Package: BIOEFIC (via r-universe)

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Type Package

Title Relative Bioefficiency via Simultaneous Regressions

Version 0.1.1

Description Fits simultaneous regression models to compare two sources (reference and test) and estimates relative bioefficiency. Includes simultaneous exponential model with common asymptote (model = 1), slope-ratio model (model = 2), quadratic model (model = 3), linear-response plateau model (model = 4), and Michaelis-Menten model (model = 5). Output style follows the 'easyreg' package. Methods are based on Finney (1978, ISBN:0-85264-252-0), Mercer et al. (1978) <doi:10.1093/jn/108.8.1244>, Robbins et al. (1979) <doi:10.1093/jn/109.10.1710>, Noll et al. (1984) <doi:10.3382/ps.0632458>, Gallant and Fuller (1973) <doi:10.1080/01621459.1973.10481356>, Littell et al. (1997) <doi:10.2527/1997.75102672x>, and Burnham and Anderson (2002, ISBN:978-0-387-95364-9).

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Encoding UTF-8

Language en-US

Imports ggplot2, minpack.lm, stats

Suggests knitr, rmarkdown

VignetteBuilder knitr

Config/roxygen2/version 8.0.0

NeedsCompilation no

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`regsim` *Regressoes Simultaneas para Bioeficacia Relativa*

Description

Ajusta modelos de regressao simultanea (referencia e teste) para estimar a bioeficacia relativa entre duas fontes.

Usage

```
regsim(
  data,
  model = 1,
  mean = FALSE,
  sd = FALSE,
  conf_level = 0.95,
  IC = NULL,
  ref_name = "Referencia",
  test_name = "Teste",
  xlab = NULL,
  ylab = NULL,
  main = NULL,
  add_eq = FALSE,
  zero_policy = c("smart", "never_drop"),
  mort = FALSE,
  digits = 6,
  resid_plot = FALSE,
  common_plateau = FALSE,
  common_asym = FALSE,
  common_int = FALSE
)

## S3 method for class 'bioefic_regsim'
print(x, ...)

## S3 method for class 'bioefic_regsim'
plot(x, ...)
```

```
## S3 method for class 'bioefic_regsim'
coef(object, ...)

## S3 method for class 'bioefic_regsim'
residuals(object, ...)

## S3 method for class 'bioefic_regsim'
fitted(object, ...)

## S3 method for class 'bioefic_regsim'
summary(object, ...)

## S3 method for class 'summary.bioefic_regsim'
print(x, ...)
```

Arguments

`data`	data.frame com 3 colunas: X (dose), Yref (resposta referencia), Ytest (resposta teste).
`model`	Inteiro de 1 a 5. 1 = exponencial, 2 = slope-ratio, 3 = quadratica, 4 = LRP, 5 = Michaelis-Menten.
`mean`	Logico. Se TRUE, plota medias por nivel de X.
`sd`	Logico. Se TRUE, plota barras de desvio padrao.
`conf_level`	Nivel de confianca (default 0.95).
`IC`	Alternativa a conf_level (ex.: 95 ou 0.95).
`ref_name`	Nome da fonte referencia (default 'Referencia').
`test_name`	Nome da fonte teste (default 'Teste').
`xlab`	Rotulo do eixo X.
`ylab`	Rotulo do eixo Y.
`main`	Titulo do grafico.
`add_eq`	Logico. Se TRUE, adiciona equacao ao grafico.
`zero_policy`	Como tratar zeros: 'smart' (default) ou 'never_drop'.
`mort`	Logico. Se TRUE, nao remove zeros (dados de mortalidade).
`digits`	Numero de casas decimais nos resultados (default 6).
`resid_plot`	Logico. Se TRUE, exibe grafico de residuos.
`common_plateau`	Logico. Forcar plato comum (models 4 e 5).
`common_asym`	Logico. Forcar assintota comum (models 1 e 5).
`common_int`	Logico. Forcar intercepto comum (models 1, 2, 3, 4 e 5).
`x`	Objeto da classe `bioefic_regsim` retornado por `regsim()`.
`...`	Argumentos adicionais (nao utilizados).
`object`	Objeto da classe `bioefic_regsim` retornado por `regsim()`.

Value

Lista de classe `bioefic_regsim` contendo:

summary Tabela resumo com parametros, metricas e bioeficacia.

params Tabela com estimativas, erros padrao e IC dos parametros.

anova Tabela de ANOVA do ajuste simultaneo.

means_by_x Medias observadas por nivel de dose.

plot Objeto ggplot2 com o grafico gerado.

residuals_df Data frame com residuos e valores ajustados.

paralel Lista com teste de paralelismo e bioeficacia relativa (IC incluso).

References

Finney, D. J. (1978). *Statistical Method in Biological Assay* (3rd ed.). Charles Griffin & Company, London. ISBN 0-85264-252-0.

Mercer, L. P., Flodin, N. W. and Morgan, P. H. (1978). New methods for comparing the biological efficiency of alternate nutrient sources. *The Journal of Nutrition*, 108(8), 1244–1249. doi:10.1093/jn/108.8.1244

Robbins, K. R., Norton, H. W. and Baker, D. H. (1979). Estimation of nutrient requirements from growth data. *The Journal of Nutrition*, 109(10), 1710–1714. doi:10.1093/jn/109.10.1710

Littell, R. C., Henry, P. R., Lewis, A. J. and Ammerman, C. B. (1997). Estimation of relative bioavailability of nutrients using SAS procedures. *Journal of Animal Science*, 75(10), 2672–2683. doi:10.2527/1997.75102672x

Bates, D. M. and Watts, D. G. (1988). *Nonlinear Regression Analysis and Its Applications*. Wiley, New York. doi:10.1002/9780470316757

Anderson, R. L. and Nelson, L. A. (1975). A family of models involving intersecting straight lines and concomitant experimental designs useful in evaluating response to fertilizer nutrients. *Biometrics*, 31(2), 303–318. doi:10.2307/2529422

Examples

```
set.seed(42)
x    <- rep(c(0, 0.05, 0.10, 0.20), each = 8)
yref <- 0.65 + 0.13 * (1 - exp(-7   * x)) + rnorm(length(x), 0, 0.01)
ytes <- 0.65 + 0.13 * (1 - exp(-5.5 * x)) + rnorm(length(x), 0, 0.01)
df   <- data.frame(x, yref, ytes)
res  <- regsim(df)
```

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