

Package ‘biodosetools’

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Title 'shiny' Application for Biological Dosimetry

Version 3.7.2

Description A tool to perform all different statistical tests and calculations needed by Biological dosimetry Laboratories. Detailed documentation is available in <<https://biodosetools-team.github.io/documentation/>>.

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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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

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

Value

Numeric value of AIC.

`bar_plots`*Bar plots dosimetry*

Description

Bar plots dosimetry

Usage`bar_plots(dat, curve, place)`**Arguments**

<code>dat</code>	data frame of data values.
<code>curve</code>	manual or auto.
<code>place</code>	UI or save.

Value

plot

Examples

```
dat <- data.frame(
  "Lab" = c("A1", "A2"),
  "Module" = c("dicentrics", "dicentrics"),
  "Type" = c("manual", "manual"),
  "radiation quality" = c("Cs-137", "Co-60"),
  "calibration" = c("air kerma", "air kerma"),
  "irradiation" = c("air", "air"),
  "temperature" = c(20, 37),
  "dose rate" = c(0.446, 0.27),
  "curve origin" = c("own", "own"),
  "C" = c(0.001189589, 0.0005),
  "alpha" = c(0.01903783, 0.0142),
  "beta" = c(0.0968831, 0.0759),
  "C std.error" = c(0.0001040828, 0.0005),
  "alpha std.error" = c(0.004119324, 0.0044),
  "beta std.error" = c(0.003505209, 0.0027),
  "max curve dose" = c(6.00, 5.05),
  stringsAsFactors = FALSE,
  check.names = FALSE
)

bar_plots(
  dat = dat,
  curve = "manual",
  place = "UI"
)
```

calc.zValue.new	<i>Calculate ZScore</i>
-----------------	-------------------------

Description

Calculate ZScore

Usage

```
calc.zValue.new(X, type, alg, c)
```

Arguments

X	vector of estimated doses.
type	dose or freq.
alg	algorithm. Choose between algA, algB or QHampel
c	value for reference dose.

Value

Numeric value of zscore.

Examples

```
calc.zValue.new(X = c(3.65, 2.5, 4.85),  
               type = "dose",  
               alg = "algA" ,  
               c = c(3.5, 3, 4.25))
```

calculate_aberr	<i>Aberration calculation functions</i>
-----------------	---

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 = c("dicentrics", "translocations", "micronuclei")
)

```

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 <i>u</i> -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_IRR *Calculate IRR (this is the same as the Odds-Ratio calculation in IAEA2011)*

Description

Calculate IRR (this is the same as the Odds-Ratio calculation in IAEA2011)

Usage

```
calculate_aberr_IRR(case_data, fit_coeffs, badge_dose)
```

Arguments

case_data	Case data in data frame form.
fit_coeffs	Fitting coefficients matrix.
badge_dose	Suspected (e.g. badge) dose

Value

character variable representing IRR in the for (P(X=k|D=0 Gy):P(X=k|D=badge_dose)).

calculate_aberr_table *Calculate aberrations table*

Description

Calculate aberrations table

Usage

```
calculate_aberr_table(  
  data,  
  type = c("count", "case"),  
  aberr_module = c("dicentrics", "translocations", "micronuclei"),  
  assessment_u = 1  
)
```

Arguments

data	Count or case data.
type	Type of input data. Either "count" and "case".
aberr_module	Aberration module, required for type = "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.

Examples

```
data <- data.frame(  
  ID = c("example1", "example2"),  
  C0 = c(302, 160),  
  C1 = c(28, 55),  
  C2 = c(22, 19),  
  C3 = c(8, 17),  
  C4 = c(1, 9),  
  C5 = c(0, 4)  
)  
  
calculate_aberr_table(data,  
  type = "case",  
  aberr_module = "dicentrics",  
  assessment_u = 1)
```

`calculate_characteristic_limits`*Characteristic limits function*

Description

Characteristic limits function

Usage

```
calculate_characteristic_limits(  
  mu0 = NULL,  
  n1 = NULL,  
  y0 = NULL,  
  n0 = NULL,  
  alpha = 0.05,  
  beta = 0.1,  
  ymax = 100,  
  type = "const"  
)
```

Arguments

<code>mu0</code>	Background rate
<code>n1</code>	Number of cells that will be analysed.
<code>y0</code>	Background number of dicentrics.
<code>n0</code>	Background number of cells analysed.
<code>alpha</code>	Type I error rate, 0.05 by default.
<code>beta</code>	Type II error rate, 0.1 by default.
<code>ymax</code>	Max dicentrics to evaluate.
<code>type</code>	Type.

Value

List of characteristic limits (`decision_threshold`, `detection_limit`).

Examples

```
control_data <- c(aberr = 4,  
                 cells = 1000)  
  
calculate_characteristic_limits(  
  y0 = control_data["aberr"],  
  n0 = control_data["cells"],  
  n1 = 20,  
  alpha = 0.05,
```

```
    beta = 0.1,  
    ymax = 100,  
    type = "var"  
  )
```

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.

Examples

```
#dna_table can be: dna_content_fractions_morton OR dna_content_fractions_ihgsc  
  
calculate_genome_factor(  
  dna_table = dna_content_fractions_morton,  
  chromosome = c(1, 2, 3, 4, 5, 6),  
  color = c("Red", "Red", "Green", "Red", "Green", "Green"),  
  sex = "male"  
)
```

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"),  
  model_family  
)
```

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".
model_family	Model family.

Value

Data frame of model statistics.

calculate_table	<i>Calculate the characteristic limits table</i>
-----------------	--

Description

Calculate the characteristic limits table

Usage

```
calculate_table(input, project_yield, fit_coeffs)
```

Arguments

input	all input UI parameters
project_yield	function for calculating yield, in utils_estimation.R
fit_coeffs	curve coefficients

Value

list with all the table columns.

calculate_trans_rate_manual	<i>Calculate manual translocation rate</i>
-----------------------------	--

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.

Examples

```
calculate_trans_rate_manual(cells = 1000,
                           genome_factor = 0.58,
                           expected_aberr_value = 0.3)
```

```
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.

Examples

```
calculate_trans_rate_sigurdson(
  cells = 1000,
  genome_factor = 0.58,
  age_value = 30,
  sex_bool = FALSE,
  sex_value = "none",
  smoker_bool = FALSE,
  ethnicity_value = "none",
  region_value = "none"
)
```

calculate_yield	<i>Calculate yield from dose</i>
-----------------	----------------------------------

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	<i>Correct yield confidence interval</i>
------------------	--

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	<i>Correct negative values</i>
-----------------------	--------------------------------

Description

Correct negative values

Usage

```
correct_negative_vals(x)
```

Arguments

x Numeric value.

Value

Numeric value corrected to zero if negative.

correct_yield	<i>Correct yields if they are below the curve</i>
---------------	---

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.

`curves_plot`*Plot curves*

Description

Plot curves

Usage`curves_plot(dat, curve, curve_type = "lin_quad", place)`**Arguments**

<code>dat</code>	data frame of data values.
<code>curve</code>	manual or auto.
<code>curve_type</code>	lin or lin_quad.
<code>place</code>	UI or save.

Value

ggplot2 object.

Examples

```
dat <- data.frame(  
  "Lab" = c("A1", "A2"),  
  "Module" = c("dicentrics", "dicentrics"),  
  "Type" = c("manual", "manual"),  
  "radiation quality" = c("Cs-137", "Co-60"),  
  "calibration" = c("air kerma", "air kerma"),  
  "irradiation" = c("air", "air"),  
  "temperature" = c(20, 37),  
  "dose rate" = c(0.446, 0.27),  
  "curve origin" = c("own", "own"),  
  "C" = c(0.001189589, 0.0005),  
  "alpha" = c(0.01903783, 0.0142),  
  "beta" = c(0.0968831, 0.0759),  
  "C std.error" = c(0.0001040828, 0.0005),  
  "alpha std.error" = c(0.004119324, 0.0044),  
  "beta std.error" = c(0.003505209, 0.0027),  
  "max curve dose" = c(6.00, 5.05),  
  stringsAsFactors = FALSE,  
  check.names = FALSE  
)
```

```
curves_plot(  
  dat = dat,
```

```

curve = "manual",
curve_type = "lin_quad",
place = "UI"
)

```

DI_plot

Dispersion index

Description

Dispersion index

Usage

```
DI_plot(dat, place)
```

Arguments

dat	data frame of data values.
place	UI or save.

Value

plot

Examples

```

dat <- data.frame(
  Lab = c("A1", "A2", "A1", "A2", "A1", "A2"),
  Module = c("dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics"),
  Type = c("manual", "manual", "manual", "manual", "manual", "manual"),
  Sample = c(1, 1, 2, 2, 3, 3),
  N = c(200, 200, 200, 200, 200, 200),
  X = c(140, 111, 204, 147, 368, 253),
  estimate = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  lower = c(2.083403, 2.231150, 2.614931, 2.622748, 3.882349, 3.552963),
  upper = c(3.208857, 3.045616, 3.785879, 3.471269, 4.688910, 4.487336),
  y = c(0.700, 0.555, 1.020, 0.735, 1.840, 1.265),
  y.err = c(0.0610, 0.0495, 0.0733, 0.0556, 0.0923, 0.0785),
  DI = c(1.0625, 0.8818, 1.0539, 0.8406, 0.9255, 0.9731),
  u = c(0.6252, -1.1840, 0.5389, -1.5951, -0.7442, -0.2692),
  stringsAsFactors = FALSE
)

DI_plot(
  dat = dat,
  place = "UI"
)

```

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](https://doi.org/10.1073/pnas.88.17.7474)

dose_boxplot

Boxplot dose estimates

Description

Boxplot dose estimates

Usage

```
dose_boxplot(dat, place)
```

Arguments

dat data frame of data values.
place UI or save.

Value

plot

Examples

```
dat <- data.frame(
  Lab = c("A1", "A2", "A1", "A2", "A1", "A2"),
  Module = c("dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics"),
  Type = c("manual", "manual", "manual", "manual", "manual", "manual"),
  Sample = c(1, 1, 2, 2, 3, 3),
  N = c(200, 200, 200, 200, 200, 200),
  X = c(140, 111, 204, 147, 368, 253),
  estimate = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  lower = c(2.083403, 2.231150, 2.614931, 2.622748, 3.882349, 3.552963),
  upper = c(3.208857, 3.045616, 3.785879, 3.471269, 4.688910, 4.487336),
  y = c(0.700, 0.555, 1.020, 0.735, 1.840, 1.265),
  y.err = c(0.0610, 0.0495, 0.0733, 0.0556, 0.0923, 0.0785),
  DI = c(1.0625, 0.8818, 1.0539, 0.8406, 0.9255, 0.9731),
  u = c(0.6252, -1.1840, 0.5389, -1.5951, -0.7442, -0.2692),
  stringsAsFactors = FALSE
```

```

)

dose_boxplot(
  dat = dat,
  place = "UI"
)

```

dose_estimation_mx *Prepare data to dose estimate using mixed fields manual*

Description

Prepare data to dose estimate using mixed fields manual

Usage

```
dose_estimation_mx(input, reactive_data, data_type)
```

Arguments

input	what you upload in the UI
reactive_data	access to the reactive data
data_type	gamma or neutron

Value

data for dose estimation using manual input.

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, AIC, and conf_int_* used.

Examples

#The fitting RDS result from the fitting module is needed. Alternatively, manual data #frames that match the structure of the RDS can be used:

```
fit_coeffs <- data.frame(
  estimate = c(0.001280319, 0.021038724, 0.063032534),
  std.error = c(0.0004714055, 0.0051576170, 0.0040073856),
  statistic = c(2.715961, 4.079156, 15.729091),
  p.value = c(6.608367e-03, 4.519949e-05, 9.557291e-56),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

fit_var_cov_mat <- data.frame(
  coeff_C = c(2.222231e-07, -9.949044e-07, 4.379944e-07),
  coeff_alpha = c(-9.949044e-07, 2.660101e-05, -1.510494e-05),
  coeff_beta = c(4.379944e-07, -1.510494e-05, 1.605914e-05),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

case_data <- data.frame(
  ID= "example1",
  N = 361,
  X = 100,
  C0 = 302,
  C1 = 28,
  C2 = 22,
  C3 = 8,
  C4 = 1,
  C5 = 0,
```

```

    y = 0.277,
    y_err = 0.0368,
    DI = 1.77,
    u = 10.4
  )

#FUNCTION ESTIMATE_HETERO_MIXED_POISSON
estimate_hetero_mixed_poisson(
  case_data[1, ],
  fit_coeffs = as.matrix(fit_coeffs),
  fit_var_cov_mat = as.matrix(fit_var_cov_mat),
  conf_int = 0.95,
  protracted_g_value = 1,
  gamma = 1 / 2.7,
  gamma_error = 0
)

```

```
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(
  num_cases,
  case_data,
  fit_coeffs,
  fit_var_cov_mat,
  conf_int = 0.95,
  protracted_g_value = 1,
  genome_factor = 1,
  gamma,
  aberr_module = c("dicentrics", "translocations", "micronuclei")
)

```

Arguments

num_cases	number of cases.
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, observed fraction of cells scored which were irradiated, estimated fraction of irradiated blood data frame, AIC, and `conf_int_*` used.

Examples

```

#The fitting RDS result from the fitting module is needed. Alternatively, manual data
#frames that match the structure of the RDS can be used:

```

```

fit_coeffs <- data.frame(
  estimate   = c(0.001280319, 0.021038724, 0.063032534),
  std.error  = c(0.0004714055, 0.0051576170, 0.0040073856),
  statistic  = c(2.715961, 4.079156, 15.729091),
  p.value    = c(6.608367e-03, 4.519949e-05, 9.557291e-56),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

fit_var_cov_mat <- data.frame(
  coeff_C     = c(2.22231e-07, -9.949044e-07, 4.379944e-07),
  coeff_alpha = c(-9.949044e-07, 2.660101e-05, -1.510494e-05),
  coeff_beta  = c(4.379944e-07, -1.510494e-05, 1.605914e-05),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

case_data <- data.frame(
  ID= "example1",
  N = 361,
  X = 100,
  C0 = 302,
  C1 = 28,
  C2 = 22,
  C3 = 8,
  C4 = 1,
  C5 = 0,
  y = 0.277,
  y_err = 0.0368,
  DI = 1.77,
  u = 10.4
)

```

```
#FUNCTION ESTIMATE_PARTIAL_BODY_DOLPHIN
estimate_partial_body_dolphin(
  num_cases = 1,
  case_data = case_data,
  fit_coeffs = as.matrix(fit_coeffs),
  fit_var_cov_mat = as.matrix(fit_var_cov_mat),
  conf_int = 0.95,
  gamma = 1 / 2.7,
  aberr_module = "dicentrics"
)
```

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(
  num_cases,
  case_data,
  fit_coeffs,
  fit_var_cov_mat,
  conf_int = 0.95,
  protracted_g_value = 1,
  aberr_module = c("dicentrics", "translocations", "micronuclei")
)
```

Arguments

num_cases	number of cases.
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, AIC, and conf_int used.

Examples

#The fitting RDS result from the fitting module is needed. Alternatively, manual data #frames that match the structure of the RDS can be used:

```
fit_coeffs <- data.frame(
  estimate = c(0.001280319, 0.021038724, 0.063032534),
  std.error = c(0.0004714055, 0.0051576170, 0.0040073856),
  statistic = c(2.715961, 4.079156, 15.729091),
  p.value = c(6.608367e-03, 4.519949e-05, 9.557291e-56),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

fit_var_cov_mat <- data.frame(
  coeff_C = c(2.222231e-07, -9.949044e-07, 4.379944e-07),
  coeff_alpha = c(-9.949044e-07, 2.660101e-05, -1.510494e-05),
  coeff_beta = c(4.379944e-07, -1.510494e-05, 1.605914e-05),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)
```

```
case_data <- data.frame(
  ID= "example1",
  N = 361,
  X = 100,
  C0 = 302,
  C1 = 28,
  C2 = 22,
  C3 = 8,
  C4 = 1,
  C5 = 0,
  y = 0.277,
  y_err = 0.0368,
  DI = 1.77,
  u = 10.4
)
```

```
#FUNCTION ESTIMATE_WHOLE_BODY_DELTA
estimate_whole_body_delta(
  num_cases = 1,
  case_data = case_data,
  fit_coeffs = as.matrix(fit_coeffs),
  fit_var_cov_mat = as.matrix(fit_var_cov_mat),
  conf_int = 0.95,
  protracted_g_value = 1,
  aberr_module = "dicentrics"
)
```

`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(  
  num_cases,  
  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 = c("dicentrics", "translocations", "micronuclei")  
)
```

Arguments

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

Value

List containing estimated doses data frame, AIC, and `conf_int_*` used.

Examples

#The fitting RDS result from the fitting module is needed. Alternatively, manual data #frames that match the structure of the RDS can be used:

```
fit_coeffs <- data.frame(
  estimate   = c(0.001280319, 0.021038724, 0.063032534),
  std.error  = c(0.0004714055, 0.0051576170, 0.0040073856),
  statistic  = c(2.715961, 4.079156, 15.729091),
  p.value    = c(6.608367e-03, 4.519949e-05, 9.557291e-56),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

fit_var_cov_mat <- data.frame(
  coeff_C      = c(2.222231e-07, -9.949044e-07, 4.379944e-07),
  coeff_alpha  = c(-9.949044e-07, 2.660101e-05, -1.510494e-05),
  coeff_beta   = c(4.379944e-07, -1.510494e-05, 1.605914e-05),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)
```

```
case_data <- data.frame(
  ID= "example1",
  N = 361,
  X = 100,
  C0 = 302,
  C1 = 28,
  C2 = 22,
  C3 = 8,
  C4 = 1,
  C5 = 0,
  y = 0.277,
  y_err = 0.0368,
  DI = 1.77,
  u = 10.4
)
```

```
#FUNCTION ESTIMATE_WHOLE_BODY_MERKLE
estimate_whole_body_merkle(
  num_cases = 1,
  case_data = case_data,
  fit_coeffs = as.matrix(fit_coeffs),
  fit_var_cov_mat = as.matrix(fit_var_cov_mat),
  conf_int_yield = 0.83,
  conf_int_curve = 0.83,
  protracted_g_value = 1,
  aberr_module = "dicentrics"
)
```

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 = c("dicentrics", "translocations", "micronuclei"),
  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 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>.

Value

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

Examples

```
count_data <- data.frame(
  D = c(0, 0.1, 0.25, 0.5, 0.75, 1, 1.5, 2, 3, 4, 5),
  N = c(5000, 5002, 2008, 2002, 1832, 1168, 562, 333, 193, 103, 59),
  X = c(8, 14, 22, 55, 100, 109, 100, 103, 108, 103, 107),
  C0 = c(4992, 4988, 1987, 1947, 1736, 1064, 474, 251, 104, 35, 11),
  C1 = c(8, 14, 20, 55, 92, 99, 76, 63, 72, 41, 19),
  C2 = c(0, 0, 1, 0, 4, 5, 12, 17, 15, 21, 11),
  C3 = c(0, 0, 0, 0, 0, 0, 0, 2, 2, 4, 9),
```

```

C4 = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 6),
C5 = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 3),
mean = c(0.0016, 0.0028, 0.0110, 0.0275, 0.0546, 0.0933, 0.178, 0.309, 0.560, 1, 1.81),
var = c(0.00160, 0.00279, 0.0118, 0.0267, 0.0560, 0.0933, 0.189, 0.353, 0.466, 0.882, 2.09),
DI = c(0.999, 0.997, 1.08, 0.973, 1.03, 0.999, 1.06, 1.14, 0.834, 0.882, 1.15),
u = c(-0.0748, -0.135, 2.61, -0.861, 0.790, -0.0176, 1.08, 1.82, -1.64, -0.844, 0.811)
)

fit(count_data = count_data,
    model_formula = "lin-quad",
    model_family = "automatic",
    fit_link = "identity",
    aberr_module = "dicentrics",
    algorithm = "maxlik")

```

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 = c("dicentrics", "translocations", "micronuclei")
)

```

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	<i>Perform max-likelihood optimization fitting</i>
-------------------	--

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 = c("dicentrics", "translocations", "micronuclei")  
)
```

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.

fun.curve	<i>Calculate curve</i>
-----------	------------------------

Description

Calculate curve

Usage

```
fun.curve(d, coef, curve_type)
```

Arguments

d	dose
coef	curve coefficients
curve_type	type of curve: lin_quad, lin

Value

Numeric value.

fun.estimate.criticality

Calculate absorbed dose for mixed fields exposure

Description

Calculate absorbed dose for mixed fields exposure

Usage

```
fun.estimate.criticality(
  num_cases,
  dics,
  cells,
  coef_gamma,
  cov_gamma,
  coef_neutron,
  cov_neutron,
  ratio,
  p
)
```

Arguments

num_cases	number of cases to estimate.
dics	dicentrics.
cells	total cells.
coef_gamma	Coefficients for gamma curve.
cov_gamma	Covariance matrix for gamma curve.
coef_neutron	Coefficients for neutron curve.
cov_neutron	Covariance matrix for neutron curve.
ratio	gamma-neutron ratio.
p	photon contribution in mixed curve.

Value

dose estimation

Examples

```
#Results from the fitting module
fit_results_gamma <- system.file("extdata",
                                "gamma_dicentrics-fitting-results.rds",
                                package = "biosetools") %>%
  readRDS()

fit_results_neutrons <- system.file("extdata",
                                    "neutrons-mixed-dicentrics-fitting-results.rds",
                                    package = "biosetools") %>%
  readRDS()

#FUNCTION TO ESTIMATE DOSE IN CRITICALITY ACCIDENTS
fun.estimate.criticality(num_cases = 2,
                        dics = c(380,456),
                        cells = c(218,567),
                        coef_gamma = fit_results_gamma[["fit_coeffs"]][,1],
                        cov_gamma = fit_results_gamma[["fit_var_cov_mat"]],
                        coef_neutron = fit_results_neutrons[["fit_coeffs"]][,1],
                        cov_neutron = fit_results_neutrons[["fit_var_cov_mat"]],
                        ratio = 1.2,
                        p = 0)
```

generate_plot_and_download

Plot at the UI and save

Description

Plot at the UI and save

Usage

```
generate_plot_and_download(
  data_type,
  reactive_data,
  output,
  input,
  manual,
  dose_plot,
  name_num
)
```

Arguments

data_type	gamma or neutron
reactive_data	access to the reactive data
output	connection with UI
input	what you upload in the UI
manual	logical, indicates if using manual input or file data.
dose_plot	the number of the dose case to plot.
name_num	associates a number to the name.

Value

plot at UI and saving plot server logic

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 $X = (x_1, x_2, \dots)$, 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	<i>Include Markdown help</i>
--------------	------------------------------

Description

Include Markdown help

Usage

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

Arguments

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

load_manual_data	<i>Load manual data</i>
------------------	-------------------------

Description

Load manual data

Usage

```
load_manual_data(data_type, input, reactive_data, output, session)
```

Arguments

data_type	gamma or neutron
input	what you upload in the UI
reactive_data	access to the reactive data
output	output for the UI
session	let interaction with the shiny UI

Value

manual curve information tables.

load_rds_data	<i>Load and show rds files</i>
---------------	--------------------------------

Description

Load and show rds files

Usage

```
load_rds_data(input_data, data_type, reactive_data, output, session)
```

Arguments

input_data	what you upload as rds file in the UI.
data_type	gamma or neutron.
reactive_data	access to the reactive data.
output	output for the UI.
session	let interaction with the shiny UI.

Value

uploaded rds file's curve information-tables.

load_rmd_report	<i>Load RMarkdown report</i>
-----------------	------------------------------

Description

Load RMarkdown report

Usage

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

Arguments

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

M_estimate	<i>Calculate algB</i>
------------	-----------------------

Description

Calculate algB

Usage

```
M_estimate(x, iter_loc = 50, iter_scale = 1000)
```

Arguments

x	vector of n observations.
iter_loc	number of iteration steps for location estimate (default=50).
iter_scale	number of iteration steps for scale estimate (default=1000).

Value

Numeric value of zscore using algB.

Examples

```
X = c(3.65, 2.5, 4.85)

M_estimate(x = as.numeric(X),
           iter_loc=50,
           iter_scale=1000)
```

plot_deviation_all	<i>Plot Deviaition from ref dose all blind samples</i>
--------------------	--

Description

Plot Deviaition from ref dose all blind samples

Usage

```
plot_deviation_all(zscore, select_method, place)
```

Arguments

zscore	zscore vector to plot for each lab.
select_method	chosen algorithm for zscore.
place	UI or save.

Value

ggplot2 object.

Examples

```
data_frame_zscore <- data.frame(
  Lab = factor(c("A1", "A2", "A1", "A2", "A1", "A2")),
  Sample = factor(c(1, 1, 2, 2, 3, 3)),
  Type = rep("manual", 6),
  Reference = c(2.56, 3.41, 4.54, 2.56, 3.41, 4.54),
  Dose = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  Deviation = c(0.02922998, -0.79902999, -1.39394510, 0.45868228, 0.84939953, -0.55077813),
  Zscore = c(1.677656, 2.925426, -2.585664, -3.833434, -1.295906, -2.543676),
  stringsAsFactors = FALSE
)

plot_deviation_all(
  zscore = data_frame_zscore,
  select_method = "algA",
  place = "UI"
)
```

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,
  place
)
```

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.
place                UI or save.

```

Value

ggplot2 object.

Examples

```

#The fitting RDS result from the fitting module is needed. Alternatively, manual data
#frames that match the structure of the RDS can be used:
fit_coeffs <- data.frame(
  estimate = c(0.001280319, 0.021038724, 0.063032534),
  std.error = c(0.0004714055, 0.0051576170, 0.0040073856),
  statistic = c(2.715961, 4.079156, 15.729091),
  p.value = c(6.608367e-03, 4.519949e-05, 9.557291e-56),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

fit_var_cov_mat <- data.frame(
  coeff_C = c(2.222231e-07, -9.949044e-07, 4.379944e-07),
  coeff_alpha = c(-9.949044e-07, 2.660101e-05, -1.510494e-05),
  coeff_beta = c(4.379944e-07, -1.510494e-05, 1.605914e-05),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

results_whole_merkle <- list(
  list(
    est_doses = data.frame(
      lower = 1.541315,
      estimate = 1.931213,
      upper = 2.420912
    ),
    est_yield = data.frame(
      lower = 0.1980553,
      estimate = 0.277,
      upper = 0.3841655
    ),
    AIC = 7.057229,
    conf_int = c(yield_curve = 0.83)
  )
)

#FUNCTION PLOT_ESTIMATED_DOSE_CURVE
plot_estimated_dose_curve(

```

```

est_doses = list(whole = results_whole_merkle),
fit_coeffs = as.matrix(fit_coeffs),
fit_var_cov_mat = as.matrix(fit_var_cov_mat),
protracted_g_value = 1,
conf_int_curve = 0.95,
aberr_name = "Micronuclei",
place = "UI"
)

```

plot_estimated_dose_curve_mx
Criticality Plot

Description

Criticality Plot

Usage

```

plot_estimated_dose_curve_mx(
  name,
  est_doses,
  fit_coeffs,
  fit_var_cov_mat,
  curve_type,
  protracted_g_value = 1,
  conf_int_curve = 0.95,
  place
)

```

Arguments

name	the dose to plot.
est_doses	List of dose estimations results.
fit_coeffs	Fitting coefficients matrix.
fit_var_cov_mat	Fitting variance-covariance matrix.
curve_type	gamma or neutron.
protracted_g_value	Protracted $G(x)$ value.
conf_int_curve	Confidence interval of the curve.
place	UI, report or save. Where the plot will be displayed.

Value

ggcurve

Examples

#The fitting RDS result from the fitting module is needed. Alternatively, manual data #frames that match the structure of the RDS can be used:

```
fit_coeffs <- data.frame(
  estimate = c(0.001280319, 0.021038724, 0.063032534),
  std.error = c(0.0004714055, 0.0051576170, 0.0040073856),
  statistic = c(2.715961, 4.079156, 15.729091),
  p.value = c(6.608367e-03, 4.519949e-05, 9.557291e-56),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

fit_var_cov_mat <- data.frame(
  coeff_C = c(2.222231e-07, -9.949044e-07, 4.379944e-07),
  coeff_alpha = c(-9.949044e-07, 2.660101e-05, -1.510494e-05),
  coeff_beta = c(4.379944e-07, -1.510494e-05, 1.605914e-05),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

est_doses <- list(
  list(
    gamma = c(est = 2.173586, lwr = 1.784314, upr = 2.562857),
    neutron = c(est = 1.811322, lwr = 1.486929, upr = 2.135715),
    total = c(est = 3.984907, lwr = 3.271243, upr = 4.698572)
  )
)

#FUNCTION PLOT_ESTIMATED_DOSE_CURVE_MX
plot_estimated_dose_curve_mx(
  name = "Sample1",
  est_doses = est_doses[[1]],
  fit_coeffs = as.matrix(fit_coeffs)[,1],
  fit_var_cov_mat = as.matrix(fit_var_cov_mat),
  curve_type = "gamma",
  protracted_g_value = 1,
  conf_int_curve = 0.95,
  place = "UI")
```

plot_fit_dose_curve *Plot fit dose curve*

Description

Plot fit dose curve

Usage

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

Arguments

`fit_results_list` List of fit results.

`aberr_name` Name of the aberration to use in the y-axis.

`place` Where the plot will be displayed.

Value

ggplot2 object.

Examples

```
#In order to plot the fitted curve we need the output of the fit() function:
count_data <- data.frame(
  D = c(0, 0.1, 0.25, 0.5, 0.75, 1, 1.5, 2, 3, 4, 5),
  N = c(5000, 5002, 2008, 2002, 1832, 1168, 562, 333, 193, 103, 59),
  X = c(8, 14, 22, 55, 100, 109, 100, 103, 108, 103, 107),
  C0 = c(4992, 4988, 1987, 1947, 1736, 1064, 474, 251, 104, 35, 11),
  C1 = c(8, 14, 20, 55, 92, 99, 76, 63, 72, 41, 19),
  C2 = c(0, 0, 1, 0, 4, 5, 12, 17, 15, 21, 11),
  C3 = c(0, 0, 0, 0, 0, 0, 0, 2, 2, 4, 9),
  C4 = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 6),
  C5 = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 3),
  mean = c(0.0016, 0.0028, 0.0110, 0.0275, 0.0546, 0.0933, 0.178, 0.309, 0.560, 1, 1.81),
  var = c(0.00160, 0.00279, 0.0118, 0.0267, 0.0560, 0.0933, 0.189, 0.353, 0.466, 0.882, 2.09),
  DI = c(0.999, 0.997, 1.08, 0.973, 1.03, 0.999, 1.06, 1.14, 0.834, 0.882, 1.15),
  u = c(-0.0748, -0.135, 2.61, -0.861, 0.790, -0.0176, 1.08, 1.82, -1.64, -0.844, 0.811)
)

fit_results <- fit(count_data = count_data,
                  model_formula = "lin-quad",
                  model_family = "automatic",
                  fit_link = "identity",
                  aberr_module = "dicentrics",
                  algorithm = "maxlik")

#FUNCTION PLOT_FIT_DOSE_CURVE()
plot_fit_dose_curve(
  fit_results,
  aberr_name = "Dicentrics",
  place = "UI"
)
```

plot_interlab_deviation

Plot deviation

Description

Plot deviation

Usage

```
plot_interlab_deviation(zscore, sum_table, place)
```

Arguments

zscore	data frame with Lab, Sample, Type, Reference, Dose, Deviation and Zscore.
sum_table	summary table.
place	UI or save.

Value

ggplot2 object.

Examples

```
data_frame_zscore <- data.frame(
  Lab = factor(c("A1", "A2", "A1", "A2", "A1", "A2")),
  Sample = factor(c(1, 1, 2, 2, 3, 3)),
  Type = rep("manual", 6),
  Reference = c(2.56, 3.41, 4.54, 2.56, 3.41, 4.54),
  Dose = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  Deviation = c(0.02922998, -0.79902999, -1.39394510, 0.45868228, 0.84939953, -0.55077813),
  Zscore = c(1.677656, 2.925426, -2.585664, -3.833434, -1.295906, -2.543676),
  stringsAsFactors = FALSE
)

sum_table <- data.frame(
  Lab = c("A1", "A2", "A1", "A2", "A1", "A2"),
  Module = c("dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics"),
  Type = rep("manual", 6),
  Sample = c(1, 1, 2, 2, 3, 3),
  N = c(200, 200, 200, 200, 200, 200),
  X = c(140, 111, 204, 147, 368, 253),
  estimate = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  lower = c(2.083403, 2.231150, 2.614931, 2.622748, 3.882349, 3.552963),
  upper = c(3.208857, 3.045616, 3.785879, 3.471269, 4.688910, 4.487336),
  y = c(0.700, 0.555, 1.020, 0.735, 1.840, 1.265),
  y.err = c(0.0610, 0.0495, 0.0733, 0.0556, 0.0923, 0.0785),
  DI = c(1.0625, 0.8818, 1.0539, 0.8406, 0.9255, 0.9731),
  u = c(0.6252, -1.1840, 0.5389, -1.5951, -0.7442, -0.2692),
  stringsAsFactors = FALSE
)

#FUNCTION PLOT_INTERLAB_DEVIATION:
plot_interlab_deviation(
  zscore = data_frame_zscore,
```

```

    sum_table = sum_table,
    place = "UI"
  )

```

plot_interlab_v2 *Plot zscore v2*

Description

Plot zscore v2

Usage

```
plot_interlab_v2(zscore, select_method, sum_table, place)
```

Arguments

zscore	data frame with Lab, Sample, Type, Reference, Dose, Deviation and Zscore.
select_method	Zscore algorithm.
sum_table	summary table.
place	UI or save.

Value

ggplot2 object.

Examples

```

data_frame_zscore <- data.frame(
  Lab = factor(c("A1", "A2", "A1", "A2", "A1", "A2")),
  Sample = factor(c(1, 1, 2, 2, 3, 3)),
  Type = rep("manual", 6),
  Reference = c(2.56, 3.41, 4.54, 2.56, 3.41, 4.54),
  Dose = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  Deviation = c(0.02922998, -0.79902999, -1.39394510, 0.45868228, 0.84939953, -0.55077813),
  Zscore = c(1.677656, 2.925426, -2.585664, -3.833434, -1.295906, -2.543676),
  stringsAsFactors = FALSE
)

```

```

sum_table <- data.frame(
  Lab = c("A1", "A2", "A1", "A2", "A1", "A2"),
  Module = c("dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics"),
  Type = rep("manual", 6),
  Sample = c(1, 1, 2, 2, 3, 3),
  N = c(200, 200, 200, 200, 200, 200),
  X = c(140, 111, 204, 147, 368, 253),
  estimate = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  lower = c(2.083403, 2.231150, 2.614931, 2.622748, 3.882349, 3.552963),
)

```

```

upper = c(3.208857, 3.045616, 3.785879, 3.471269, 4.688910, 4.487336),
y = c(0.700, 0.555, 1.020, 0.735, 1.840, 1.265),
y.err = c(0.0610, 0.0495, 0.0733, 0.0556, 0.0923, 0.0785),
DI = c(1.0625, 0.8818, 1.0539, 0.8406, 0.9255, 0.9731),
u = c(0.6252, -1.1840, 0.5389, -1.5951, -0.7442, -0.2692),
stringsAsFactors = FALSE
)

#FUNCTION PLOT_INTERLAB_V2
plot_interlab_v2(zscore = data_frame_zscore,
                select_method = "algA",
                sum_table = sum_table,
                place = "UI"
                )

```

plot_triage

Plot triage

Description

Plot triage

Usage

```
plot_triage(num_cases, est_doses_whole, est_doses_partial, assessment, place)
```

Arguments

num_cases	number of cases.
est_doses_whole	dose estimation list of cases.
est_doses_partial	dose estimation list of cases.
assessment	partial or whole.
place	UI or save.

Value

ggplot2 object.

Examples

```

est_doses_whole <- data.frame(
  ID = c("example1", "example2"),
  lower = c(1.407921, 2.604542),
  estimate = c(1.931245, 3.301014),
  upper = c(2.632199, 4.221749)
)

```

```

)

plot_triage(
  num_cases = 2,
  est_doses_whole ,
  est_doses_partial = NULL,
  assessment = "whole",
  place = "UI"
)

```

plot_triage_interlab *Plot triage interlab*

Description

Plot triage interlab

Usage

```
plot_triage_interlab(line_triage, sum_table, place)
```

Arguments

line_triage	reference value for selected sample.
sum_table	summary table.
place	UI or save.

Value

ggplot2 object.

Examples

```

line_triage <- list(`1` = 2.56, `2` = 3.41, `3` = 4.54)

sum_table <- data.frame(
  Lab = c("A1", "A2", "A1", "A2", "A1", "A2"),
  Module = c("dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics"),
  Type = c("manual", "manual", "manual", "manual", "manual", "manual"),
  Sample = c(1, 1, 2, 2, 3, 3),
  N = c(200, 200, 200, 200, 200, 200),
  X = c(140, 111, 204, 147, 368, 253),
  estimate = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  lower = c(2.083403, 2.231150, 2.614931, 2.622748, 3.882349, 3.552963),
  upper = c(3.208857, 3.045616, 3.785879, 3.471269, 4.688910, 4.487336),
  y = c(0.700, 0.555, 1.020, 0.735, 1.840, 1.265),
  y.err = c(0.0610, 0.0495, 0.0733, 0.0556, 0.0923, 0.0785),

```

```

DI = c(1.0625, 0.8818, 1.0539, 0.8406, 0.9255, 0.9731),
u = c(0.6252, -1.1840, 0.5389, -1.5951, -0.7442, -0.2692),
stringsAsFactors = FALSE
)

plot_triage_interlab(
  line_triage = line_triage,
  sum_table = sum_table,
  place = "UI"
)

```

plot_zscore_all *Plot Z-scores all blind samples*

Description

Plot Z-scores all blind samples

Usage

```
plot_zscore_all(zscore, select_method, place)
```

Arguments

zscore	zscore vector to plot for each lab.
select_method	chosen algorithm for zscore.
place	UI or save.

Value

ggplot2 object.

Examples

```

data_frame_zscore <- data.frame(
  Lab = factor(c("A1", "A2", "A1", "A2", "A1", "A2")),
  Sample = factor(c(1, 1, 2, 2, 3, 3)),
  Type = rep("manual", 6),
  Reference = c(2.56, 3.41, 4.54, 2.56, 3.41, 4.54),
  Dose = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  Deviation = c(0.02922998, -0.79902999, -1.39394510, 0.45868228, 0.84939953, -0.55077813),
  Zscore = c(1.677656, 2.925426, -2.585664, -3.833434, -1.295906, -2.543676),
  stringsAsFactors = FALSE
)

plot_zscore_all(
  zscore = data_frame_zscore,
  select_method = "algA",

```

```

    place = "UI"
  )

```

```

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 = c("dicentrics", "translocations", "micronuclei")
)

```

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.

Examples

```
fit_coeffs <- data.frame(
  estimate = c(0.001280319, 0.021038724, 0.063032534),
  std.error = c(0.0004714055, 0.0051576170, 0.0040073856),
  statistic = c(2.715961, 4.079156, 15.729091),
  p.value = c(6.608367e-03, 4.519949e-05, 9.557291e-56),
  row.names = c("coeff_C", "coeff_alpha", "coeff_beta")
)

project_yield(yield = 0.67,
             type = "estimate",
             general_fit_coeffs = fit_coeffs[, "estimate"],
             general_fit_var_cov_mat = NULL,
             protracted_g_value = 1,
             conf_int = 0.95)
```

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 $G(x)$.

Examples

```
protracted_g_function(time = 3,
                      time_0 = 2)
```

QHampel

Calculate QHampel

Description

Calculate QHampel

Usage

```
QHampel(y, lab, tol.G1 = 1e-06)
```

Arguments

y vector of data values.
lab corresponding lab numbers.
tol.G1 decimal place accuracy of the numerator of s.star.

Value

Numeric value of zscore using QHampel algorithm.

Examples

```
X = c(3.65, 2.5, 4.85)
```

```
QHampel(y = as.numeric(X),
        lab = 1:length(X),
        tol.G1=0.000001)
```

run_app	<i>Run the Shiny Application</i>
---------	----------------------------------

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	<i>Calculate R regression confidence factor</i>
----------	---

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.

summary_curve_tables *Summary and curve tables*

Description

Summary and curve tables

Usage

```
summary_curve_tables(num_labs, list_lab_names, all_rds)
```

Arguments

num_labs number of laboratories participating.
list_lab_names list with the laboratory names.
all_rds list with the rds files.

Value

list(sorted_table_ilc, sorted_table_curve)

Examples

```
#fit_results_X is the output from the Estimation module

fit_results_A1 <- system.file("extdata", "A1_Estimation_results.rds", package = "biosetools") %>%
  readRDS()

fit_results_A2 <- system.file("extdata", "A2_Estimation_results.rds", package = "biosetools") %>%
  readRDS()

summary_curve_tables(num_labs = 2,
                     list_lab_names = c("A", "B"),
                     all_rds = list(fit_results_A1, fit_results_A2)
                     )
```

update_outputs *Update dose estimation box with yield values*

Description

Update dose estimation box with yield values

Usage

```
update_outputs(num_cases, reactive_data, output, yield_fun, manual, table)
```

Arguments

num_cases number of cases to estimate.
 reactive_data to access reactive data.
 output output for the UI.
 yield_fun function for calculating yield, in utils_estimation.R
 manual logical, indicates if using manual input or file data.
 table the data input table.

Value

yield per dose. Numeric

u_test_plot	<i>U-test</i>
-------------	---------------

Description

U-test

Usage

```
u_test_plot(dat, place)
```

Arguments

dat data frame of data values.
 place UI or save.

Value

plot

Examples

```
dat <- data.frame(
  Lab = c("A1", "A2", "A1", "A2", "A1", "A2"),
  Module = c("dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics"),
  Type = c("manual", "manual", "manual", "manual", "manual", "manual"),
  Sample = c(1, 1, 2, 2, 3, 3),
  N = c(200, 200, 200, 200, 200, 200),
  X = c(140, 111, 204, 147, 368, 253),
  estimate = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
```

```

lower = c(2.083403, 2.231150, 2.614931, 2.622748, 3.882349, 3.552963),
upper = c(3.208857, 3.045616, 3.785879, 3.471269, 4.688910, 4.487336),
y = c(0.700, 0.555, 1.020, 0.735, 1.840, 1.265),
y.err = c(0.0610, 0.0495, 0.0733, 0.0556, 0.0923, 0.0785),
DI = c(1.0625, 0.8818, 1.0539, 0.8406, 0.9255, 0.9731),
u = c(0.6252, -1.1840, 0.5389, -1.5951, -0.7442, -0.2692),
stringsAsFactors = FALSE
)

u_test_plot(
  dat = dat,
  place = "UI"
)

```

yield_boxplot

Boxplot yield

Description

Boxplot yield

Usage

```
yield_boxplot(dat, place)
```

Arguments

dat	data frame of data values.
place	UI or save.

Value

plot

Examples

```

dat <- data.frame(
  Lab = c("A1", "A2", "A1", "A2", "A1", "A2"),
  Module = c("dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics", "dicentrics"),
  Type = c("manual", "manual", "manual", "manual", "manual", "manual"),
  Sample = c(1, 1, 2, 2, 3, 3),
  N = c(200, 200, 200, 200, 200, 200),
  X = c(140, 111, 204, 147, 368, 253),
  estimate = c(2.589230, 2.610970, 3.146055, 3.018682, 4.259400, 3.989222),
  lower = c(2.083403, 2.231150, 2.614931, 2.622748, 3.882349, 3.552963),
  upper = c(3.208857, 3.045616, 3.785879, 3.471269, 4.688910, 4.487336),
  y = c(0.700, 0.555, 1.020, 0.735, 1.840, 1.265),
  y.err = c(0.0610, 0.0495, 0.0733, 0.0556, 0.0923, 0.0785),
  DI = c(1.0625, 0.8818, 1.0539, 0.8406, 0.9255, 0.9731),

```

```

    u = c(0.6252, -1.1840, 0.5389, -1.5951, -0.7442, -0.2692),
    stringsAsFactors = FALSE
  )

  yield_boxplot(
    dat = dat,
    place = "UI"
  )

```

yield_error_fun	<i>Calculate yield error</i>
-----------------	------------------------------

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	<i>Calculate yield</i>
-----------	------------------------

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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