Fitting Mathematical Models to Biological Data using Non-Linear Least-Squares (NLLS)

Samraat Pawar

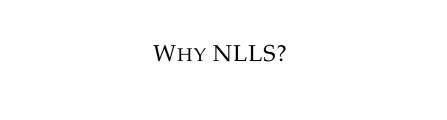
Department of Life Sciences (Silwood Park)

Imperial College London

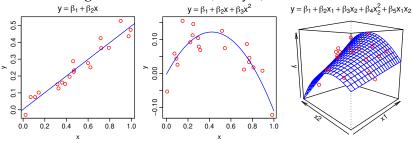
November 9, 2022

OUTLINE

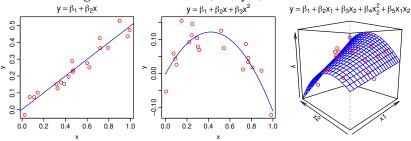
- Why NLLS?
- The NLLS fitting method
- Practicals (in R) overview



• These are *all* good *Linear Models* (really?!):

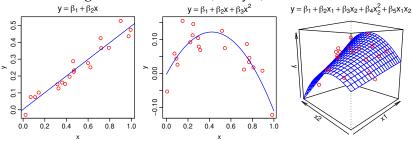


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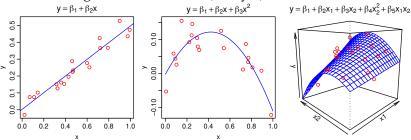
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- Linear models can include curved responses (e.g. Polynomial regression)

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In all of these, at least one term is non-linear (e.g., $x_i^{\beta_2}$, $e^{\beta_2 x_i}$, etc.)

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RSS =
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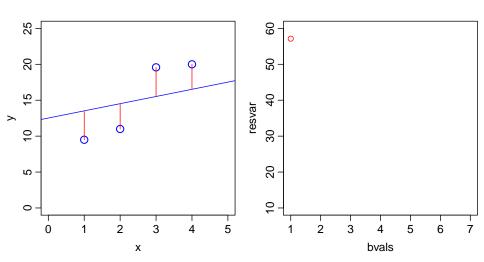
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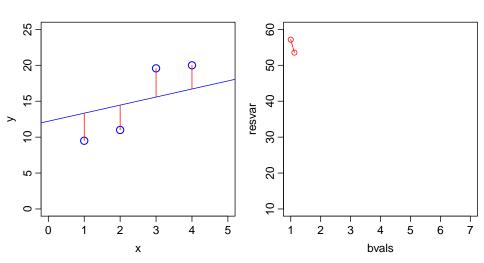
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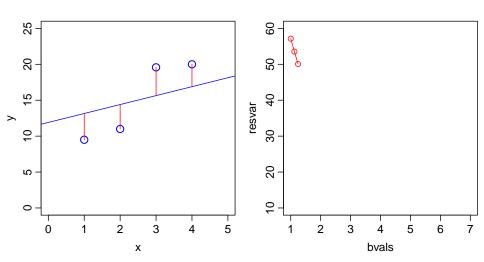
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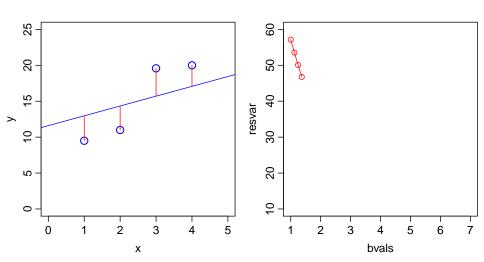
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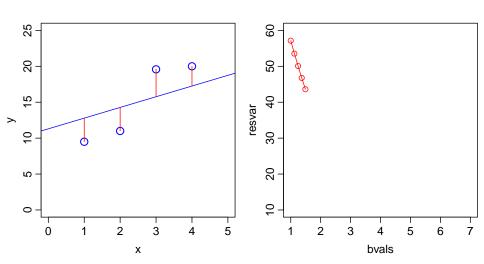
• Let's picture this using a simple (OLS) example; fitting the model $y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$...

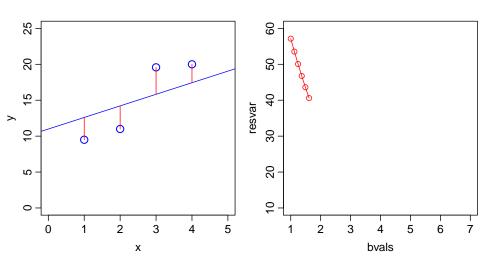


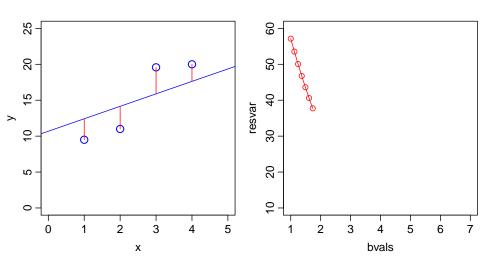


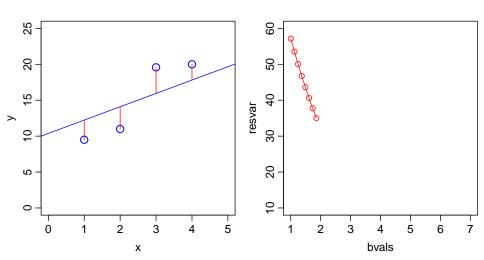


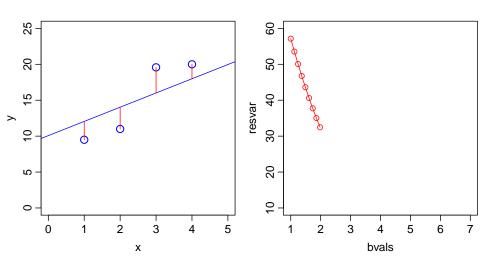


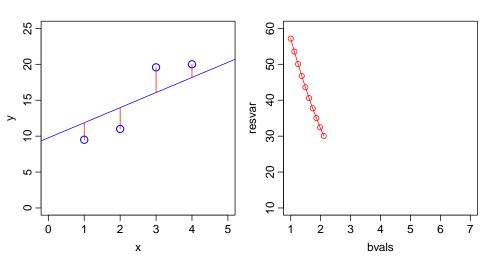


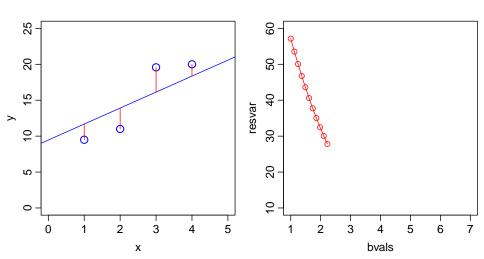


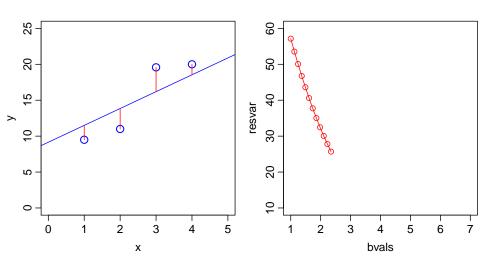


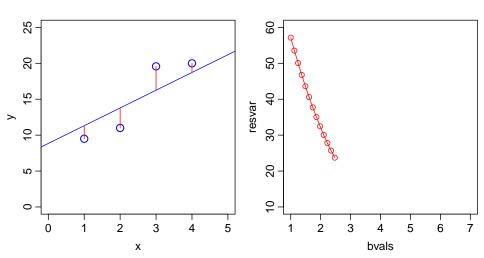


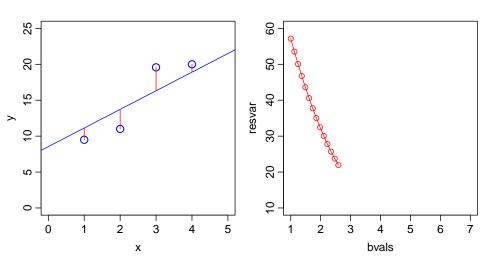


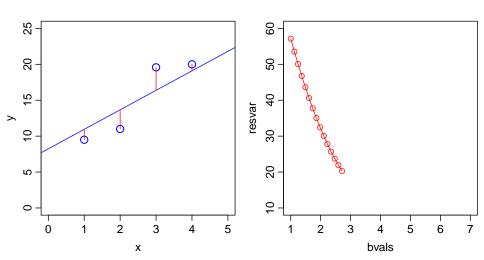


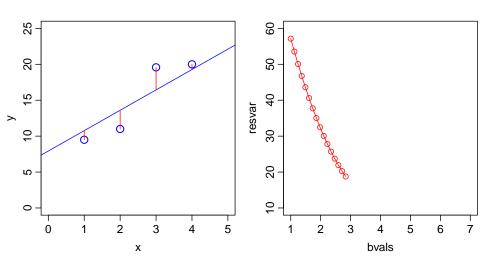


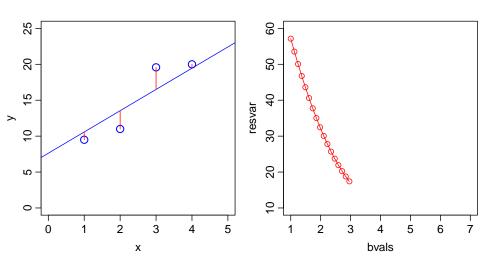


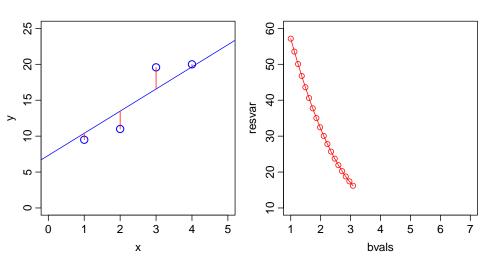


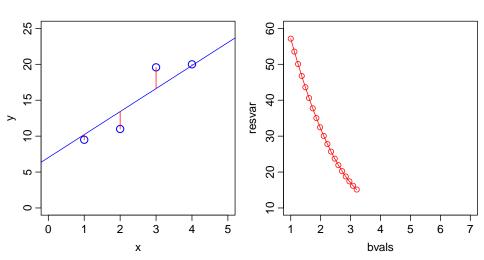


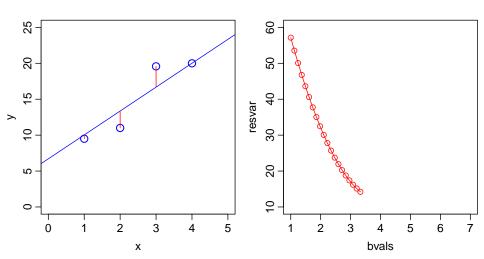


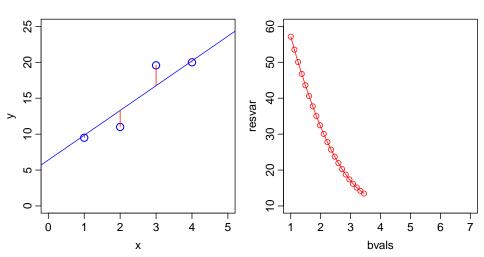


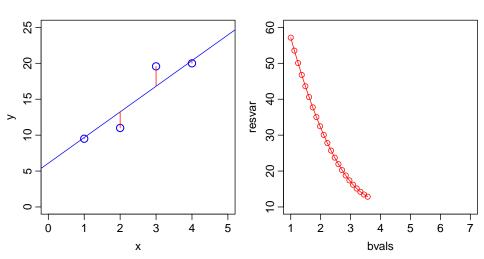


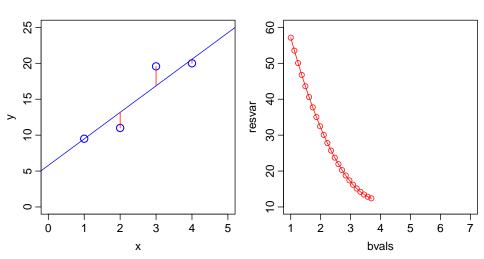


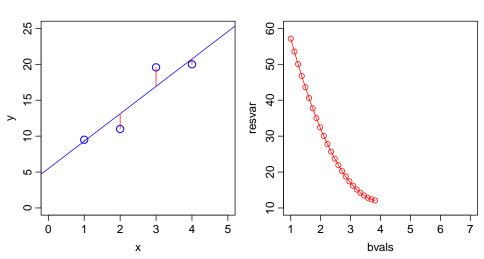


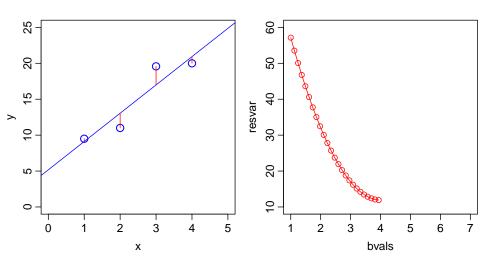


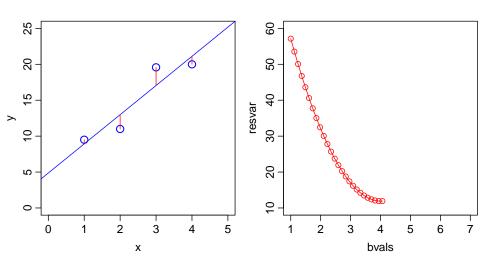


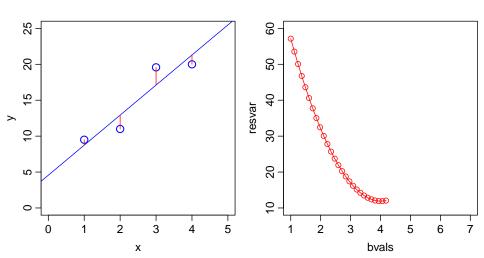


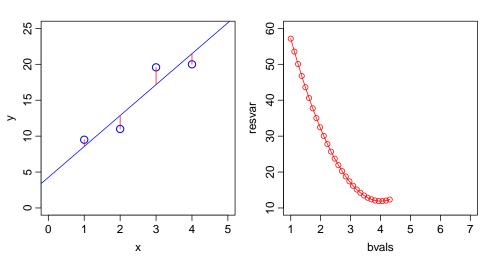


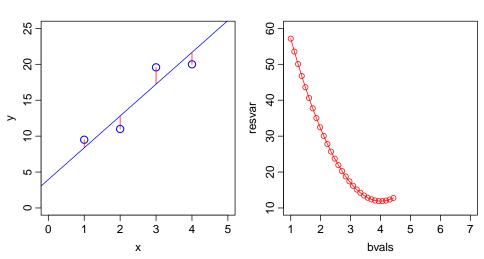


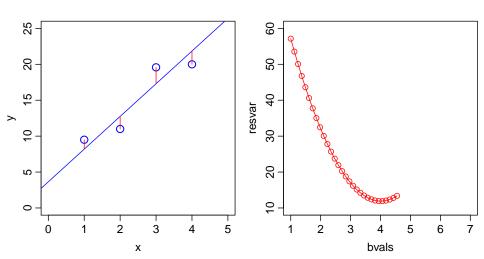


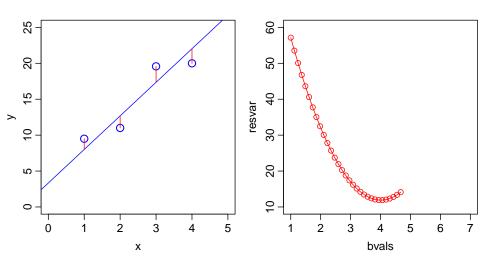


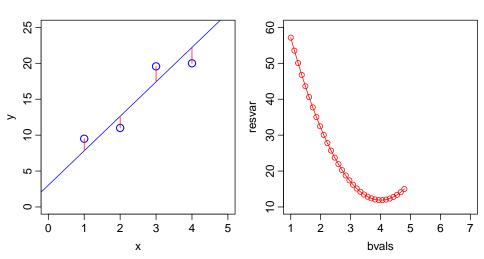


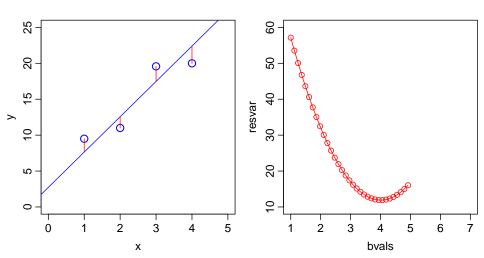


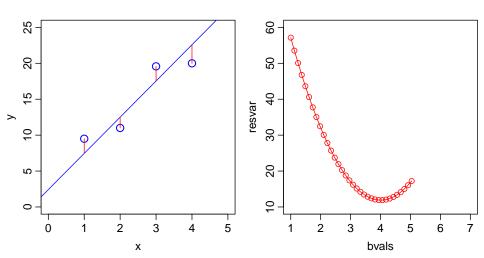


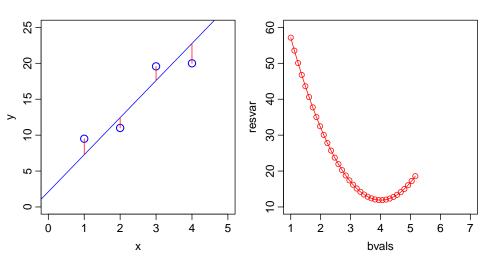


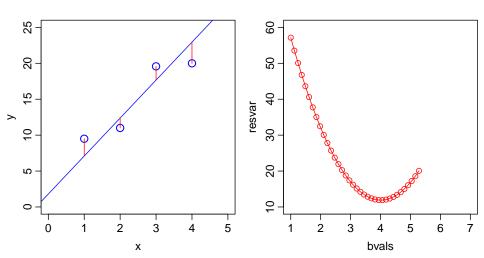


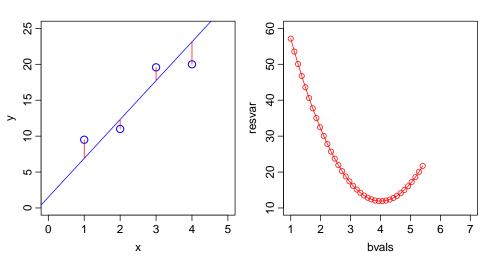


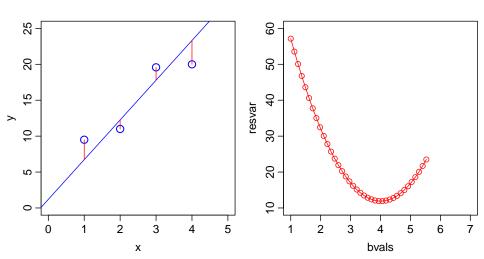


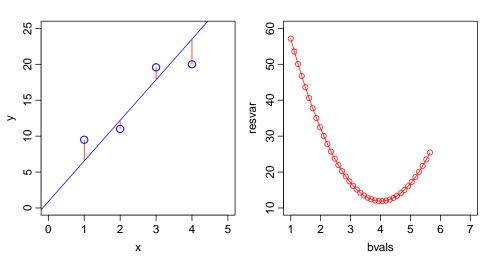


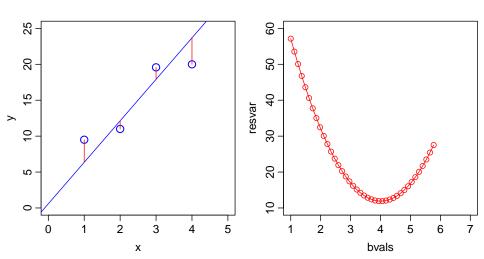


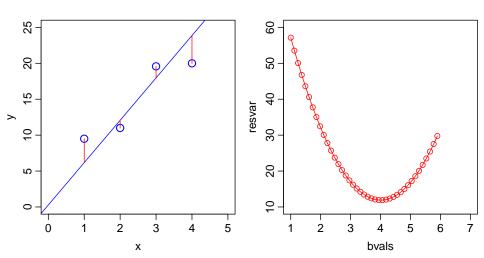


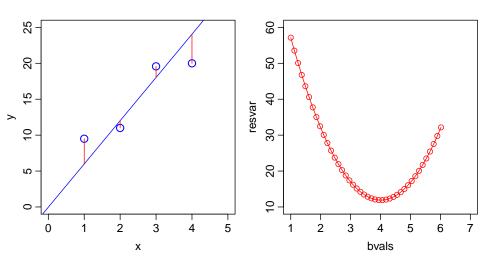


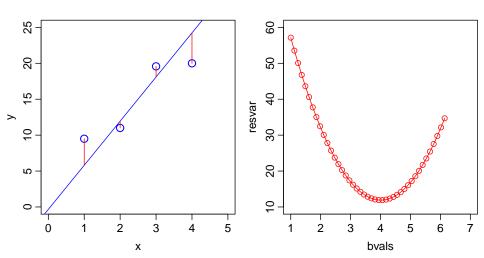


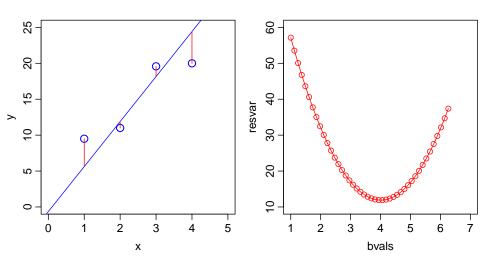


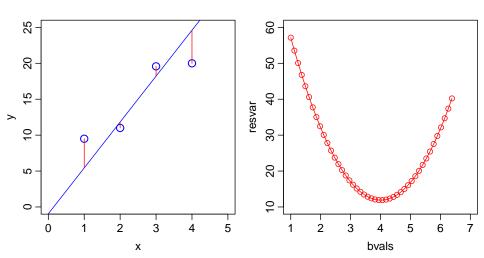


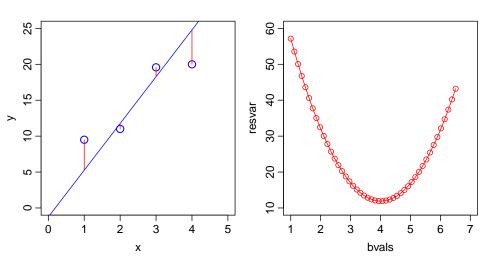


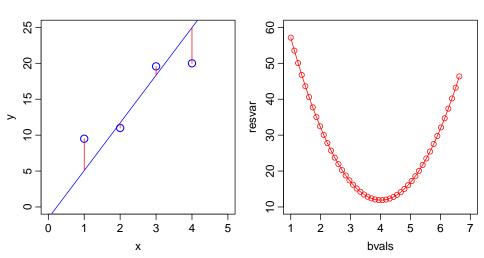


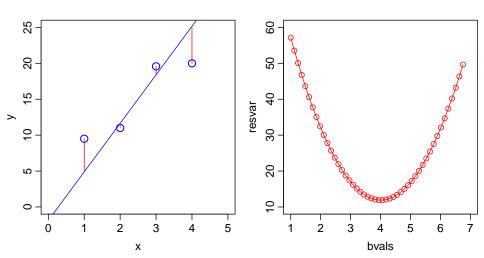


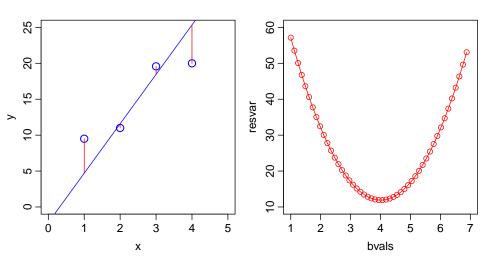


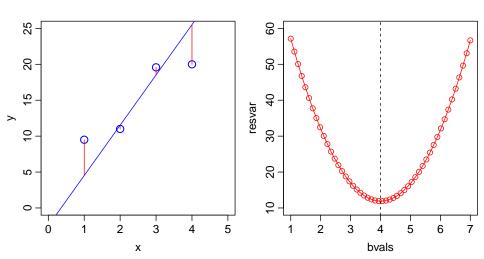




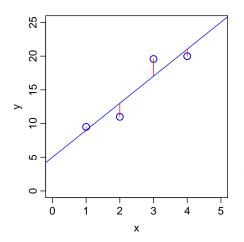








IF THE MODEL IS LINEAR, THE LEAST-SQUARE SOLUTION IS EXACT



$$y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$

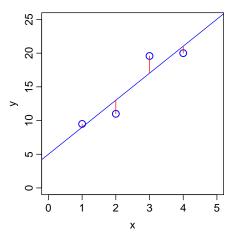
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• This system of (linear) equations can be compactly represented (and solved using matrix algebra) as $\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$

INTRINSIC NON-LINEARITY MAKES LEAST-AQUARES MODEL FITTING DIFFICULT

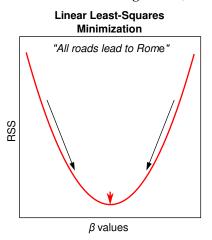
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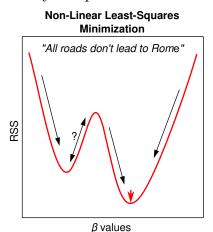
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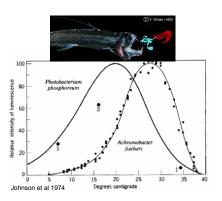
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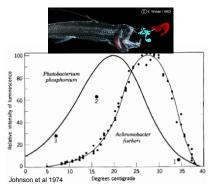
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- Can you think of some examples?

NON-LINEAR MODEL EXAMPLE: TEMPERATURE AND METABOLISM

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$$B = B_0 e^{-\frac{E}{kT}} f(T, T_{pk}, E_D)$$

T = temperature (K)

 $k = \text{Boltzmann constant (eV K}^{-1})$

E = Activation energy (eV)

 T_{pk} = Temperature of peak performance

 E_D = Deactivation energy (eV)

(J H van't Hoff 1884, S Arrhenius 1889)

THE NLLS FITTING METHOD

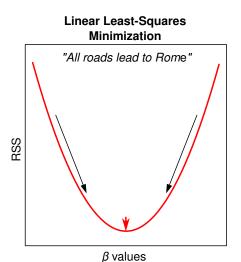
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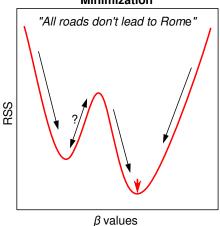
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 - Eventually, if it all goes well, a combination of β_j 's that is *very close* to the desired solution (where the RSS is *approximately* minimized) can be found



Non-Linear Least-Squares Minimization



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THE NLLS FITTING / OPTIMIZATION PROCESS

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

NLLS FITTING / OPTIMIZATION ALGORITHMS

The tricky part — adjust parameters to make curve come closer to the data points (step 4) — has two main algorithms that are generally used:

• The **Gauss-Newton** algorithm is often used, but doesn't work very well if the model to be fitted is mathematically complicated (the parameter search "landscape" is difficult) and the *starting values* for parameters are far-off-optimal

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- The Levenberg-Marquardt algorithm switches between Gauss-Newton and "gradient descent" and is more robust against starting values that are far-off-optimal and is more reliable in most scenarios.

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- You may also want to compare and select between multiple competing models
- Unlike in Linear Models, R² values *should not* be used to interpret the quality of a NLLS fit (more on this in the practicals).

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- What if the errors are not normal? Interpret results cautiously, and use Maximum Likelihood or Bayesian fitting methods instead

PRACTICALS OVERVIEW

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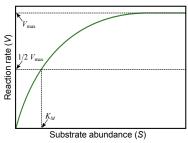
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 - It offers additional features like the ability to "bound" parameters to realistic values

 We will start with NLLS fitting of the Michaelis-Menten model of biochemical reaction kinetics:

$$V = \frac{V_{\max}[S]}{K_m + [S]}$$

- S = Substrate density
- V_{max} = Maximum reaction rate (at saturating substrate concentration)
- K_M = Half-saturation constant; the S at which reaction rate reaches half of possible maximum (= ½V_{max})



- ullet You will use NLLS fitting to obtain estimates of $V_{\rm max}$ and K_M
- Note that $V_{\text{max}} \le 0$ and $K_M \le 0$ are physically impossible (useful fir picking starting values)

READINGS

 Motulsky, Harvey, and Arthur Christopoulos. Fitting models to biological data using linear and nonlinear regression: a practical guide to curve fitting. OUP USA, 2004.