Package 'biodosetools'

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Title An R Shiny Application for Biological Dosimetry

Version 3.6.0

Description A tool to perform all different statistical tests and calculations needed by Biological Dosimetry Laboratories.

License GPL-3

URL https://biodosetools-team.github.io/biodosetools/,
https://github.com/biodosetools-team/biodosetools/

BugReports https://github.com/biodosetools-team/biodosetools/issues/

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R topics documented:

`AIC_from_data` *Calculate AIC (Akaike's 'An Information Criterion')*

Description

Calculate AIC (Akaike's 'An Information Criterion')

Usage

```
AIC_from_data(
  general_fit_coeffs,
  data,
  dose_var = "dose",
  yield_var = "yield",
  fit_link = "identity"
)
```

Arguments

`general_fit_coeffs`	Generalised fit coefficients matrix.
`data`	Data (dose, yield) to calculate AIC from.
`dose_var`	Name of the dose variable (enquoted).
`yield_var`	Name of the yield variable (enquoted).
`fit_link`	A specification for the model link function.

Value

Numeric value of AIC.

`biodosetools` `biodosetools` *package*

Description

Shiny App To Be Used By Biological Dosimetry Laboratories

Details

See the README on GitHub

`calculate_aberr` *Aberration calculation functions*

Description

Aberration calculation functions

Usage

```
calculate_aberr_power(data, aberr_prefix = "C", power = 1)

calculate_aberr_mean(X, N)

calculate_aberr_var(X, X2, N)

calculate_aberr_disp_index(mean, var)

calculate_aberr_u_value(X, N, mean, var, assessment_u = 1)

init_aberr_table(data, type = c("count", "case"), aberr_module)
```

Arguments

`data`	Count or case data.
`aberr_prefix`	Prefix of the aberrations in the data.
`power`	Power of aberration.
`X`	Sum of detected aberrations.
`N`	Number of cells analysed.
`X2`	Quadratic sum of detected aberrations.
`mean`	Mean.
`var`	Variance.
`assessment_u`	Expected u-value of the assessment. For a Poisson distribution this should be unity.
`type`	Type of input data. Either "count" and "case".
`aberr_module`	Aberration module.

`calculate_aberr_table` *Calculate aberrations table*

Description

Calculate aberrations table

Usage

```
calculate_aberr_table(data, type = c("count", "case"), assessment_u = 1)
```

Arguments

`data`	Count or case data.
`type`	Type of input data. Either "count" and "case".
`assessment_u`	Expected u-value of the assessment. For a Poisson distribution this should be unity.

Value

Data frame containing cell count (N), aberrations (X), and other coefficients (dispersion index, u-value, ...), as well as raw count or case `data`.

`calculate_decision_threshold` *Calculate decision thresholds*

Description

Calculate decision thresholds

Arguments

`fit_results_list`	List of fit results.
`cells`	Number of cells `N`.
`count_data`	Count data in data frame form.
`model_formula`	Model formula.
`model_family`	Model family.
`frequency_select`	Whether to use measured frequency or full genome frequency.
`conf_int`	Confidence interval.
`aberr_module`	Aberration module.

`calculate_genome_factor` *Calculate genomic conversion factor*

Description

Method based on the paper by Lucas, J. N. et al. (1992). Rapid Translocation Frequency Analysis in Humans Decades after Exposure to Ionizing Radiation. International Journal of Radiation Biology, 62(1), 53-63. <doi:10.1080/09553009214551821>.

Usage

```
calculate_genome_factor(dna_table, chromosomes, colors, sex)
```

Arguments

`dna_table`	DNA content fractions table. Can be `dna_content_fractions_morton` or `dna_content_table_ihgsc`.
`chromosomes`	Vector of stained chromosomes.
`colors`	Vector of colors of the stains.
`sex`	Sex of the individual.

Value

Numeric value of genomic conversion factor.

`calculate_model_stats` *Calculate model statistics*

Description

Calculate model statistics

Usage

```
calculate_model_stats(
  model_data,
  fit_coeffs_vec,
  glm_results = NULL,
  fit_algorithm = NULL,
  response = "yield",
  link = c("identity", "log"),
  type = c("theory", "raw"),
  Y = NULL,
  mu = NULL,
  n = NULL,
```

```
  npar = NULL,
  genome_factor = NULL,
  calc_type = c("fitting", "estimation")
)
```

Arguments

`model_data`	Data of the model.
`fit_coeffs_vec`	Vector of fitting coefficients.
`glm_results`	Results of glm.
`fit_algorithm`	String of the algorithm used.
`response`	Type of response.
`link`	Fit link.
`type`	Theoretical or raw glm model statistics.
`Y`	Y response (required in constraint-maxlik-optimization).
`mu`	mu response required in constraint-maxlik-optimization).
`n`	number of parameters (required in constraint-maxlik-optimization).
`npar`	number of parameters (required in constraint-maxlik-optimization).
`genome_factor`	Genomic conversion factor used in translocations.
`calc_type`	Calculation type, either "fitting" or "estimation".

Value

Data frame of model statistics.

`calculate_trans_rate_manual`

Calculate manual translocation rate

Description

Calculate manual translocation rate

Usage

```
calculate_trans_rate_manual(cells, genome_factor, expected_aberr_value)
```

Arguments

`cells`	Number of cells `N`.
`genome_factor`	Genomic conversion factor.
`expected_aberr_value`	Expected aberrations.

Value

Numeric value of translocation rate.

`calculate_trans_rate_sigurdson`

Calculate Sigurdson's translocation rate

Description

Method based on the paper by Sigurdson, A. J. et al. (2008). International study of factors affecting human chromosome translocations. Mutation Research/Genetic Toxicology and Environmental Mutagenesis, 652(2), 112-121. <doi:10.1016/j.mrgentox.2008.01.005>.

Usage

```
calculate_trans_rate_sigurdson(
  cells,
  genome_factor,
  age_value,
  sex_bool = FALSE,
  sex_value = "none",
  smoker_bool = FALSE,
  ethnicity_value = "none",
  region_value = "none"
)
```

Arguments

`cells`	Number of cells `N`.
`genome_factor`	Genomic conversion factor.
`age_value`	Age of the individual.
`sex_bool`	If `TRUE`, `sex_value` will be used.
`sex_value`	Sex of the individual, either "male" of "female".
`smoker_bool`	Whether the individual smokes or not.
`ethnicity_value`	Ethnicity of the individual.
`region_value`	Region of the individual.

Value

Numeric value of translocation rate.

`calculate_yield` *Calculate yield from dose*

Description

Calculate yield from dose

Usage

```
calculate_yield(
  dose,
  type = c("estimate", "lower", "upper"),
  general_fit_coeffs,
  general_fit_var_cov_mat = NULL,
  protracted_g_value = 1,
  conf_int = 0.95
)
```

Arguments

`dose`	Numeric value of dose.
`type`	Type of yield calculation. Can be "estimate", "lower", or "upper".
`general_fit_coeffs`	Generalised fit coefficients matrix.
`general_fit_var_cov_mat`	Generalised variance-covariance matrix.
`protracted_g_value`	Protracted $G(x)$ value.
`conf_int`	Curve confidence interval, 95% by default.

Value

Numeric value of yield.

`calculate_yield_infimum` *Calculate theoretical yield infimum*

Description

Calculate theoretical yield infimum

Usage

```
calculate_yield_infimum(
  type = c("estimate", "lower", "upper"),
  general_fit_coeffs,
  general_fit_var_cov_mat = NULL,
  conf_int = 0.95
)
```

Arguments

`type`	Type of yield calculation. Can be "estimate", "lower", or "upper".
`general_fit_coeffs`	Generalised fit coefficients matrix.
`general_fit_var_cov_mat`	Generalised variance-covariance matrix.
`conf_int`	Curve confidence interval, 95% by default.

Value

Numeric value of yield infimum.

`correct_boundary` *Correct boundary of irradiated fractions to be bounded by 0 and 1*

Description

Correct boundary of irradiated fractions to be bounded by 0 and 1

Usage

```
correct_boundary(x)
```

Arguments

`x`	Numeric value.

Value

Numeric value in [0, 1] range.

`correct_conf_int` *Correct yield confidence interval*

Description

Correct yield confidence interval if simple method is required.

Usage

```
correct_conf_int(
  conf_int,
  general_fit_var_cov_mat,
  protracted_g_value = 1,
  type,
  dose = seq(0, 10, 0.2)
)
```

Arguments

`conf_int`	Confidence interval.
`general_fit_var_cov_mat`	Generalised variance-covariance matrix.
`protracted_g_value`	Protracted $G(x)$ value.
`type`	Type of yield calculation. Can be "estimate", "lower", or "upper".
`dose`	Numeric value of dose.

Value

Numeric value of corrected confidence interval.

`correct_negative_vals` *Correct negative values*

Description

Correct negative values

Usage

```
correct_negative_vals(x)
```

Arguments

`x`	Numeric value.

Value

Numeric value corrected to zero if negative.

`correct_yield` *Correct yields if they are below the curve*

Description

Correct yields if they are below the curve

Usage

```
correct_yield(
  yield,
  type = "estimate",
  general_fit_coeffs,
  general_fit_var_cov_mat,
  conf_int
)
```

Arguments

`yield`	Numeric value of yield.
`type`	Type of yield calculation. Can be "estimate", "lower", or "upper".
`general_fit_coeffs`	Generalised fit coefficients matrix.
`general_fit_var_cov_mat`	Generalised variance-covariance matrix.
`conf_int`	Curve confidence interval.

Value

Numeric value of corrected yield.

`dna_content_fractions_ihgsc` *DNA Content Fractions of Human Chromosomes (IHGSC)*

Description

Normalised DNA Content of Human Chromosomes from the International Human Genome Sequencing Consortium.

Usage

```
dna_content_fractions_ihgsc
```

Format

A data frame with 24 rows and 3 variables:

chromosome Chromosome.

fraction_male Normalised content of megabases on male human DNA.

fraction_female Normalised content of megabases on female human DNA.

Details

Last accessed in July 2020.

Source

`https://www.ncbi.nlm.nih.gov/grc/human/data`

`dna_content_fractions_morton` *DNA Content Fractions of Human Chromosomes (Morton 1991)*

Description

Normalised DNA Content of Human Chromosomes from Morton, N. E. (1991). Parameters of the human genome. Proceedings of the National Academy of Sciences, 88(17), 7474-7476.

Usage

```
dna_content_fractions_morton
```

Format

A data frame with 24 rows and 3 variables:

chromosome	Chromosome.
fraction_male	Normalised content of megabases on male human DNA.
fraction_female	Normalised content of megabases on female human DNA.

Source

doi: 10.1073/pnas.88.17.7474

`estimate_hetero_mixed_poisson`

Heterogeneous dose estimation (Mixed Poisson model)

Description

Method based on the paper by Pujol, M. et al. (2016). A New Model for Biological Dose Assessment in Cases of Heterogeneous Exposures to Ionizing Radiation. Radiation Research, 185(2), 151-162. <doi:10.1667/RR14145.1>.

Usage

```
estimate_hetero_mixed_poisson(
  case_data,
  fit_coeffs,
  fit_var_cov_mat,
  conf_int = 0.95,
  protracted_g_value = 1,
  gamma,
  gamma_error
)
```

Arguments

`case_data`	Case data in data frame form.
`fit_coeffs`	Fitting coefficients matrix.
`fit_var_cov_mat`	Fitting variance-covariance matrix.
`conf_int`	Confidence interval, 95% by default.
`protracted_g_value`	Protracted $G(x)$ value.
`gamma`	Survival coefficient of irradiated cells.
`gamma_error`	Error of the survival coefficient of irradiated cells.

Value

List containing estimated mixing proportions data frame, estimated yields data frame, estimated doses data frame, estimated fraction of irradiated blood data frame, and AIC.

`estimate_partial_body_dolphin` *Partial-body dose estimation (Dolphin's method)*

Description

Method based on the paper by Dolphin, G. W. (1969). Biological Dosimetry with Particular Reference to Chromosome Aberration Analysis: A Review of Methods. International Atomic Energy Agency (IAEA) Retrieved from `https://inis.iaea.org/search/search.aspx?orig_q=RN:45029080`.

Usage

```
estimate_partial_body_dolphin(
  case_data,
  fit_coeffs,
  fit_var_cov_mat,
  conf_int = 0.95,
  protracted_g_value = 1,
  genome_factor = 1,
  gamma,
  aberr_module
)
```

Arguments

`case_data`	Case data in data frame form.
`fit_coeffs`	Fitting coefficients matrix.
`fit_var_cov_mat`	Fitting variance-covariance matrix.
`conf_int`	Confidence interval, 95% by default.
`protracted_g_value`	Protracted $G(x)$ value.
`genome_factor`	Genomic conversion factor used in translocations, else 1.
`gamma`	Survival coefficient of irradiated cells.
`aberr_module`	Aberration module.

Value

List containing estimated doses data frame, estimated fraction of irradiated blood data frame, and AIC.

`estimate_whole_body_delta`

Whole-body dose estimation (delta method)

Description

Method based on 2001 manual by the International Atomic Energy Agency (IAEA). Cytogenetic Analysis for Radiation Dose Assessment, Technical Reports Series (2001). Retrieved from `https://www.iaea.org/publications/6303/cytogenetic-analysis-for-radiation-dose-assessment`.

Usage

```
estimate_whole_body_delta(
  case_data,
  fit_coeffs,
  fit_var_cov_mat,
  conf_int = 0.95,
  protracted_g_value = 1,
  aberr_module
)
```

Arguments

`case_data`	Case data in data frame form.
`fit_coeffs`	Fitting coefficients matrix.
`fit_var_cov_mat`	Fitting variance-covariance matrix.
`conf_int`	Confidence interval, 95% by default.
`protracted_g_value`	Protracted $G(x)$ value.
`aberr_module`	Aberration module.

Value

List containing estimated doses data frame and AIC.

`estimate_whole_body_merkle`

Whole-body dose estimation (Merkle's method)

Description

Method based on the paper by Merkle, W. (1983). Statistical methods in regression and calibration analysis of chromosome aberration data. Radiation and Environmental Biophysics, 21(3), 217-233. <doi:10.1007/BF01323412>.

Usage

```
estimate_whole_body_merkle(
  case_data,
  fit_coeffs,
  fit_var_cov_mat,
  conf_int_yield = 0.83,
  conf_int_curve = 0.83,
  protracted_g_value = 1,
  genome_factor = 1,
  aberr_module
)
```

Arguments

`case_data`	Case data in data frame form.
`fit_coeffs`	Fitting coefficients matrix.
`fit_var_cov_mat`	Fitting variance-covariance matrix.
`conf_int_yield`	Confidence interval of the yield, 83% by default.
`conf_int_curve`	Confidence interval of the curve, 83% by default.
`protracted_g_value`	Protracted $G(x)$ value.
`genome_factor`	Genomic conversion factor used in translocations, else 1.
`aberr_module`	Aberration module.

Value

List containing estimated doses data frame and AIC.

`fit` *Perform dose-effect fitting algorithm*

Description

Perform dose-effect fitting. A generalized linear model (GLM) is used by default, with a maximum likelihood estimation (MLE) as a fallback method.

Usage

```
fit(
  count_data,
  model_formula,
  model_family,
  fit_link = "identity",
  aberr_module,
  algorithm = c("glm", "maxlik")
)
```

Arguments

`count_data`	Count data in data frame form.
`model_formula`	Model formula.
`model_family`	Model family.
`fit_link`	Family link.
`aberr_module`	Aberration module.
`algorithm`	Optional selection of algorithm to be used, either "glm" (for GLM) or "maxlik" (for MLE). By default, "glm" is used, with "maxlik" as a fallback method.

Details

The GLM method is based on the paper by Edwards, A. A. et al. (1979). Radiation induced chromosome aberrations and the Poisson distribution. Radiation and Environmental Biophysics, 16(2), 89-100. <doi:10.1007/BF01323216>.

The MLE method is based on the paperby Oliveira, M. et al. (2016). Zero-inflated regression models for radiation-induced chromosome aberration data: A comparative study. Biometrical Journal, 58(2), 259-279. <doi:10.1002/bimj.201400233>.

Value

List object containing fit results either using GLM or maxLik optimization.

`fit_glm_method` *Perform GLM (Generalised Linear Model) fitting*

Description

Method based on the paper by Edwards, A. A. et al. (1979). Radiation induced chromosome aberrations and the Poisson distribution. Radiation and Environmental Biophysics, 16(2), 89-100. <doi:10.1007/BF01323216>.

Usage

```
fit_glm_method(
  count_data,
  model_formula,
  model_family = c("automatic", "poisson", "quasipoisson", "nb2"),
  fit_link = "identity",
  aberr_module
)
```

Arguments

`count_data`	Count data in data frame form.
`model_formula`	Model formula.
`model_family`	Model family.
`fit_link`	Family link.
`aberr_module`	Aberration module.

Value

List object containing GLM fit results.

`fit_maxlik_method` *Perform max-likelihood optimization fitting*

Description

Method based on the paper by Oliveira, M. et al. (2016). Zero-inflated regression models for radiation-induced chromosome aberration data: A comparative study. Biometrical Journal, 58(2), 259-279. <doi:10.1002/bimj.201400233>.

Usage

```
fit_maxlik_method(
  data,
  model_formula,
  model_family = c("automatic", "poisson", "quasipoisson", "nb2"),
  fit_link,
  aberr_module
)
```

Arguments

`data`	Count data.
`model_formula`	Model formula.
`model_family`	Model family.
`fit_link`	Family link.
`aberr_module`	Aberration module.

Value

List object containing maxLik fit results.

`gardner_confidence_table`

Gardner's Confidence Intervals Table

Description

Confidence intervals for the expectation of a Poisson variable.

Usage

```
gardner_confidence_table
```

Format

A data frame with 1201 rows and 3 variables:

s_est Nominal value for the Poisson variable.

s_low Lower confidence interval for the Poisson variable.

s_upp Upper confidence interval for the Poisson variable.

Source

doi: 10.1093/biomet/46.34.441

`get_deltamethod_std_err`

Get standard errors using delta method

Description

Delta method for approximating the standard error of a transformation $g(X)$ of a random variable $X = (x1, x2, ...)$, given estimates of the mean and covariance matrix of X.

Usage

```
get_deltamethod_std_err(
  fit_is_lq,
  variable = c("dose", "fraction_partial", "fraction_hetero"),
  mean_estimate,
  cov_estimate,
  protracted_g_value = NA,
  d0 = NA
)
```

Arguments

`fit_is_lq`	Whether the fit is linear quadratic (`TRUE`) or linear (`FALSE`).
`variable`	Variable resulting of the transformation $g(X)$.
`mean_estimate`	The estimated mean of X.
`cov_estimate`	The estimated covariance matrix of X.
`protracted_g_value`	Protracted $G(x)$ value.
`d0`	Survival coefficient of irradiated cells.

Value

Numeric value containing the standard error of the dose estimate.

`include_help` *Include Markdown help*

Description

Include Markdown help

Usage

```
include_help(...)
```

Arguments

`...`	Character vector specifying directory and or file to point to inside the current package.

`load_rmd_report` *Load RMarkdown report*

Description

Load RMarkdown report

Usage

```
load_rmd_report(...)
```

Arguments

`...`	Character vector specifying directory and or file to point to inside the current package.

`plot_estimated_dose_curve` *Plot dose estimation curve*

Description

Plot dose estimation curve

Usage

```
plot_estimated_dose_curve(
  est_doses,
  fit_coeffs,
  fit_var_cov_mat,
  protracted_g_value = 1,
  conf_int_curve,
  aberr_name
)
```

Arguments

`est_doses`	List of dose estimations results from `estimate_*()` family of functions.
`fit_coeffs`	Fitting coefficients matrix.
`fit_var_cov_mat`	Fitting variance-covariance matrix.
`protracted_g_value`	Protracted $G(x)$ value.
`conf_int_curve`	Confidence interval of the curve.
`aberr_name`	Name of the aberration to use in the y-axis.

Value

`ggplot2` object.

`plot_fit_dose_curve` *Plot fit dose curve*

Description

Plot fit dose curve

Usage

```
plot_fit_dose_curve(fit_results_list, aberr_name)
```

Arguments

`fit_results_list`	List of fit results.
`aberr_name`	Name of the aberration to use in the y-axis.

Value

`ggplot2` object.

`prepare_maxlik_count_data` *Prepare count data for max-likelihood optimization fitting*

Description

Prepare count data for max-likelihood optimization fitting

Usage

```
prepare_maxlik_count_data(count_data, model_formula, aberr_module)
```

Arguments

`count_data`	Count data in data frame form.
`model_formula`	Model formula.
`aberr_module`	Aberration module.

Value

Data frame of parsed count data.

`project_yield` *Project yield into dose-effect fitting curve*

Description

Project yield into dose-effect fitting curve

Usage

```
project_yield(
  yield,
  type = "estimate",
  general_fit_coeffs,
  general_fit_var_cov_mat = NULL,
  protracted_g_value = 1,
  conf_int = 0.95
)
```

Arguments

`yield`	Yield to be projected.
`type`	Type of yield calculation. Can be "estimate", "lower", or "upper".
`general_fit_coeffs`	Generalised fit coefficients matrix.
`general_fit_var_cov_mat`	Generalised variance-covariance matrix.
`protracted_g_value`	Protracted $G(x)$ value.
`conf_int`	Curve confidence interval, 95% by default.

Value

Numeric value of projected dose.

`protracted_g_function` *Calculate protracted function* $G(x)$

Description

Calculation based on the paper by Lea, D. E. & Catcheside, D. G. (1942). The mechanism of the induction by radiation of chromosome aberrations in*Tradescantia*. Journal of Genetics, 44(2-3), 216-245. <doi:10.1007/BF02982830>.

Usage

```
protracted_g_function(time, time_0 = 2)
```

Arguments

`time`	Time over which the irradiation occurred.
`time_0`	The mean lifetime of the breaks, which has been shown to be on the order of ~ 2 hours (default value).

Value

Numeric value of $G(x)$.

`run_app` *Run the Shiny Application*

Description

Run the Shiny Application

Usage

```
run_app(...)
```

Arguments

`...`	A series of options to be used inside the app.

Value

Used for side-effect.

`R_factor` *Calculate R regression confidence factor*

Description

Calculate R regression confidence factor depending on selected confidence interval and type of fit.

Usage

```
R_factor(general_fit_coeffs, conf_int = 0.95)
```

Arguments

`general_fit_coeffs`	Generalised fit coefficients matrix.
`conf_int`	Confidence interval, 95% by default.

Value

Numeric value of R regression confidence factor.

`yield_error_fun` *Calculate yield error*

Description

Calculate yield error using Merkle's method

Usage

```
yield_error_fun(dose, general_fit_var_cov_mat = NULL, protracted_g_value = 1)
```

Arguments

`dose`	Numeric value of dose.
`general_fit_var_cov_mat`	Generalised variance-covariance matrix.
`protracted_g_value`	Protracted $G(x)$ value.

Value

Numeric value of yield error.

`yield_fun` *Calculate yield*

Description

Calculate yield

Usage

```
yield_fun(dose, general_fit_coeffs, protracted_g_value = 1)
```

Arguments

`dose`	Numeric value of dose.
`general_fit_coeffs`	Generalised fit coefficients matrix.
`protracted_g_value`	Protracted $G(x)$ value.

Value

Numeric value of yield.

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