Fitting mathematical models to biological data using least-squares minimization

Samraat Pawar

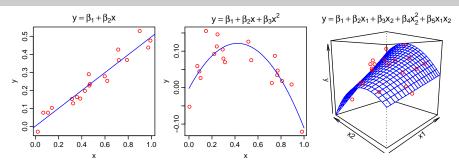
Department of Life Sciences (Silwood Park)

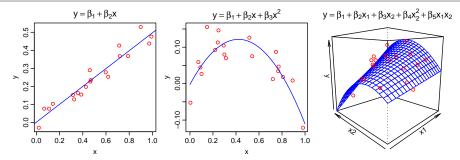
Imperial College London

January 23, 2020

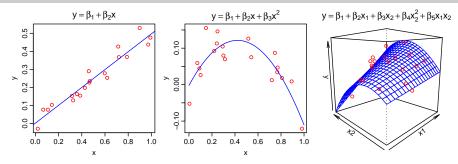
OUTLINE

- Why Non-Linear Least Squares regression / fitting?
- The NLLS fitting method
- NLLS in R
- Practicals overview

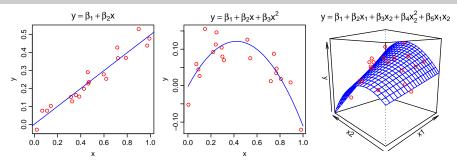




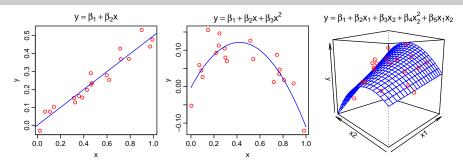
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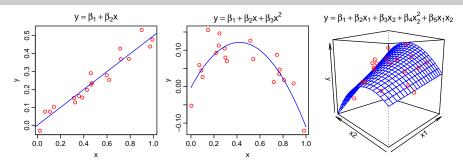
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- OK, so then why Non-Linear Least Squares (NLLS) fitting?

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NO!

SO WHAT — WHY IS INTRINSIC NON-LINEARITY A PROBLEM?

Recall what the Least Squares method does:

• Consider a predictor *x*, data *y*, *n* observations, and a model that we want to fit to the data:

$$f(x_i, \boldsymbol{\beta}) + \varepsilon_i$$
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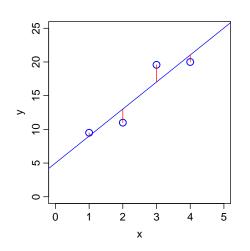
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• The objective is to find estimates of values of the k parameters $(\hat{\beta}_j)$ that minimize the sum (S) of squared residuals (r_i) (AKA RSS): $S = \sum_{i=1}^{n} [y_i - f(x_i, \beta)]^2 = \sum_{i=1}^{n} r_i^2$

THE LEAST-SQUARES SOLUTION

OLS minimizes the *sum* of the *squared* residuals

IF THE MODEL IS LINEAR, THE SOLUTION IS EASY USING ALGEBRA



$$y_1 = \beta_0 + \beta_1 x_1 + \frac{\varepsilon_i}{\varepsilon_i}$$

$$9.50 = 5 + 4 \times 1 + 0.50$$

 $11.00 = 5 + 4 \times 2 - 2.00$
 $19.58 = 5 + 4 \times 3 + 2.58$
 $20.00 = 5 + 4 \times 4 - 1.00$

$$\beta_0 = 5; \beta_1 = 4$$

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- ullet So the nice trick of solving Y=Xeta+arepsilon is impossible *mathematically*

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- Whether a refinement has taken place in any step of the iteration is determined by re-calculating the residuals at that step
- Eventually, if it all goes well, we find a combination of β_j 's that is *very close* to the desired solution $\frac{\partial S}{\partial \beta_i} = 0, j = 0, 1, 2, \dots, k$

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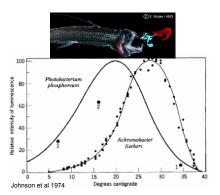
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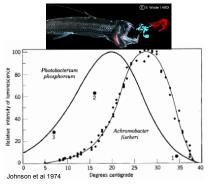
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- Can you think of some examples?





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T = temperature(K)

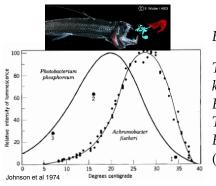
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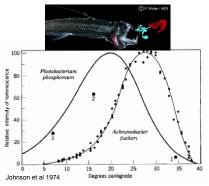
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- What about alternative models?

EXAMPLE: FUNCTIONAL RESPONSES

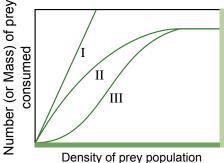
$$f(x_R) = rac{ax_R^{q+1}}{1+hax_R^{q+1}}$$
 (Holling, 1959)

 x_R = Resource density (Mass / Area or Volume)

a = Search rate (Area or Volume / Time)

h = Handling time

q =Shape parameter (dimensionless)



Note that:

- NLLS fitting can yield h < 0, q < 0, or both
- h < 0 is biologically impossible but indicates an upward curving response
- q < 0 is biologically unlikely as it indicates a decline in search rate with resource density (but is useful as a measure of deviation away from a type III response)

So the general procedure is:

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- Stop simulations when the adjustments make virtually no difference to the rss

The tricky part — adjust parameters to make curve come closer to the data points (step 4) has two main algorithms that you can choose between:

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- You may also want to compare multiple models.

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- What if the errors are not normal? use Maximum Likelihood or Bayesian methods instead.

MORE NLLS TIPS

• You can use mixed-effects modelling with NLLS in R; the package is nlme https://stat.ethz.ch/R-manual/R-devel/library/nlme/html/nlme.html (You are probably stuck with the Gauss-Newton algorithm with nlme though)

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- You can also use Python look up lmfit https://lmfit.github.io/lmfit-py/index.html. python seems to have a better Levenberg-Marqualdt implementation than R

READINGS AND RESOURCES

- Motulsky, Harvey, and Arthur Christopoulos. Fitting models to biological data using linear and nonlinear regression: a practical guide to curve fitting. OUP USA, 2004.
- Johnson, J. B. & Omland, K. S. 2004 Model selection in ecology and evolution. Trends Ecol. Evol. 19, 101–108.

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- That is, the solution of $\frac{\partial r_i}{\partial \beta_j}$ is simple (enough)

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- Then we want to solve $\frac{\partial S}{\partial \beta_0} = \sum_{i=1}^n \frac{\partial [y_i - (\beta_0 + \beta_1 x_i)]^2}{\partial \beta_0} = 0$

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just boils down to solving two simultaneous equations because $\frac{\partial r_i}{\partial \beta_i}$ is simple *because* the model is intrinsically linear:

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• That is, we need to solve $\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$ (this is what R solves when you use lm())