Dose-response modelling using R

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The outcome of dose-response experiments is the effect or stimulus on an organism in response to a dose administered. In this context *dose* can refer to any biological, chemical, radioactive stimulus, or to any other tangible stimuli that can be graduated. Major application areas include agriculture, biology, chemistry, medicine, pharmacology, and toxicology. Specific applications range from experiments in hearing and speech science over pulse oxygen saturation modelling to toxicity testing of chemicals within regulatory frameworks.

This presentation provides an overview of the extension package `drc` (on CRAN), which is designed for the statistical analysis of dose-response data that either could be individual curves or several curves considered jointly (eg. binary mixture models). Package development began in 2004 with a narrow focus on pesticide development and ecotoxicology (Ritz & Streibig, 2005). Mainly in response to user feedback and requests, the package has been improved and extended in various ways for the last 5 years. The package provides a general model fitting function, with much the same basic interface and feel as `lm()`, as well as all standard extractor methods, e.g. `anova`, `coef`, `plot`, `predict`, `residuals`, and `summary`. An arsenal of built-in dose-response functions (relying heavily on the concept of self starter functions) comes with the package. In addition, there are several special functions for after-fitting extraction of particular parameters of biological interest such as effect concentrations or doses (e.g. EC50/ED50 and LC50/LD50 values).

More specifically, the presentation will touch upon topics such as:

- unified parametric modelling framework for several data types

- elaborate infrastructure for built-in functions

- analysis of high throughput dose-response data

- simulation from parametric dose-response models (given a specified design)

- visualisation of the results

Some ideas for future developments will also be presented.

References

Ritz C. and Streibig J. C. (2005). Bioassay analysis using **R**. *Journal of Statistical Software*, **12**, Issue 5, 1–22. http://www.jstatsoft.org/v12/i05.