenol (TFM).

Source

Hlina, B.L., Birceanu, O., Robinson, C.S., Dhiyebi, H., Wilkie, M.P. *In Review*. Seasonal Variation in the Sensitivity of Invasive Sea Lampreys to the Lampricide TFM: Importance of Energy Reserves and Temperature. North American Journal of Fisheries Management

LC_logit

*Lethal Concentration Logit***Description**

Calculates lethal concentration (LC) and its fiducial confidence limits (CL) using a logit analysis according to Finney 1971, Wheeler et al. 2006, and Robertson et al. 2007.

Usage

```
LC_logit(formula, data, p = NULL, weights = NULL,
         subset = NULL, log_base = NULL,
         log_x = TRUE, het_sig = NULL,
         conf_level = NULL, conf_type = NULL,
         long_output = TRUE)
```

Arguments

| | |
|----------|---|
| formula | an object of class formula or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under Details. |
| data | an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which LC_logit is called. |
| p | Lethal Concentration (LC) values for given p, example will return a LC50 value if p equals 50. If more than one LC value wanted specify by creating a vector. LC values can be calculated down to the 1e-16 of a percentage (e.g. LC99.99). However, the tibble produced can round to nearest whole number. |
| weights | vector of 'prior weights' to be used in the fitting process. Only needs to be supplied if you are taking the response / total for your response variable within the formula call of LC_probit. Otherwise if you use cbind(response, non-response) method you do not need to supply weights. If you do the model will be incorrect. If you don't supply weights there is a warning that will help you to make sure you are using one method or the other. See the following StackExchange post about differences cbind() function in R for a logistic regression . |
| subset | allows for the data to be subseted if desired. Default set to NULL. |
| log_base | default is 10 and will be used to calculate results using the anti of log10() given that the x variable has been log10 transformed. If FALSE results will not be back transformed. |
| log_x | default is TRUE and will calculate results using the antilog of determined by log_base given that the x variable has been log() transformed. If FALSE results will not be back transformed. |
| het_sig | significance level from person's chi square goodness-of-fit test that is used to decide if a heterogeneity factor is used. NULL is set to 0.15. |

| | |
|-------------|---|
| conf_level | adjust confidence level as necessary or NULL set at 0.95. |
| conf_type | default is "f1" which will calculate fiducial confidence limits per Finney 1971. If set to "dm" the delta method will be used instead. |
| long_output | default is TRUE which will return a tibble with all 17 variables. If FALSE the tibble returned will consist of the p level, n, the predicted LC for given p level, lower and upper confidence limits. |

Value

Returns a tibble with predicted LC for given p level, lower CL (LCL), upper CL (UCL), Pearson's chi square goodness-of-fit test (pgof), slope, intercept, slope and intercept p values and standard error, and LC variance.

References

- Finney, D.J., 1971. Probit Analysis, Cambridge University Press, Cambridge, England, ISBN: 052108041X
- Wheeler, M.W., Park, R.M., and Bailey, A.J., 2006. Comparing median lethal concentration values using confidence interval overlap or ratio tests, Environ. Toxic. Chem. 25(5), 1441-1444.10.1897/05-320R.1
- Robertson, J.L., Savin, N.E., Russell, R.M. and Preisler, H.K., 2007. Bioassays with arthropods. CRC press. ISBN: 9780849323317

Examples

```
head(lamprey_tox)

# within the dataframe used, control dose, unless produced a value
# during experimentation, are removed from the dataframe,
# as glm cannot handle values of infinite. Other statistical programs
# make note of the control dose but do not include within analysis

# calculate LC50 and LC99 for May

m <- LC_logit((response / total) ~ log10(dose), p = c(50, 99),
             weights = total,
             data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
             subset = c(month == "May"))

# OR

m1 <- LC_logit(cbind(response, survive) ~ log10(dose), p = c(50, 99),
             data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
             subset = c(month == "May"))

# view calculated LC50 and LC99 for seasonal toxicity of a piscicide,
# to lamprey in 2011
```

```

m

# they are the same

m1

# dose-response curve can be plotted using 'ggplot2'
# Uncomment the below lines to run create plots

# library(ggplot2)

# lc_may <- subset(lamprey_tox, month %in% c("May"))

# p1 <- ggplot(data = lc_may[lc_may$nominal_dose != 0, ],
#             aes(x = log10(dose), y = (response / total))) +
# geom_point() +
# geom_smooth(method = "glm",
#             method.args = list(family = binomial(link = "logit")),
#             aes(weight = total), colour = "#FF0000", se = TRUE)

# p1

# calculate LC50s and LC99s for multiple toxicity tests, June, August, and September

j <- LC_logit((response / total) ~ log10(dose), p = c(50, 99),
             weights = total,
             data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
             subset = c(month == "June"))

a <- LC_logit((response / total) ~ log10(dose), p = c(50, 99),
             weights = total,
             data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
             subset = c(month == "August"))

s <- LC_logit((response / total) ~ log10(dose), p = c(50, 99),
             weights = total,
             data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
             subset = c(month == "September"))

# group results together in a dataframe to plot with 'ggplot2'

results <- rbind(m[, c(1, 3:8, 11)], j[,c(1, 3:8, 11)],
              a[, c(1, 3:8, 11)], s[, c(1, 3:8, 11)])
results$month <- factor(c(rep("May", 2), rep("June", 2),
                       rep("August", 2), rep("September", 2)),
                      levels = c("May", "June", "August", "September"))

# p2 <- ggplot(data = results, aes(x = month, y = dose,
#                                 group = factor(p), fill = factor(p))) +
# geom_col(position = position_dodge(width = 0.9), colour = "#000000") +
# geom_errorbar(aes(ymin = LCL, ymax = UCL),

```

```
#           size = 0.4, width = 0.06,
#           position = position_dodge(width = 0.9))

# p2
```

 LC_probit

Lethal Concentration Probit

Description

Calculates lethal concentration (LC) and its fiducial confidence limits (CL) using a probit analysis according to Finney 1971, Wheeler et al. 2006, and Robertson et al. 2007.

Usage

```
LC_probit(formula, data, p = NULL, weights = NULL,
           subset = NULL, log_base = NULL, log_x = TRUE,
           het_sig = NULL, conf_level = NULL, conf_type = NULL,
           long_output = TRUE)
```

Arguments

| | |
|----------|---|
| formula | an object of class formula or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under Details. |
| data | an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>LC_probit</code> is called. |
| p | Lethal Concentration (LC) values for given p, example will return a LC50 value if p equals 50. If more than one LC value wanted specify by creating a vector. LC values can be calculated down to the 1e-16 of a percentage (e.g. LC99.99). However, the tibble produced can round to nearest whole number. |
| weights | vector of 'prior weights' to be used in the fitting process. Only needs to be supplied if you are taking the response / total for your response variable within the formula call of <code>LC_probit</code> . Otherwise if you use <code>cbind(response, non-response)</code> method you do not need to supply weights. If you do the model will be incorrect. If you don't supply weights there is a warning that will help you to make sure you are using one method or the other. See the following StackExchanges post about differences cbind() function in R for a logistic regression and input format for binomial glm . |
| subset | allows for the data to be subseted if desired. Default set to NULL. |
| log_base | default is 10 and will be used to calculate results using the anti of <code>log10()</code> given that the x variable has been <code>log10</code> transformed. If FALSE results will not be back transformed. |

| | |
|-------------|---|
| log_x | default is TRUE and will calculate results using the antilog of determined by log_base given that the x variable has been log() transformed. If FALSE results will not be back transformed. |
| het_sig | significance level from person's chi square goodness-of-fit test (pgof) that is used to decide if a heterogeneity factor is used. NULL is set to 0.15. |
| conf_level | adjust confidence level as necessary or NULL set at 0.95. |
| conf_type | default is "f1" which will calculate fiducial confidence limits per Finney 1971. If set to "dm" the delta method will be used instead. |
| long_output | default is TRUE which will return a tibble with all 17 variables. If FALSE the tibble returned will consist of the p level, n, the predicted LC for given p level, lower and upper confidence limits. |

Value

Returns a tibble with predicted LC for given p level, lower CL (LCL), upper CL (UCL), Pearson's chi square goodness-of-fit test (pgof), slope, intercept, slope and intercept p values and standard error, and LC variance.

References

- Finney, D.J., 1971. Probit Analysis, Cambridge University Press, Cambridge, England, ISBN: 052108041X
- Wheeler, M.W., Park, R.M., and Bailey, A.J., 2006. Comparing median lethal concentration values using confidence interval overlap or ratio tests, Environ. Toxic. Chem. 25(5), 1441-1444.10.1897/05-320R.1
- Robertson, J.L., Savin, N.E., Russell, R.M. and Preisler, H.K., 2007. Bioassays with arthropods. CRC press. ISBN: 9780849323317

Examples

```
head(lamprey_tox)

# within the dataframe used, control dose, unless produced a value
# during experimentation, are removed from the dataframe,
# as glm cannot handle values of infinite. Other statistical programs
# make note of the control dose but do not include within analysis

# calculate LC50 and LC99

m <- LC_probit((response / total) ~ log10(dose), p = c(50, 99),
              weights = total,
              data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
              subset = c(month == "May"))

# OR

m1 <- LC_probit(cbind(response, survive) ~ log10(dose), p = c(50, 99),
               data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
               subset = c(month == "May"))
```



```

# view calculated LC50 and LC99 for seasonal toxicity of a piscicide,
# to lamprey in 2011

m

# these are the same

m1

# dose-response curve can be plotted using 'ggplot2'

# library(ggplot2)

# lc_may <- subset(lamprey_tox, month %in% c("May"))

# p1 <- ggplot(data = lc_may[lc_may$nominal_dose != 0, ],
#             aes(x = log10(dose), y = (response / total))) +
#   geom_point() +
#   geom_smooth(method = "glm",
#             method.args = list(family = binomial(link = "probit")),
#             aes(weight = total), colour = "#FF0000", se = TRUE)

# p1

# calculate LC50s and LC99s for multiple toxicity tests, June, August, and September

j <- LC_probit((response / total) ~ log10(dose), p = c(50, 99),
              weights = total,
              data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
              subset = c(month == "June"))

a <- LC_probit((response / total) ~ log10(dose), p = c(50, 99),
              weights = total,
              data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
              subset = c(month == "August"))

s <- LC_probit((response / total) ~ log10(dose), p = c(50, 99),
              weights = total,
              data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
              subset = c(month == "September"))

# group results together in a dataframe to plot with 'ggplot2'

results <- rbind(m[, c(1, 3:8, 11)], j[,c(1, 3:8, 11)],
               a[, c(1, 3:8, 11)], s[, c(1, 3:8, 11)])
results$month <- factor(c(rep("May", 2), rep("June", 2),
                        rep("August", 2), rep("September", 2)),
                      levels = c("May", "June", "August", "September"))

# p2 <- ggplot(data = results, aes(x = month, y = dose,
#                                 group = factor(p), fill = factor(p))) +
#   geom_col(position = position_dodge(width = 0.9), colour = "#000000") +
#   geom_errorbar(aes(ymin = LCL, ymax = UCL),

```

```
#           size = 0.4, width = 0.06,
#           position = position_dodge(width = 0.9))

# p2
```

 LT_logit

Lethal Time Logit

Description

Calculates lethal time (LT) and its fiducial confidence limits (CL) using a logit analysis according to Finney 1971, Wheeler et al. 2006, and Robertson et al. 2007.

Usage

```
LT_logit(formula, data, p = NULL, weights = NULL,
          subset = NULL, log_base = NULL, log_x = TRUE, het_sig = NULL,
          conf_level = NULL, long_output = TRUE)
```

Arguments

| | |
|----------|--|
| formula | an object of class formula or one that can be coerced to that class: a symbolic description of the model to be fitted. |
| data | an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>LT_logit</code> is called. |
| p | Lethal time (LT) values for given p, example will return a LT50 value if p equals 50. If more than one LT value wanted specify by creating a vector. LT values can be calculated down to the 1e-16 of a percentage (e.g. LT99.99). However, the tibble produced can and will round to nearest whole number. |
| weights | vector of 'prior weights' to be used in the fitting process. Only needs to be supplied if you are taking the response / total for your response variable within the formula call of <code>LC_probit</code> . Otherwise if you use <code>cbind(response, non-response)</code> method you do not need to supply weights. If you do the model will be incorrect. If you don't supply weights there is a warning that will help you to make sure you are using one method or the other. See the following StackExchange post about differences cbind() function in R for a logistic regression . |
| subset | allows for the data to be subseted if desired. Default set to NULL. |
| log_base | default is 10 and will be used to calculate results using the anti of <code>log10()</code> given that the x variable has been <code>log10</code> transformed. If FALSE results will not be back transformed. |
| log_x | default is TRUE and will calculate results using the antilog of determined by <code>log_base</code> given that the x variable has been <code>log()</code> transformed. If FALSE results will not be back transformed. |

| | |
|-------------|---|
| het_sig | significance level from person's chi square goodness-of-fit test that is used to decide if a heterogeneity factor is used. NULL is set to 0.15. |
| conf_level | Adjust confidence level as necessary or NULL set at 0.95. |
| long_output | default is TRUE which will return a tibble with all 17 variables. If FALSE the tibble returned will consist of the p level, n, the predicted LC for given p level, lower and upper confidence limits. |

Value

Returns a tibble with predicted LT for given p level, lower CL (LCL), upper CL (UCL), LCL, Pearson's chi square goodness-of-fit test (pgof), slope, intercept, slope and intercept p values and standard error, and LT variance.

References

- Finney, D.J., 1971. Probit Analysis, Cambridge University Press, Cambridge, England, ISBN: 052108041X
- Wheeler, M.W., Park, R.M., and Bailey, A.J., 2006. Comparing median lethal concentration values using confidence interval overlap or ratio tests, Environ. Toxic. Chem. 25(5), 1441-1444.10.1897/05-320R.1
- Robertson, J.L., Savin, N.E., Russell, R.M. and Preisler, H.K., 2007. Bioassays with arthropods. CRC press. ISBN: 9780849323317

Examples

```
head(lamprey_time)

results <- LT_logit((response / total) ~ log10(hour),
  p = c(50, 99),
  weights = total,
  data = lamprey_time,
  subset = c(month == "May"))

# view calculated LT50 and LT99 for seasonal
# toxicity of a piscicide, 3-trifluoromethyl-4-nitrophenol, to lamprey in 2011

results

# dose-response curve can be plotted using 'ggplot2'
```

LT_probit

Lethal Time Probit

Description

Calculates lethal time (LT) and its fiducial confidence limits (CL) using a probit analysis according to Finney 1971, Wheeler et al. 2006, and Robertson et al. 2007.

Usage

```
LT_probit(
  formula,
  data,
  p = NULL,
  weights = NULL,
  subset = NULL,
  log_base = NULL,
  log_x = TRUE,
  het_sig = NULL,
  conf_level = NULL,
  conf_type = NULL,
  long_output = TRUE
)
```

Arguments

| | |
|------------|--|
| formula | an object of class formula or one that can be coerced to that class: a symbolic description of the model to be fitted. |
| data | an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>LT_probit</code> is called. |
| p | Lethal time (LT) values for given p, example will return a LT50 value if p equals 50. If more than one LT value wanted specify by creating a vector. LT values can be calculated down to the 1e-16 of a percentage (e.g. LT99.99). However, the tibble produced can and will round to nearest whole number. |
| weights | vector of 'prior weights' to be used in the fitting process. Only needs to be supplied if you are taking the response / total for your response variable within the formula call of <code>LC_probit</code> . Otherwise if you use <code>cbind(response, non-response)</code> method you do not need to supply weights. If you do the model will be incorrect. If you don't supply weights there is a warning that will help you to make sure you are using one method or the other. See the following StackExchange post about differences cbind() function in R for a logistic regression . |
| subset | allows for the data to be subseted if desired. Default set to NULL. |
| log_base | default is 10 and will be used to calculate results using the anti of <code>log10()</code> given that the x variable has been <code>log10</code> transformed. If FALSE results will not be back transformed. |
| log_x | default is TRUE and will calculate results using the antilog of determined by <code>log_base</code> given that the x variable has been <code>log()</code> transformed. If FALSE results will not be back transformed. |
| het_sig | significance level from person's chi square goodness-of-fit test that is used to decide if a heterogeneity factor is used. NULL is set to 0.15. |
| conf_level | Adjust confidence level as necessary or NULL set at 0.95. |
| conf_type | default is "f1" which will calculate fiducial confidence limits per Finney 1971. If set to "dm" the delta method will be used instead. |

long_output default is TRUE which will return a tibble with all 17 variables. If FALSE the tibble returned will consist of the p level, n, the predicted LC for given p level, lower and upper confidence limits.

Value

Returns a tibble with predicted LT for given p level, lower CL (LCL), upper CL (UCL), LCL, Pearson's chi square goodness-of-fit test (pgof), slope, intercept, slope and intercept p values and standard error, and LT variance.

References

Finney, D.J., 1971. Probit Analysis, Cambridge University Press, Cambridge, England, ISBN: 052108041X

Wheeler, M.W., Park, R.M., and Bailey, A.J., 2006. Comparing median lethal concentration values using confidence interval overlap or ratio tests, Environ. Toxic. Chem. 25(5), 1441-1444.10.1897/05-320R.1

Robertson, J.L., Savin, N.E., Russell, R.M. and Preisler, H.K., 2007. Bioassays with arthropods. CRC press. ISBN: 9780849323317

Examples

```
head(lamprey_time)

results <- LT_probit((response / total) ~ log10(hour),
  p = c(50, 99),
  weights = total,
  data = lamprey_time,
  subset = c(month == "May"))

# view calculated LT50 and LT99 for seasonal
# toxicity of a piscicide, 3-trifluoromethyl-4-nitrophenol, to lamprey in 2011

results

# dose-response curve can be plotted using 'ggplot2'
```

ratio_test

Ratio test

Description

Calculates a ratio test to compare two LC or LT values from two separate probit or logit models. This function is based on the ratio test developed in [Wheeler et al. 2006. 10.1897/05-320R.1](#) which has been suggested as a replacement to the common method of comparing confidence intervals to determine differences.

Usage

```
ratio_test(model_1, model_2, percentage = NULL,
           type = NULL, compare = NULL, log_base = NULL, log_x = TRUE,
           obj_type = NULL, conf_type = NULL)
```

Arguments

| | |
|------------|--|
| model_1 | first model used in the ratio test. Should be an object of either a probit or logit model created using the <code>glm()</code> function. See example. |
| model_2 | second model used in the ratio test. Should be an object of either a probit or logit model created using the <code>glm()</code> function. See example. |
| percentage | either a single value or a vector for given LC or LT percentage desired to compare. Percentage is the same value used for the argument <code>p</code> in all <code>LC_</code> and <code>LT_</code> functions. For example, 50 will return and compare LC50 values for the two models. If more than one LC value is desired specify by creating a vector. LC values can be calculated down to the 1e-16 of a percentage (e.g. LC99.99). However, the tibble produced can and will round to nearest whole number. |
| type | Link type needs to be specified to either "probit" which is default and will return and used in calculations for a probit model for the desired LCs or LTs. If specified to "logit" then <code>ratio_test</code> will return and calculate using a logit model for the desired LCs or LTs. |
| compare | Supply a character string to be used in the output letting the user know what models the LCs or LTs are being compared. Default output is "Model 1 - Model 2". See example. |
| log_base | default is 10 and will be used to calculate results using the anti of <code>log10()</code> given that the <code>x</code> variable has been <code>log10</code> transformed. If FALSE results will not be back transformed. |
| log_x | default is TRUE and will calculate results using the antilog of determined by <code>log_base</code> given that the <code>x</code> variable has been <code>log()</code> transformed. If FALSE results will not be back transformed. |
| obj_type | default is "list" which requires both <code>model_1</code> and <code>model_2</code> arguments to be model objects, in the form of a list, from <code>glm()</code> functions. Alternatively "df" can be used which will require both <code>model_1</code> and <code>model_2</code> arguments to be <code>data.frame</code> objects created when running either <code>LC_</code> or <code>LT_</code> functions. |
| conf_type | default is "f1" which if "df" is supplied will correct covariance values if <code>h</code> is above 1 as fiducial confidence limits use a heterogeneity factor, <code>h</code> , to correct variances when chi-square <code>p</code> value is less than 0.15. <code>conf_type</code> can also be "dm", delta method, which doesn't use a heterogeneity correction factor therefore covariance will not be uncorrected. This argument is only needed if you are using the <code>dataframe</code> objects from <code>LC_</code> or <code>LT_</code> functions and have used the delta method in that analysis. |

Value

A tibble with `percentage` for the LC or LT value desired for the above `percentage` argument, `dose_1` and `dose_2` displayed calculated backtransformed or untransformed doses for the desired

LC or LT values. Standard Error (se), Z test statistic (test_stat) and p_value determined using Z test statistic as determined using formulas in [Wheeler et al. 2006](#).

References

Wheeler, M.W., Park, R.M., and Bailey, A.J., 2006. Comparing median lethal concentration values using confidence interval overlap or ratio tests, Environ. Toxic. Chem. 25(5), 1441-1444. [10.1897/05-320R.1](#)

Examples

```
# view lamprey_tox data

head(lamprey_tox)

# using glm() to determine LC values using probit model for May and June

m <- glm((response / total) ~ log10(dose),
        data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
        subset = c(month == "May"),
        weights = total,
        family = binomial(link = "probit"))

j <- glm((response / total) ~ log10(dose),
        data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
        subset = c(month == "June"),
        weights = total,
        family = binomial(link = "probit"))

# now that both May and June models have been made. use ratio_test to
# compare LC50 values or whatever LC values of interest.

ratios <- ratio_test(model_1 = m, model_2 = j, percentage = 50,
                    compare = "May - June")

# view ratio test results

ratios

# you can also use LC_probit to create the models and use ratio test

m_1 <- LC_probit((response / total) ~ log10(dose), p = c(50, 99),
                weights = total,
                data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
                subset = c(month == "May"))

j_1 <- LC_probit((response / total) ~ log10(dose), p = c(50, 99),
                weights = total,
                data = lamprey_tox[lamprey_tox$nominal_dose != 0, ],
```

```
subset = c(month == "June")
```

```
ratios_2 <- ratio_test(model_1 = m_1, model_2 = j_1, percentage = 50,  
compare = "May - June", obj_type = "df")
```

```
ratios_2
```


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