Package: ordinalMIC (via r-universe)

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Type Package

Title Minimum Inhibitory Concentration Estimation from Ordinal Regression Models

Version 1.0.0

Description Provides tools to estimate minimum inhibitory concentration (MIC) and conduct rigorous pairwise comparisons (delta, fold-change, and difference of difference tests) from cumulative-link models fitted with 'ordinal::clm'.

Depends R (>= 4.1)

Imports ggplot2, stats, utils, cli, tibble

Suggests ordinal, testthat (>= 3.0.0)

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Contents

`autoplot.mic_solve` *autoplot method for mic_solve objects*

Description

Quick ggplot2 visualisations of the main outputs from `mic_solve()`. Three panels are supported:

- **"mic"** - forest plot of group-wise MIC estimates with asymmetric CIs.
- **"delta"** - forest plot of deltaMIC pairwise differences.
- **"ratio"** - forest plot of MIC ratios (log scale).

Usage

```
## S3 method for class 'mic_solve'
autoplot(
  object,
  type = c("mic", "delta", "ratio", "DoD_delta", "DoD_ratio"),
  x = NULL,
  color_by = NULL,
  dot_size = 0.5,
  ...
)
```

Arguments

`object`	An object returned by `mic_solve()`.
`type`	One of `"mic"`, `"delta"`, or `"ratio"`, `"DoD_delta"`, or `"DoD_ratio"`.
`x`	Variable for x axis plotting
`color_by`	Optional column name used to color and dodge replicate points. Default: first column in `newdata`.
`dot_size`	Size of the dots in the dotplot. Default: `0.5`.
`...`	Additional arguments passed to `ggplot2::ggplot()`.

Value

A **ggplot** object.

Author(s)

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Examples

```
if (requireNamespace("ordinal", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE)) {
  df <- data.frame(score  = ordered(sample(0:4, 120, TRUE)),
                   conc   = runif(120, 0, 4),
                   strain = factor(sample(c("A","B"), 120, TRUE)))
  fit <- ordinal::clm(score ~ strain * log1p(conc), data = df)
  res <- mic_solve(fit, expand.grid(strain = levels(df$strain)),
                   conc_name = "conc")
  ggplot2::autoplot(res, type = "mic")
}
```

`mic_solve` *Estimate MICs and Compare Groups*

Description

High-level wrapper that returns:

- `delta_mic_results` – additive pairwise differences (Δ-MIC).
- `ratio_mic_results` – multiplicative pairwise ratios.
- `dod_ratio_results` – **difference-of-differences on the ratio scale** (ratio-of-ratios, a classic interaction on the log scale).
- `dod_delta_results` – **difference-of-differences on the additive scale** (Δ of Δs).

Usage

```
mic_solve(
  clm_fit,
  newdata = NULL,
  conc_name,
  transform_fun = log1p,
  inv_transform_fun = expm1,
  alpha = 0.05,
  compare_pairs = "all",
  pvalue_scale = c("lp", "logmic")
)
```

Arguments

`clm_fit`	Fitted object from `ordinal::clm()`.
`newdata`	Data frame with factor combinations to evaluate.
`conc_name`	Character string giving the **raw** concentration column.
`transform_fun`	Transformation used in the model (default `log1p`).

`inv_transform_fun`	Inverse transformation (default `expm1`).
`alpha`	Confidence-level significance (default 0.05).
`compare_pairs`	One of `"all"` (default) to retain every pairwise comparison, or `"share_any"` to exclude contrasts where the two groups share no covariate levels in `newdata`.
`pvalue_scale`	Which pivot the main P_value uses for pairwise tests: ”lp” (difference in lp = log1p(MIC), recommended for calibration) or ”logmic” (current Wald on log(MIC) for ratios and MIC scale for deltas).

Value

An object of class `"mic_solve"` containing the tables above plus `mic_estimates`.

Examples

```
if (requireNamespace("ordinal", quietly = TRUE)) {
  ## Toy ordinal dataset
  set.seed(1)
  fit <- ordinal::clm(score ~ strain * treatment + log1p(conc), data = yeast_df)
  res <- mic_solve(fit, conc_name = "conc")
  head(res$ratio_mic_results)
}
```

`tidy.mic_solve` *tidy method for mic_solve objects*

Description

tidy method for mic_solve objects

Usage

```
tidy.mic_solve(
  x,
  table = c("mic", "delta", "ratio", "DoD_delta", "DoD_ratio"),
  ...
)
```

Arguments

`x`	An object of class `mic_solve`.
`table`	A character string specifying which table to return. Options are `"mic"`, `"delta"`, `"ratio"`, `"DoD_delta"`, and `"DoD_ratio"`.
`...`	Additional arguments (not used).

Value

A tibble containing the requested table from the `mic_solve` object.

`yeast_df` *Simulated Yeast Stress-Survival Data*

Description

An example dataset with ordinal spot scores (0 = no growth … 4 = full growth) for treated and untreated wild-type and mutant yeast across a peroxide gradient.

Usage

```
data(yeast_df)
```

Format

A data frame with 132 rows and 4 variables:

score Ordered factor `0 < 1 < 2 < 3 < 4`

conc Numeric concentration units

strain Factor: `"WT"` or `"Mut"`

treatment Factor: `"None"` or `"Salt"`

rep Replicate id (integer)

Examples

```
data(yeast_df)
head(yeast_df)
```

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