

An overview of dose-response analysis

Christian Ritz

NEXS, University of Copenhagen
e-mail: ritz@nexs.ku.dk

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About dose and response

Basic data structure:

dose: certain amount of biological, chemical or radiation stress
(*also called explanatory variable or predictor or x*
– *usually a non-negative quantity*)

response: biological reaction to a given dose of stress
(*also called endpoint or outcome or y*)

Various ways to quantify the response:

- continuous/quantitative (length, optical density, weight)
- discrete/quantal
 - ▶ binary (dead/alive, immobile/mobile, present/absent)
 - ▶ counts (number of offspring, roots)
 - ▶ multinomial (severity of damage, ordinal score)
- survival in terms of event times (e.g., Ritz *et al.* (2013))
- ...



Dose-response modelling

Basic building block:

- a **parametric** model for each observed dose-response curve

Extensions:

- combining data from several dose-response curves obtained from the same experiment into a single dose-response model
- nonlinear mixed-effects dose-response models for combining dose-response curves from different experiments
- model averaging to include model selection uncertainty
- mixture models describing the joint action of several substances
- ...



Parametric models

- log-logistic (and logistic) models
 - ▶ special cases: exponential decay, logit and Michaelis-Menten models
 - ▶ asymmetric extension: generalized log-logistic
- other monotonous models:
 - ▶ log-normal models (*probit analysis with log-dose a special case*)
 - ▶ asymmetric Weibull models (*related to extreme value distributions*)
 - ▶ fractional polynomial models (Namata *et al.*, 2008)
 - ▶ threshold models (Pires *et al.*, 2002)
- non-monotonous models (often tend to be too flexible):
 - ▶ inverse j-shaped/u-shaped *hormesis* models (Cedergreen *et al.*, 2005)
 - ▶ biphasic models (Cornou *et al.*, 2013)

(see also Ritz (2010) for additional details)



Log-logistic model: Definition

The classic: Four-parameter log-logistic model:

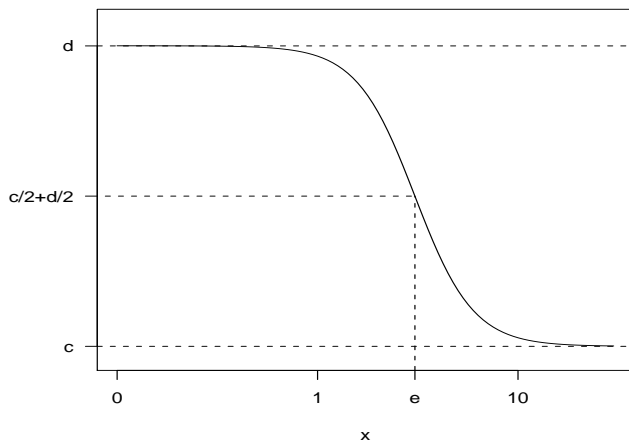
$$f(\text{dose}) = c + \frac{d - c}{1 + \exp[b\{\log(\text{dose}) - \log(e)\}]} = c + \frac{d - c}{1 + (\text{dose}/e)^b}$$

Details:

- *empirically established* for s-shaped dose-response data
- parameters have biological interpretation
- used in biology, hearing and speech science, medicine, pharmacology
- used extensively in toxicology for evaluating toxicity
- for binary data with $c = 0$ and $d = 1$ the *logistic regression model* is obtained (but in a somewhat different parameterization)



Log-logistic model: Parameter interpretation



Alternative asymmetric models

... if you know the type of asymmetry!

Slow descent from upper limit (Weibull type 1):

$$f(\text{dose}) = c + (d - c)\exp(-\exp[b\{\log(\text{dose}) - \log(e)\}])$$

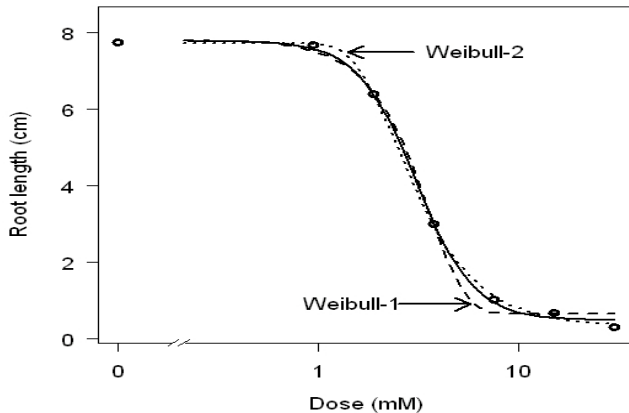
Rapid descent from upper limit (Weibull type 2):

$$f(\text{dose}) = c + (d - c)\{1 - \exp(-\exp[b\{\log(\text{dose}) - \log(e)\}])\}$$

Note: Only the model parameters c and d have biological interpretations



Asymmetric dose-response curves



Hormesis models – formulas

Brain-Cousens model:

$$f(\text{dose}) = c + \frac{d - c + f \text{dose}}{1 + \exp \{b(\log(\text{dose}) - \log(e))\}}$$

Cedergreen *et al.* (2005) model:

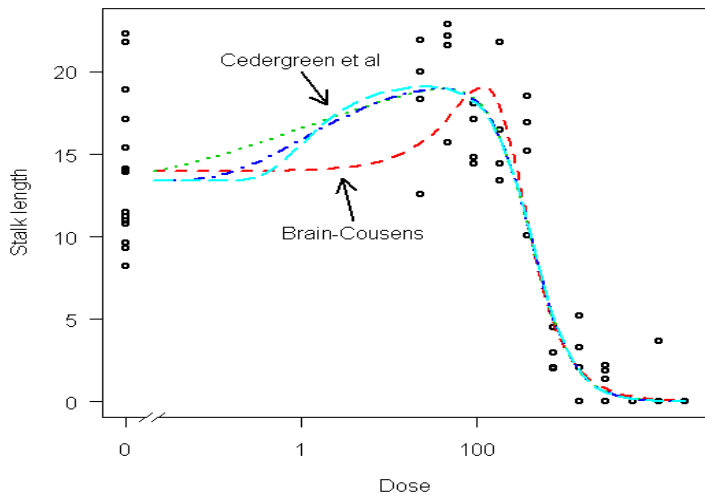
$$f(\text{dose}) = c + \frac{d - c + f \exp \{-1/\text{dose}^\alpha\}}{1 + \exp \{b(\log(\text{dose}) - \log(e))\}}$$

Note: The resulting curve has always both a minute local minimum and a global maximum that corresponds to the maximum hormesis response

There exist other hormesis models with even more model parameters
(Beckon *et al.* (2008))



Hormesis models – visualization



What are dose-response models used for?

- A single dose-response curve:
 - ▶ estimating relevant parameters such as *effective concentrations/doses* (inverse regression problem)
 - ▶ quantifying the uncertainty associated with the estimates
- Several dose-response curves:
 - ▶ calculating *relative potency* between curves (ratios of effective concentrations/doses)
 - ▶ comparing entire dose-response curves
 - ▶ comparing only specific model parameters or derived parameters



Resources in **R**

Bits and pieces found in several packages:

- `nls()` – part of the standard **R** installation
- `nls2`, `nlstools`, `MASS`
- `drc` and extensions: `bmd`, `medrc`
- `calib`, `drfit`, `grofit`, `qpcR`, `PK`
- ...



Key features of drc

- Unified framework for different types of responses
- Convenient model specification through a range of built-in mean functions
- Special cases can be obtained by fixing parameters at given values (so not estimated)
- All standard **R** methods available (e.g., `anova`, `confint`, `predict`, `summary`, `vcov`)
- Estimation in most cases as smooth as for `lm()`
*(no need to think about starting values for the model parameters ... a consequence of the programming flexibility in **R**!)*
- Convenient plotting functionality (in contrast to `nls()`)
- Built-in calculation of derived parameters



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