

Package ‘BKMutate’

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Type Package

Title Statistical Analysis of Induced Mutagenesis Experiments in Crop Plants

Version 0.1.0

Description A colour-first toolkit for the statistical analysis of induced mutagenesis experiments in crop plants. It fits dose-response models to physical and chemical mutagen data and estimates the median lethal and growth-reduction doses (LD50, GR50) with confidence intervals obtained from Fieller's theorem; quantifies first-generation biological damage (lethality, injury and pollen sterility); and estimates mutagenic effectiveness and mutagenic efficiency. Effectiveness and efficiency are conventionally reported as point estimates only; this package treats them as functions of binomial proportions and supplies interval estimates by the delta method on the logarithmic scale and by the nonparametric bootstrap. It further provides chlorophyll mutation spectrum analysis with tests of homogeneity and diversity, generalised linear models for second-generation mutant counts with formal assessment of overdispersion, and formal comparison of mutagens including relative biological effectiveness. Every analysis returns a tidy result object and a publication-ready 'ggplot2' figure. Methods follow Konzak et al. (1965, ISBN:9789201150653), Fieller (1954) <doi:10.1111/j.2517-6161.1954.tb00159.x> and Katz et al. (1978) <doi:10.2307/2530610>.

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BugReports <https://github.com/bkpraveenars-del/BKMutate/issues>

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Contents

BKMutate-package	2
bm_compare	3
bm_data	3
bm_dose	4
bm_effect	5
bm_m2	6
bm_palette	7
bm_plot	8
bm_spectrum	8
scale_colour_bm	9
theme_bm	10

Index	11
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BKMutate-package	<i>BKMutate: Statistical Analysis of Induced Mutagenesis Experiments</i>
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Description

A colour-first toolkit for analysing induced mutagenesis experiments in crop plants: dose-response and LD50/GR50 with Fieller intervals, mutagenic effectiveness and efficiency with confidence intervals, chlorophyll mutation spectrum analysis, generalised linear models for M2 counts, and formal comparison of mutagens.

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See Also

[bm_dose](#), [bm_effect](#), [bm_spectrum](#), [bm_m2](#), [bm_compare](#), [bm_plot](#).

bm_compare	<i>Formal comparison of mutagens</i>
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Description

Compares mutagens using interval estimates: pooled mutation frequency with Wilson intervals, pairwise ratios of mutation frequency with Katz intervals and chi-square tests, and relative biological effectiveness computed from LD50 values.

Usage

```
bm_compare(effect, dose_fit = NULL, reference = NULL, conf = 0.95)
```

Arguments

effect	An object returned by bm_effect .
dose_fit	An object returned by bm_dose , optional; used for the RBE table.
reference	Character; the reference mutagen. Defaults to the first alphabetically.
conf	Confidence level (default 0.95).

Value

An object of class `bm_compare` with pooled frequencies, pairwise ratios and relative biological effectiveness.

Examples

```
m <- bm_data("m2")
ef <- bm_effect(m, "mutagen", "dose", "M2_plants", "M2_mutants",
               lethality_n = "lethality_n", lethality_x = "lethality_x",
               boot = 0)
cmp <- bm_compare(ef)
cmp
bm_plot(cmp)
```

bm_data	<i>Load a bundled BKMutate example dataset</i>
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Description

Convenience loader for the demonstration datasets shipped with the package.

Usage

```
bm_data(name = c("dose", "m2", "spectrum", "counts"))
```

Arguments

name One of "dose", "m2", "spectrum", "counts".

Value

A data frame.

Examples

```
head(bm_data("dose"))
```

bm_dose	<i>Dose-response analysis: LD50 and GR50 with Fieller confidence intervals</i>
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Description

Fits a dose-response model and estimates the median lethal dose (LD50) or median growth-reduction dose (GR50). Because the median effective dose is a ratio of two correlated coefficients, its confidence interval is obtained from Fieller's theorem, which is correctly asymmetric; the symmetric delta-method interval is reported alongside.

Usage

```
bm_dose(data, dose, n_total = NULL, n_affected = NULL, response = NULL,
        mutagen = NULL, link = c("probit", "logit", "cloglog"), conf = 0.95)
```

Arguments

data A data frame with one row per dose.
dose Character; the dose column.
n_total Character; number of individuals treated (quantal response).
n_affected Character; number affected, e.g. dead or surviving (quantal response).
response Character; a continuous response such as seedling height.
mutagen Character or NULL; optional grouping column so a separate curve is fitted per mutagen.
link Link for the quantal model: probit (default), logit or cloglog.
conf Confidence level (default 0.95).

Value

An object of class `bm_dose` containing the estimates, fitted curve and observed points.

References

Fieller EC (1954). Some problems in interval estimation. *Journal of the Royal Statistical Society B* **16**, 175–185. doi:[10.1111/j.25176161.1954.tb00159.x](https://doi.org/10.1111/j.25176161.1954.tb00159.x)

See Also[bm_effect](#), [bm_plot](#)**Examples**

```
d <- bm_data("dose")
res <- bm_dose(d, dose = "dose", n_total = "n_treated",
              n_affected = "n_survived", mutagen = "mutagen")

res
bm_plot(res)
```

bm_effect

*Mutagenic effectiveness and efficiency with confidence intervals***Description**

Estimates mutagenic effectiveness (mutation frequency per unit dose) and mutagenic efficiency (mutation frequency per unit biological damage) with interval estimates. Effectiveness intervals rescale a Wilson score interval. Efficiency is a ratio of two binomial proportions, formally a relative risk, so intervals are obtained by the delta method on the log scale (Katz) and by the nonparametric bootstrap. Conventional practice reports these quantities as point estimates only.

Usage

```
bm_effect(data, mutagen, dose, m2_total, m2_mutants,
          lethality_n = NULL, lethality_x = NULL,
          sterility_n = NULL, sterility_x = NULL, injury = NULL,
          conf = 0.95, boot = 2000, seed = 1L)
```

Arguments

data	A data frame with one row per mutagen-dose combination.
mutagen	Character; the mutagen column.
dose	Character; the dose column.
m2_total	Character; number of M2 plants or families scored.
m2_mutants	Character; number of mutants observed.
lethality_n, lethality_x	Characters; denominator and count for M1 lethality. Optional.
sterility_n, sterility_x	Characters; denominator and count for pollen sterility. Optional.
injury	Character; percentage seedling injury. Optional.
conf	Confidence level (default 0.95).
boot	Bootstrap replicates for efficiency; 0 disables (default 2000).
seed	Random seed for the bootstrap.

Value

An object of class `bm_effect` containing point estimates and interval estimates for mutation frequency, effectiveness and efficiency.

References

Konzak CF, Nilan RA, Wagner J, Foster RJ (1965). Efficient chemical mutagenesis.
 Katz D, Baptista J, Azen SP, Pike MC (1978). Obtaining confidence intervals for the risk ratio in cohort studies. *Biometrics* **34**, 469–474. doi:10.2307/2530610

See Also

[bm_compare](#)

Examples

```
m <- bm_data("m2")
res <- bm_effect(m, mutagen = "mutagen", dose = "dose",
  m2_total = "M2_plants", m2_mutants = "M2_mutants",
  lethality_n = "lethality_n", lethality_x = "lethality_x",
  boot = 200)

res
bm_plot(res)
bm_plot(res, type = "efficiency")
```

bm_m2

Generalised linear models for M2 mutant counts

Description

Fits a Poisson log-linear model to per-family mutant counts, tests for overdispersion, and refits as quasi-Poisson when the counts are overdispersed. The number of plants scored enters as an offset so the model describes the mutation rate per plant.

Usage

```
bm_m2(data, counts, mutagen, dose = NULL, plants = NULL,
  family = c("auto", "poisson", "quasipoisson"),
  scale_dose = TRUE, disp_threshold = 1.5)
```

Arguments

<code>data</code>	A data frame with one row per M2 family.
<code>counts</code>	Character; column of mutant counts.
<code>mutagen</code>	Character; the mutagen column.
<code>dose</code>	Character or NULL; dose column.
<code>plants</code>	Character or NULL; plants scored per family, used as an offset.

family	Model family: auto (default), poisson or quasipoisson.
scale_dose	Logical; rescale dose to [0, 1] within each mutagen so that a pooled dose coefficient is interpretable when mutagens use different units.
disp_threshold	Dispersion above which overdispersion is declared (default 1.5).

Value

An object of class `bm_m2` with the coefficient table, dispersion statistic and fitted model.

Examples

```
cts <- bm_data("counts")
res <- bm_m2(cts, counts = "mutants", mutagen = "mutagen",
             dose = "dose", plants = "plants")
res
bm_plot(res)
```

bm_palette	<i>BKMutate colour palettes</i>
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Description

Palettes designed for mutagenesis figures, including a chlorophyll palette echoing the mutant classes themselves.

Usage

```
bm_palette(name = c("mutagen", "chloro", "dose", "damage", "contrast"),
           n = NULL, reverse = FALSE)
```

Arguments

name	Palette name.
n	Number of colours to return.
reverse	Logical; reverse the palette.

Value

A character vector of hex colours.

Examples

```
bm_palette("chloro")
bm_palette("dose", 8)
```

bm_plot	<i>Draw the signature figure for a BKMutate result</i>
---------	--

Description

Generic entry point returning the publication-ready figure for whichever analysis produced x.

Usage

```
bm_plot(x, ...)
```

Arguments

x	A BKMutate result object.
...	Passed to the specific method, for example type.

Value

A ggplot2 object.

Examples

```
bm_plot(bm_dose(bm_data("dose"), "dose", "n_treated", "n_survived",
  mutagen = "mutagen"))
```

bm_spectrum	<i>Chlorophyll mutation spectrum analysis</i>
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Description

Summarises the spectrum of chlorophyll-deficient mutants, tests whether the spectrum differs between mutagens by a chi-square test of homogeneity, and quantifies spectrum breadth by the Shannon-Weaver diversity index and its evenness.

Usage

```
bm_spectrum(data, mutagen, classes, dose = NULL)
```

Arguments

data	A data frame with one row per mutagen-dose combination.
mutagen	Character; the mutagen column.
classes	Character vector; the count columns for each mutant class.
dose	Character or NULL; optional dose column.

Value

An object of class `bm_spectrum` with counts, relative frequencies, diversity indices and a homogeneity test.

Examples

```
s <- bm_data("spectrum")
res <- bm_spectrum(s, mutagen = "mutagen",
                  classes = c("albina", "xantha", "chlorina", "viridis"),
                  dose = "dose")

res
bm_plot(res)
```

scale_colour_bm

Discrete BKMutate colour and fill scales

Description

Discrete colour and fill scales built on the BKMutate palettes.

Usage

```
scale_colour_bm(pal_name = "mutagen", reverse = FALSE, ...)

scale_color_bm(pal_name = "mutagen", reverse = FALSE, ...)

scale_fill_bm(pal_name = "mutagen", reverse = FALSE, ...)
```

Arguments

<code>pal_name</code>	Palette name (see bm_palette).
<code>reverse</code>	Logical; reverse the palette.
<code>...</code>	Passed to <code>ggplot2::discrete_scale</code> .

Value

A `ggplot2` scale.

Examples

```
library(ggplot2)
ggplot(iris, aes(Sepal.Length, Sepal.Width, colour = Species)) +
  geom_point() + scale_colour_bm("contrast")
```

theme_bm*A clean ggplot2 theme for BKMutate figures*

Description

The BKMutate figure theme.

Usage

```
theme_bm(base_size = 12, base_family = "", grid = TRUE)
```

Arguments

base_size	Base font size in points.
base_family	Font family.
grid	Logical; draw light major grid lines.

Value

A ggplot2 theme object.

Examples

```
library(ggplot2)
ggplot(mtcars, aes(wt, mpg)) + geom_point() + theme_bm()
```

Index

BKMutate (BKMutate-package), [2](#)
BKMutate-package, [2](#)
bm_compare, [2](#), [3](#), [6](#)
bm_data, [3](#)
bm_dose, [2](#), [3](#), [4](#)
bm_effect, [2](#), [3](#), [5](#), [5](#)
bm_m2, [2](#), [6](#)
bm_palette, [7](#), [9](#)
bm_plot, [2](#), [5](#), [8](#)
bm_spectrum, [2](#), [8](#)

scale_color_bm (scale_colour_bm), [9](#)
scale_colour_bm, [9](#)
scale_fill_bm (scale_colour_bm), [9](#)

theme_bm, [10](#)