

# Package ‘ecotox’

March 6, 2020

**Type** Package

**Title** Analysis of Ecotoxicology

**Version** 1.4.2

**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>;  
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

**License** GPL-3 | file LICENSE

**Encoding** UTF-8

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**Author** Benjamin L Hlina [aut, cre]

**Maintainer** Benjamin L Hlina <benjamin.hlina@gmail.com>

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## R topics documented:

lamprey_time . . . . .	2
lamprey_tox . . . . .	3
LC_logit . . . . .	4
LC_probit . . . . .	7
LT_logit . . . . .	10
LT_probit . . . . .	11
ratio_test . . . . .	13

<b>Index</b>	<b>16</b>
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lamprey_time	<i>Lethal time data for seasonal exposure to TFM for larval sea lamprey</i>
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### 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

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lamprey_tox	<i>Lethal concentration data for seasonal exposure to TFM for larval sea lamprey</i>
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### 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, 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> ) 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_logit</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 StackExchange post about differences <a href="#">cbind() function in R for a logistic regression</a> .
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 19 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 and their distances.

### Value

Returns a tibble with predicted LC for given p level, lower CL (LCL), upper CL (UCL), LCL and UCL distance away from LC (LCL\_dis & UCL\_dis; important for creating a plot), 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 = (dose - LCL_dis), ymax = (dose + UCL_dis)),
#              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,
          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 StackExchange post about differences <a href="#">cbind() function in R for a logistic regression</a> .
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> tranformed. 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> tranformed. 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.
long_output	default is TRUE which will return a tibble with all 19 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 and their distances.

### Value

Returns a tibble with predicted LC for given p level, lower CL (LCL), upper CL (UCL), LCL and UCL distance away from LC (LCL\_dis & UCL\_dis; important for creating a plot), 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 = (dose - LCL_dis), ymax = (dose + UCL_dis)),
#               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 <a href="#">cbind() function in R for a logistic regression</a> .
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 19 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 and their distances.

**Value**

Returns a tibble with predicted LT for given p level, lower CL (LCL), upper CL (UCL), LCL and UCL distance away from LT (LCL\_dis & UCL\_dis; important for creating a plot), 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,
  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> ) 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 <a href="#">cbind() function in R for a logistic regression</a> .
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> tranformed. 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> tranformed. 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 19 variabless. If FALSE the tibble returned will consist of the p level, n, the predicted LC for given p level, lower and upper confidence limits and their distances.

**Value**

Returns a tibble with predicted LT for given p level, lower CL (LCL), upper CL (UCL), LCL and UCL distance away from LT (`LCL_dis` & `UCL_dis`; important for creating a plot), 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	<i>Ratio test</i>
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---

## 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)
```

## 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 <code>LC50</code> 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. <code>LC99.99</code> ). 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 ratio_test 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 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.

### 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
```

# Index

## \*Topic **datasets**

lamprey\_time, 2

lamprey\_tox, 3

lamprey\_time, 2

lamprey\_tox, 3

LC\_logit, 4

LC\_probit, 7

LT\_logit, 10

LT\_probit, 11

ratio\_test, 13