

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

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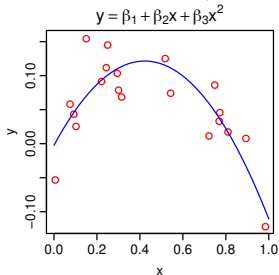
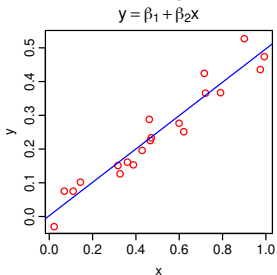
# OUTLINE

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

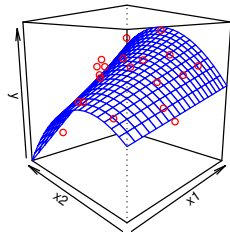
WHY NLLS?

# LINEAR MODELS

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

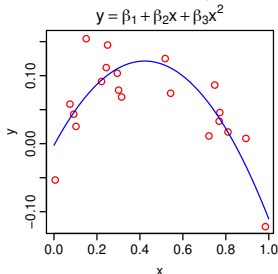
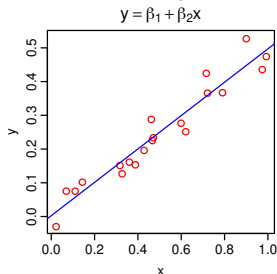


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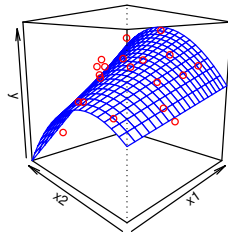


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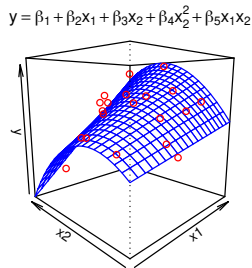
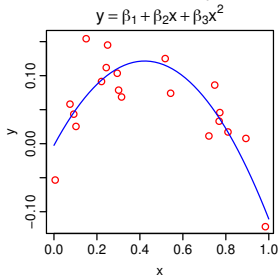
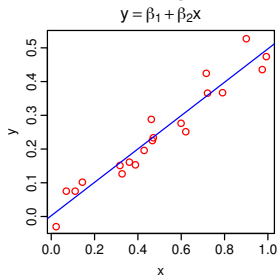
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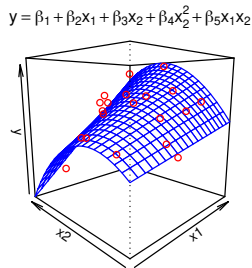
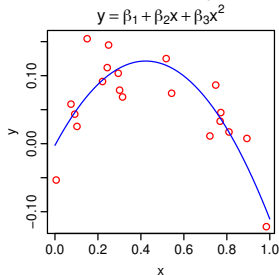
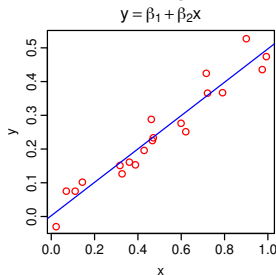
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- Linear models can *include curved responses* (e.g. Polynomial regression)

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

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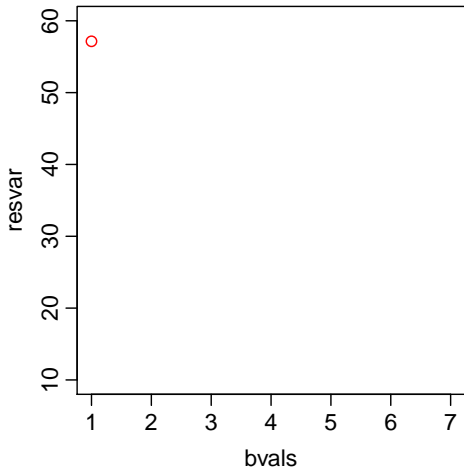
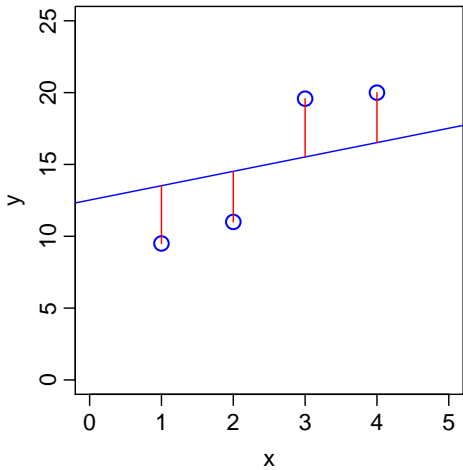


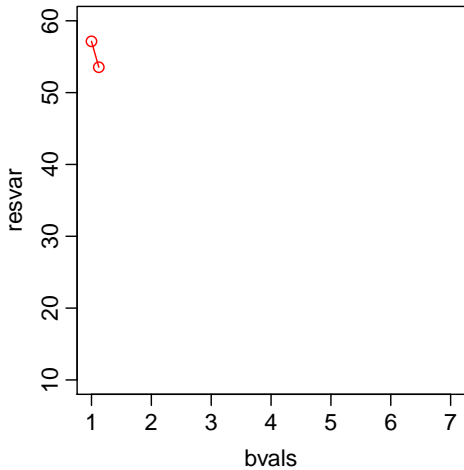
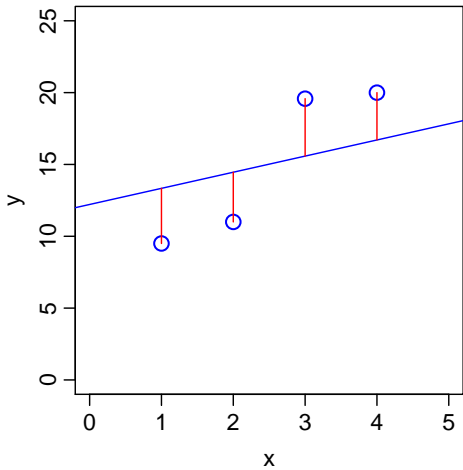
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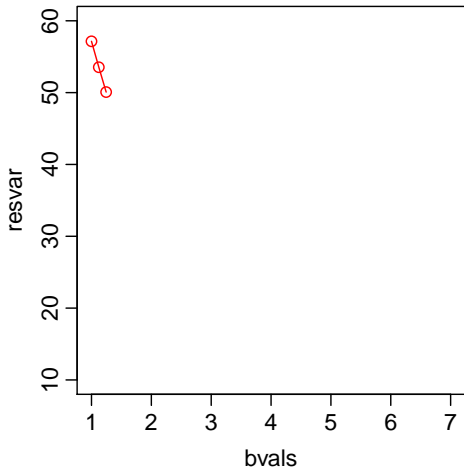
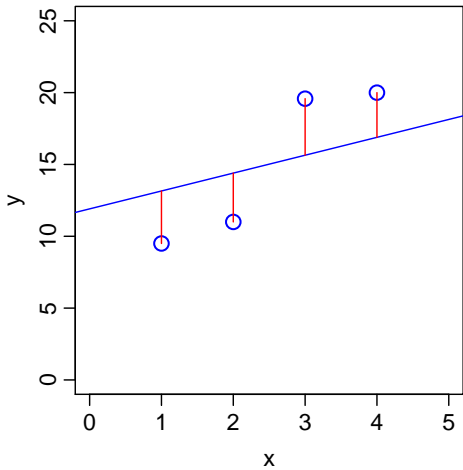
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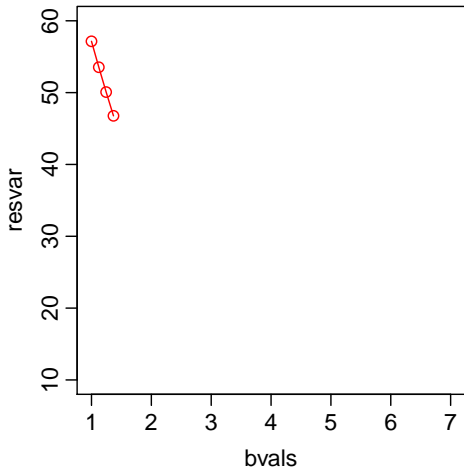
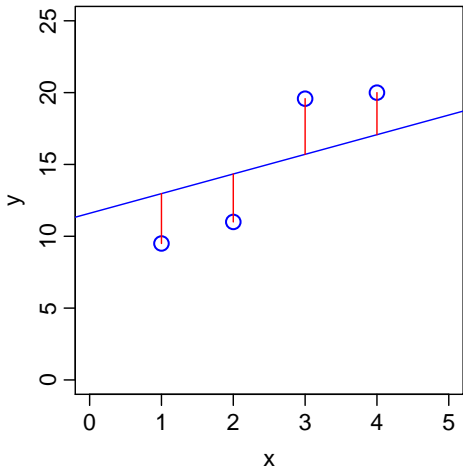
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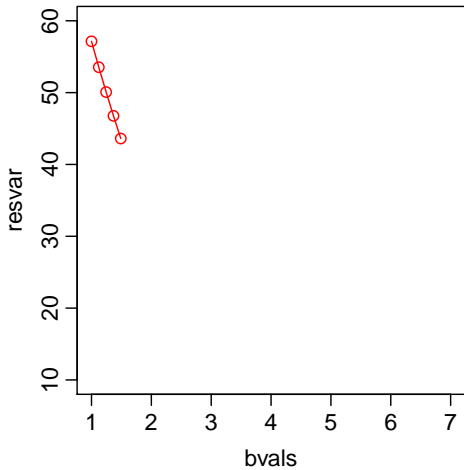
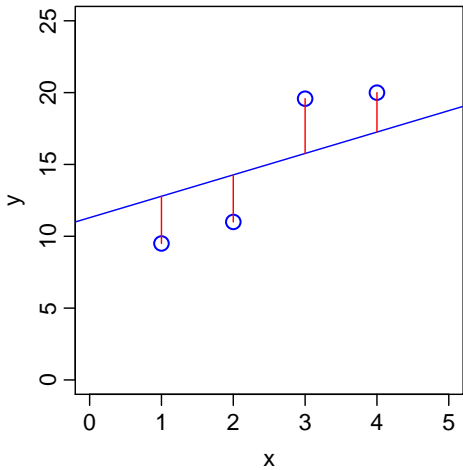
- Let's picture this using a simple (OLS) example; fitting the model  $y_i = \beta_0 + \beta_1 x_i + \varepsilon_i \dots$

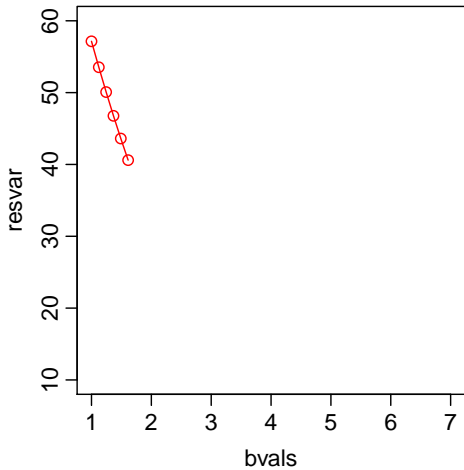
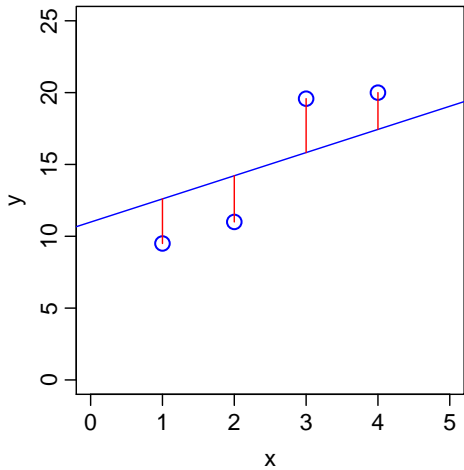


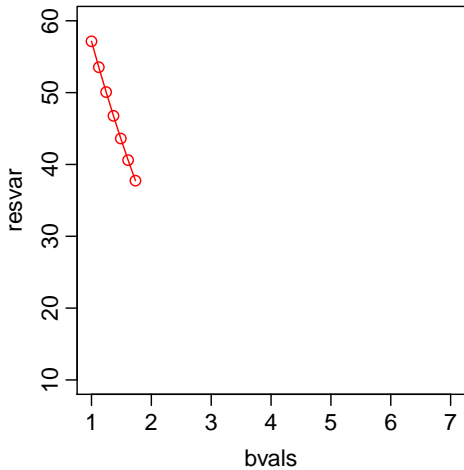
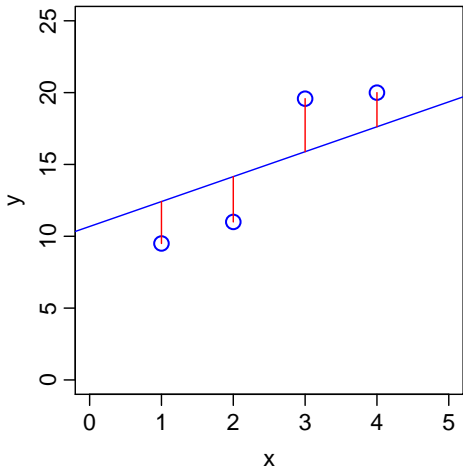




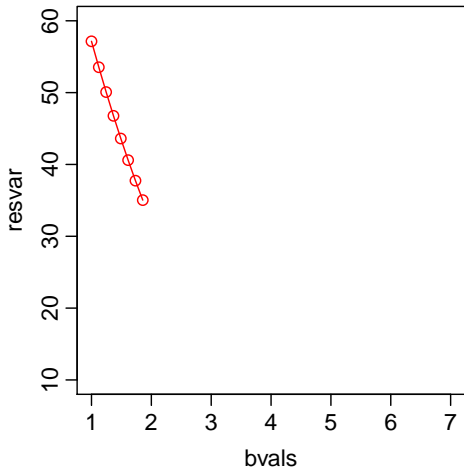
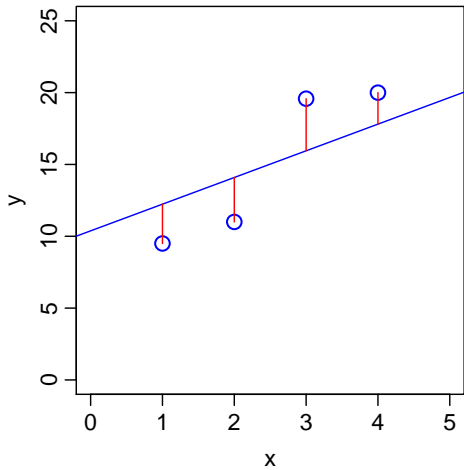


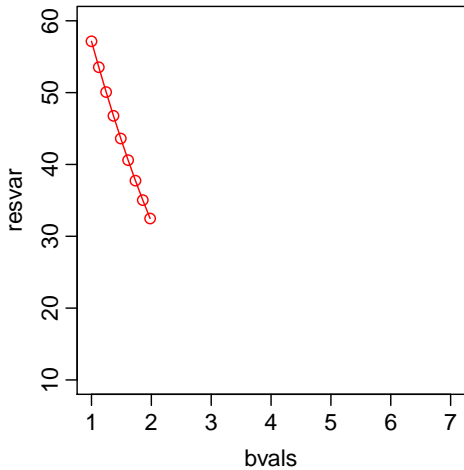
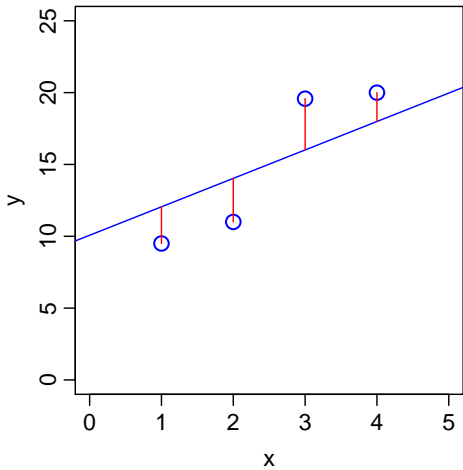


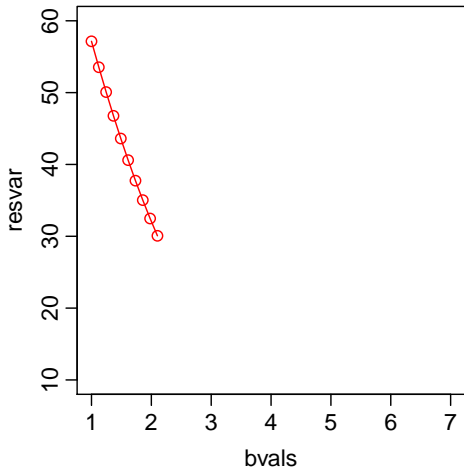
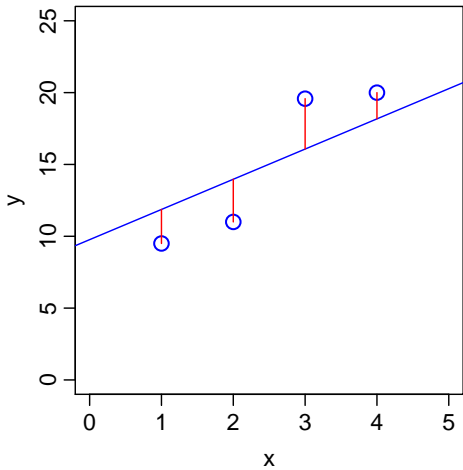


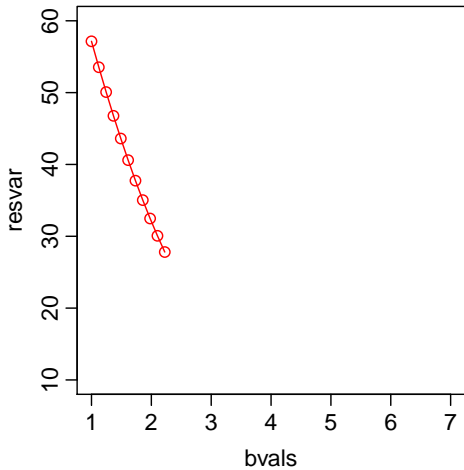
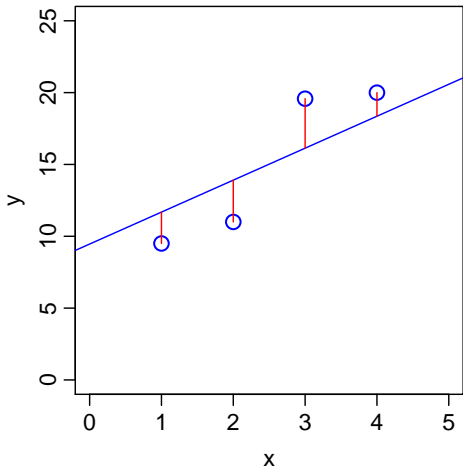


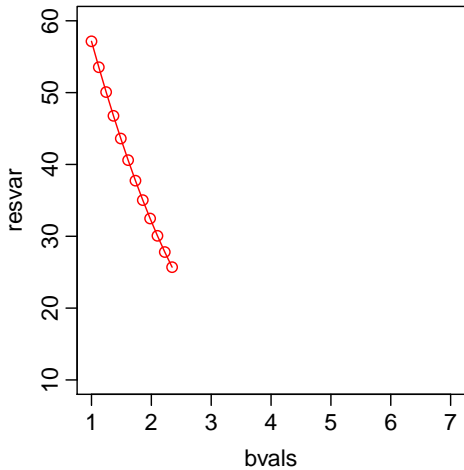
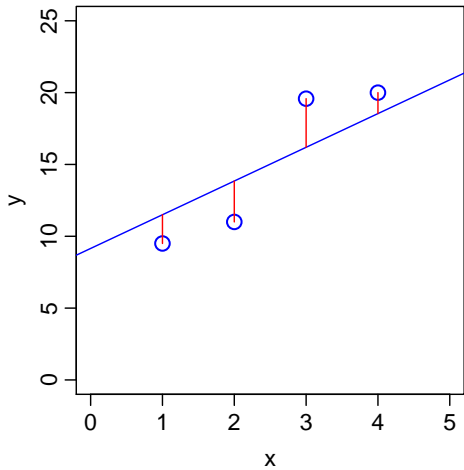


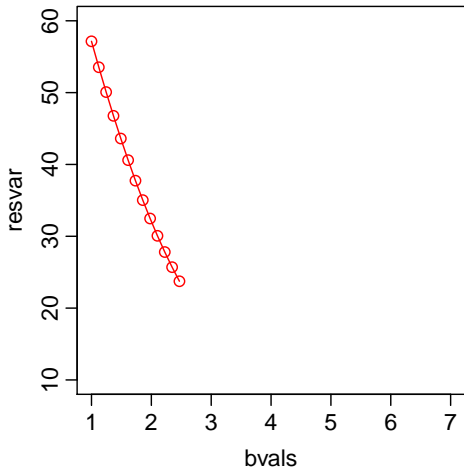
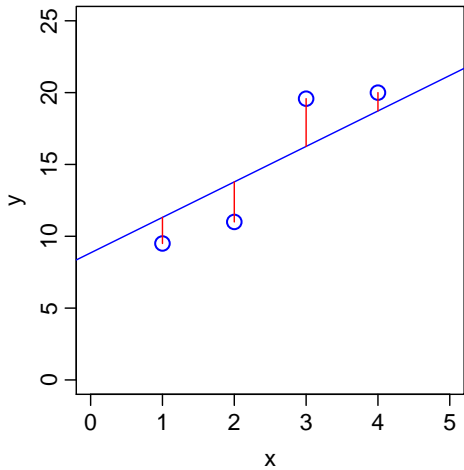


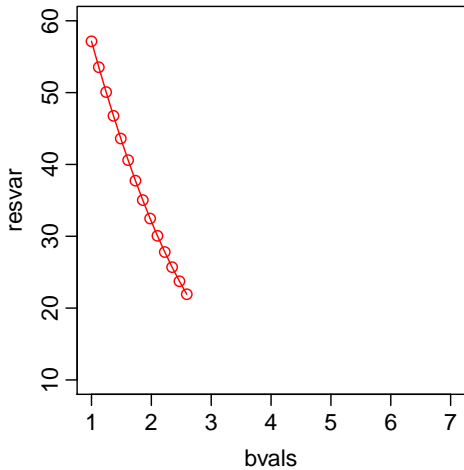
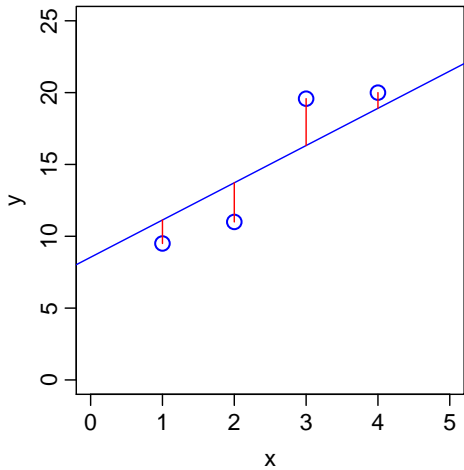


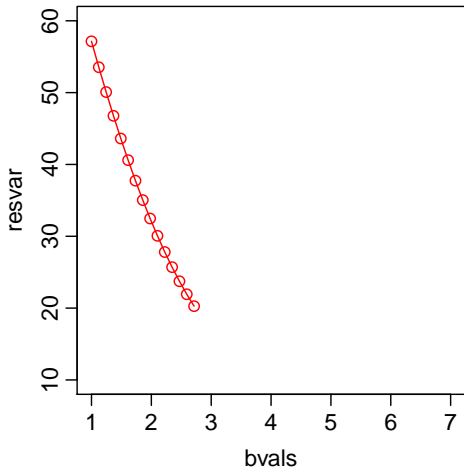
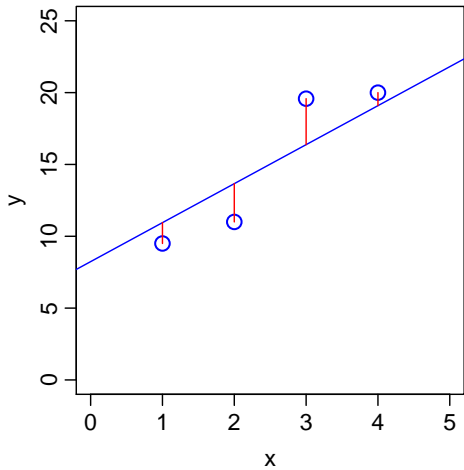




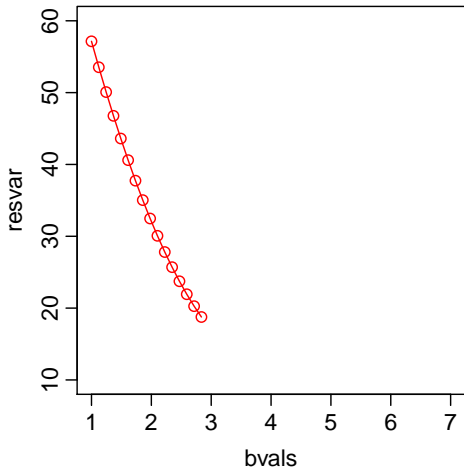
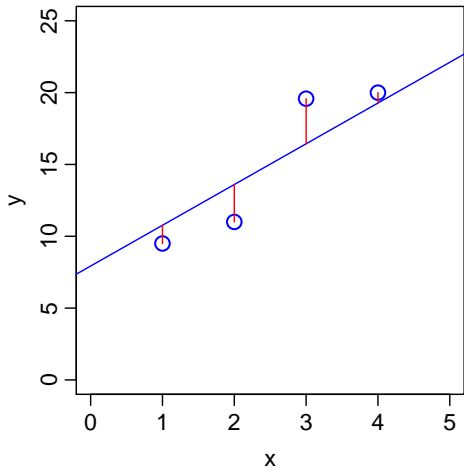


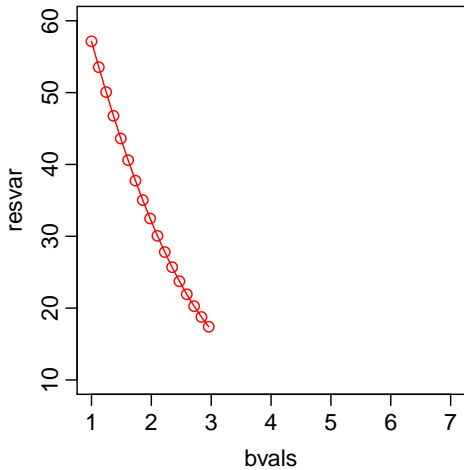
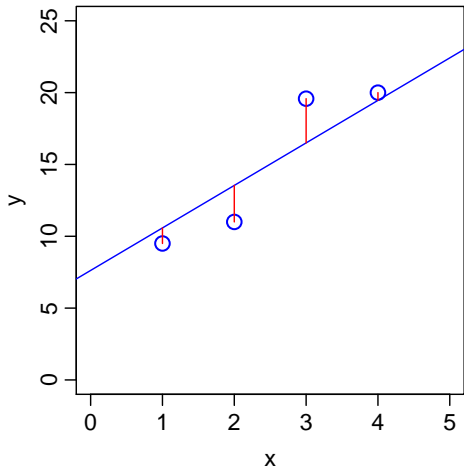


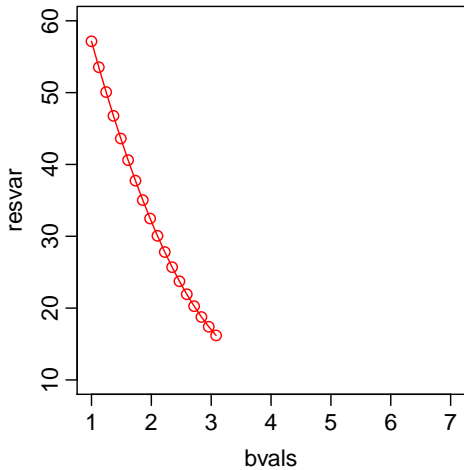
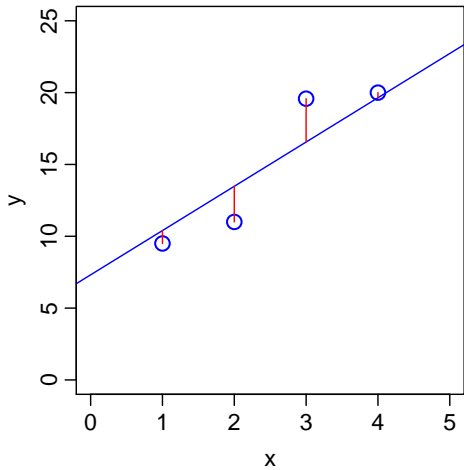


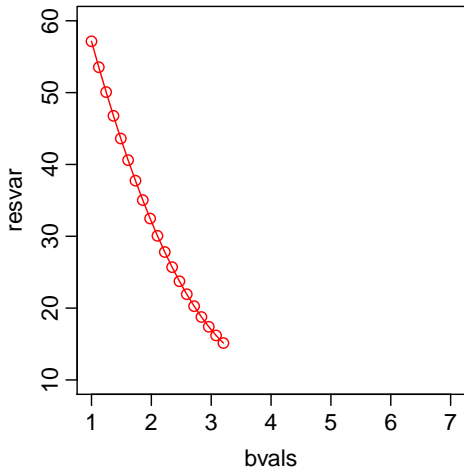
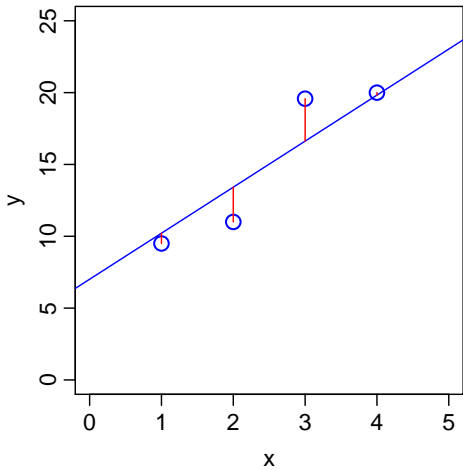


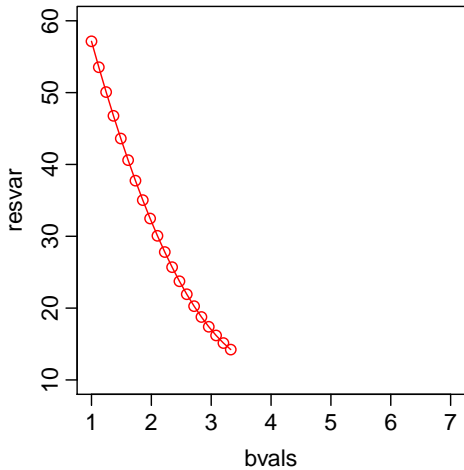
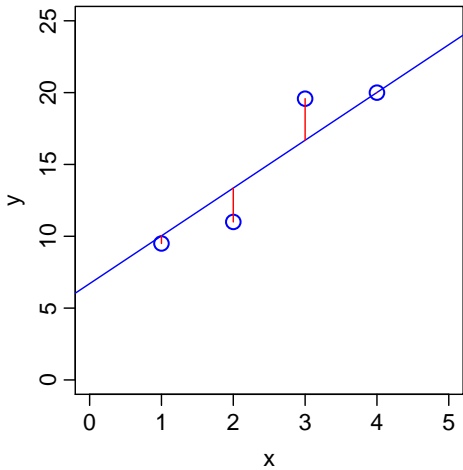


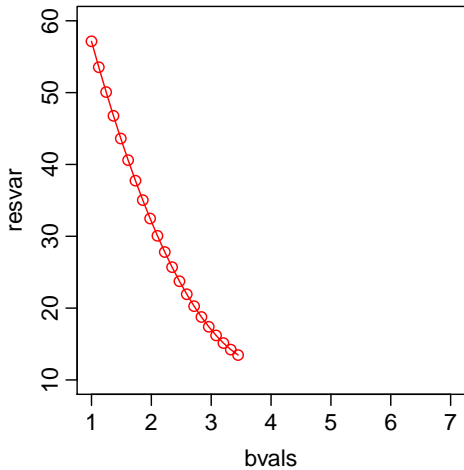
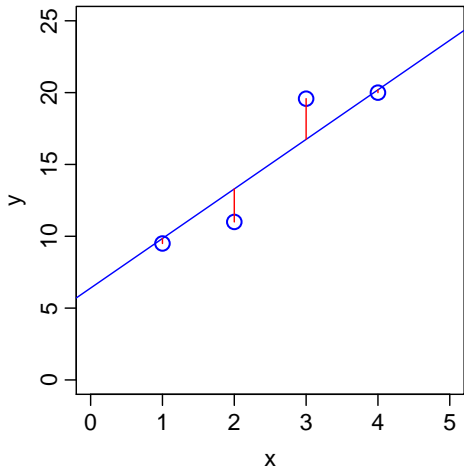


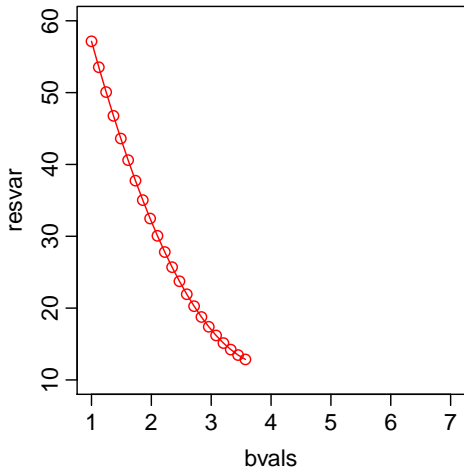
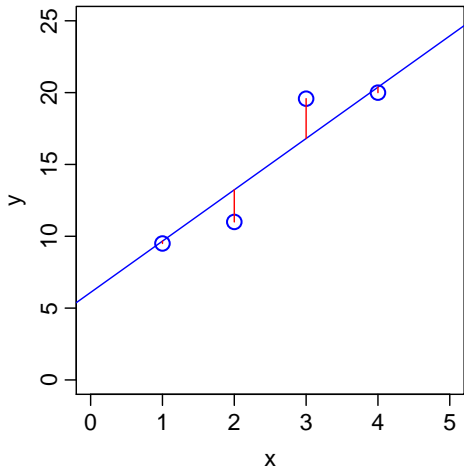


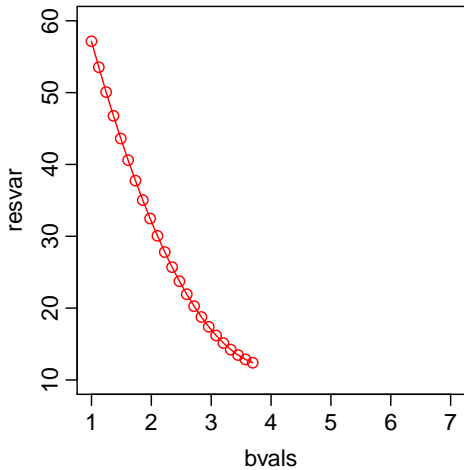
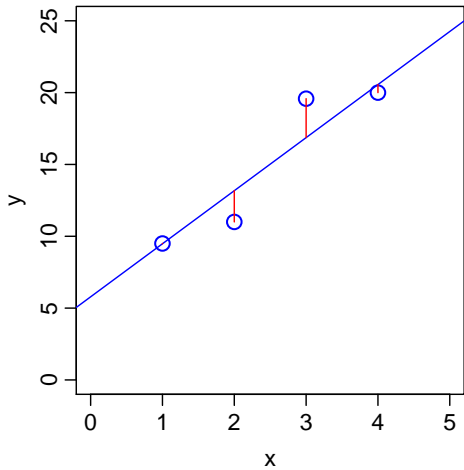




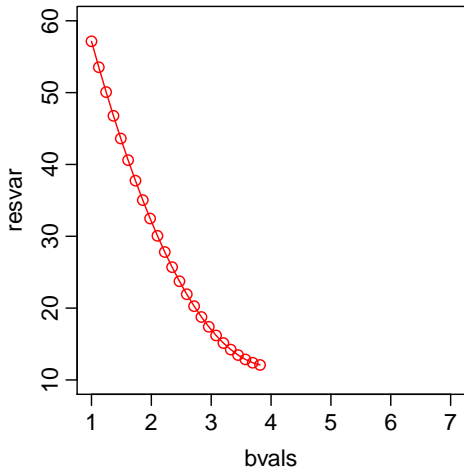
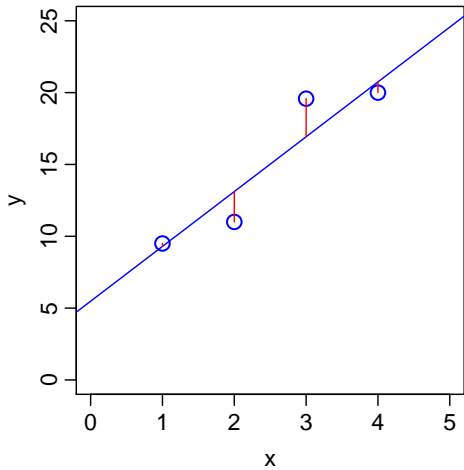


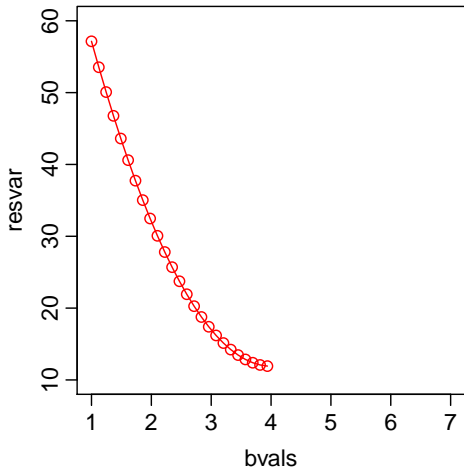
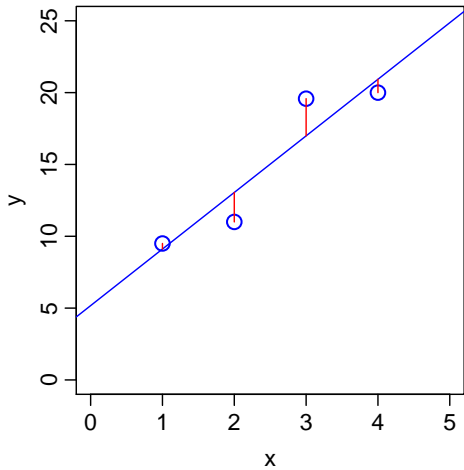


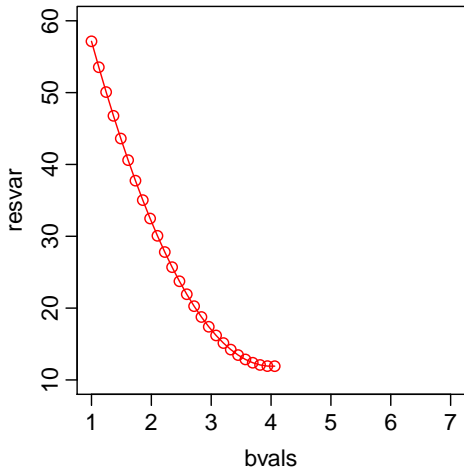
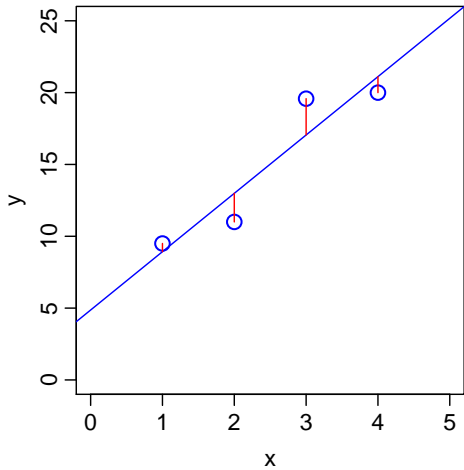


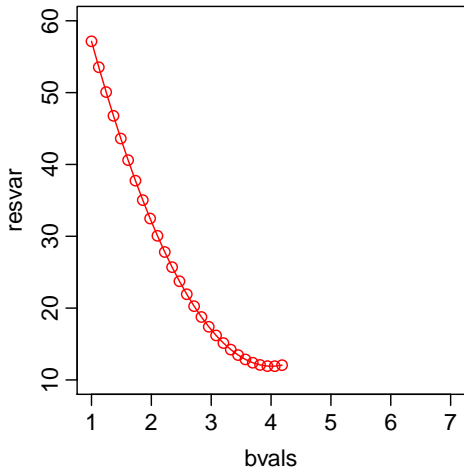
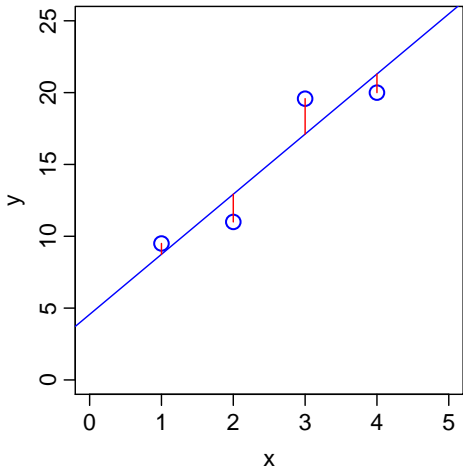


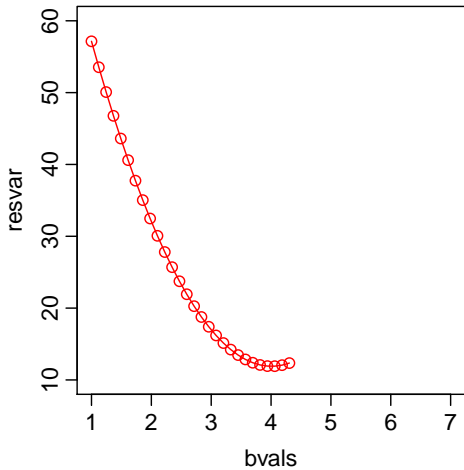
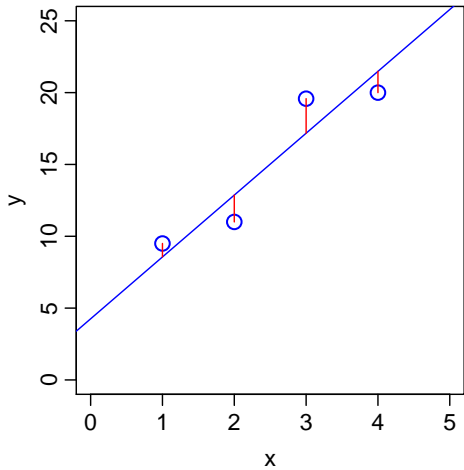


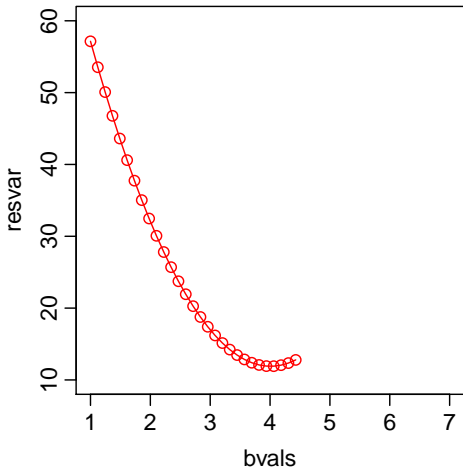
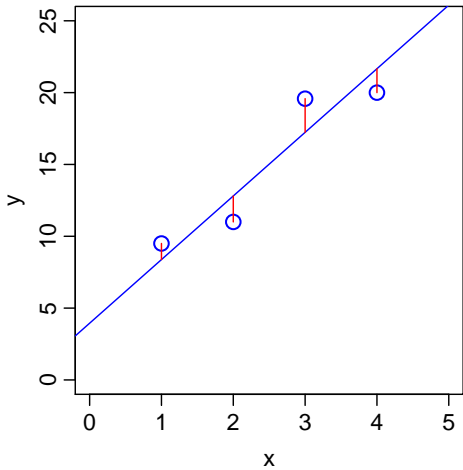


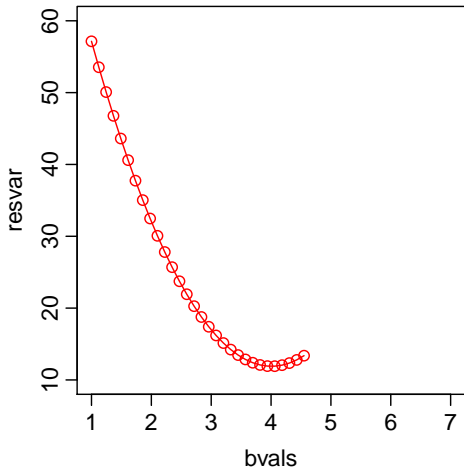
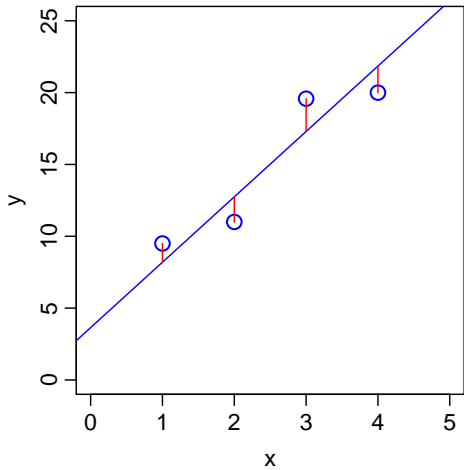


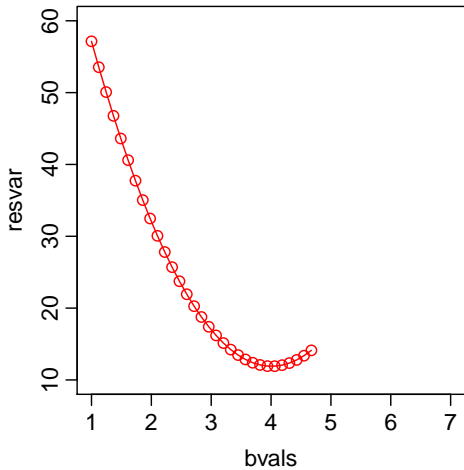
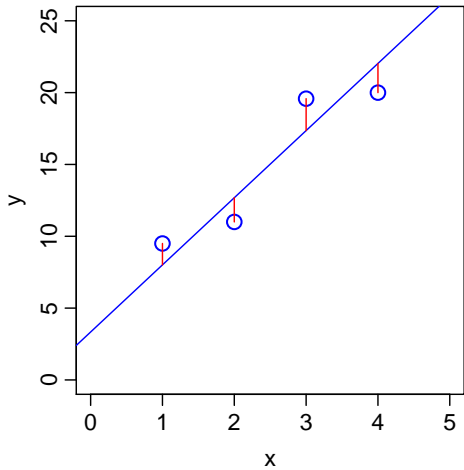




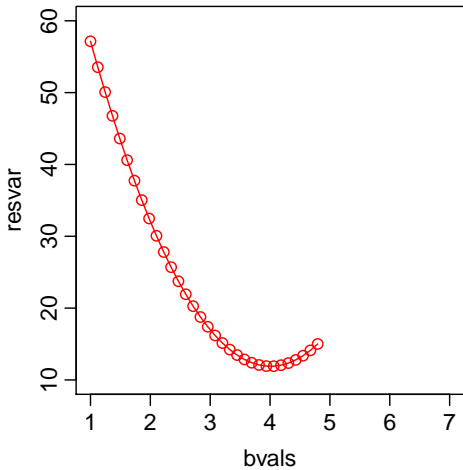
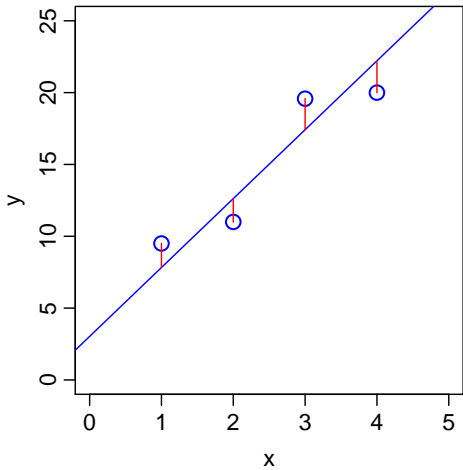


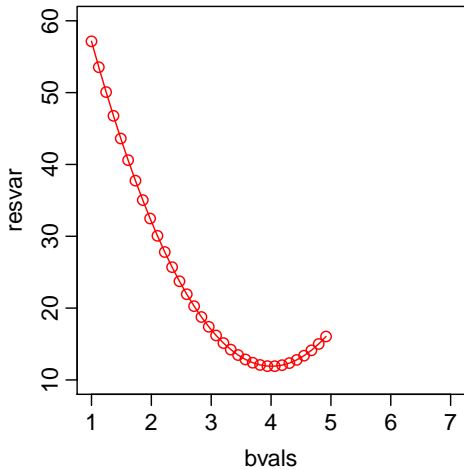
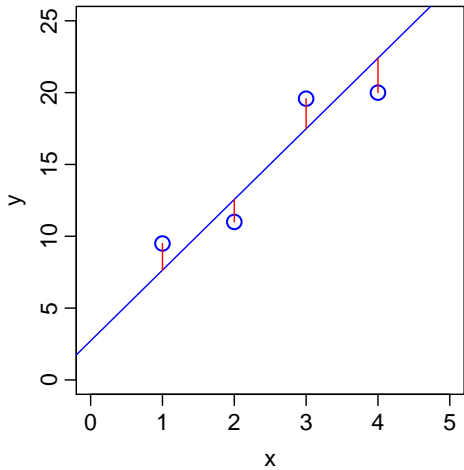


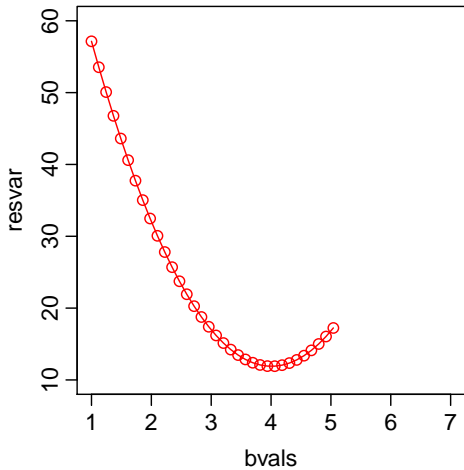
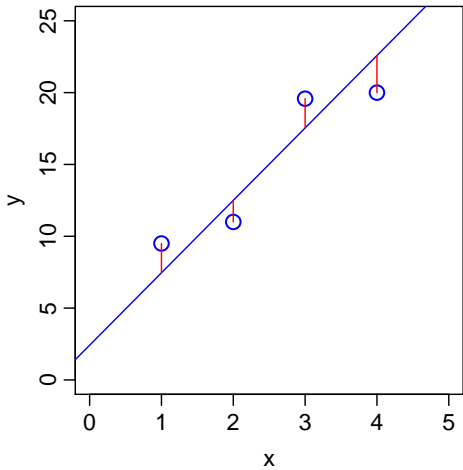


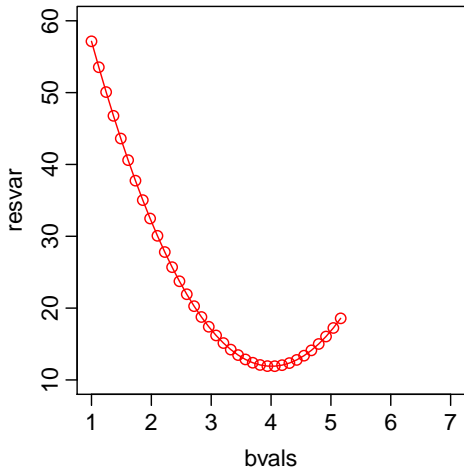
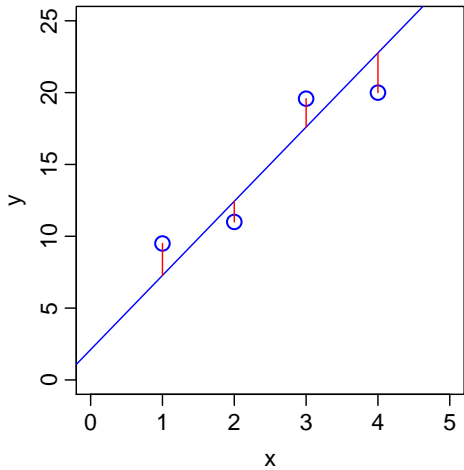


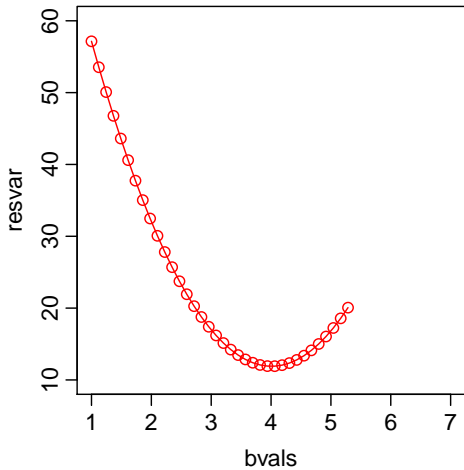
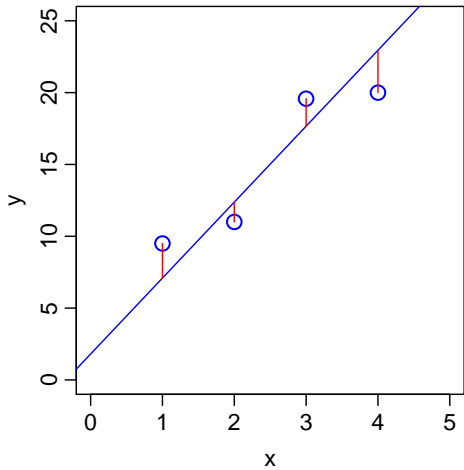


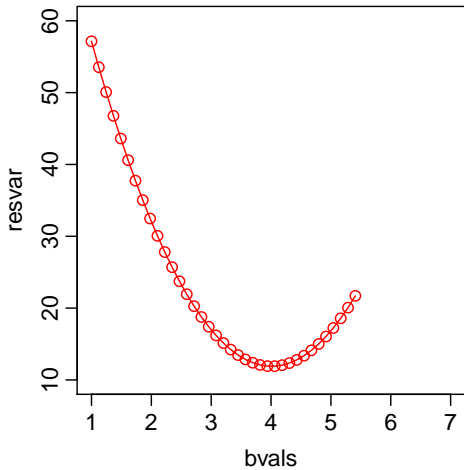
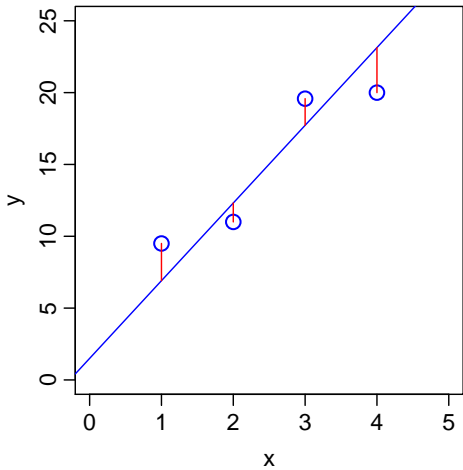


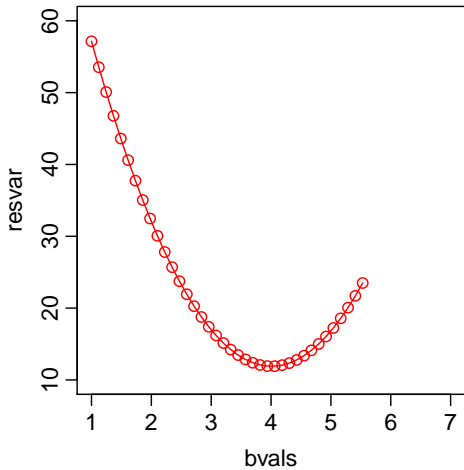
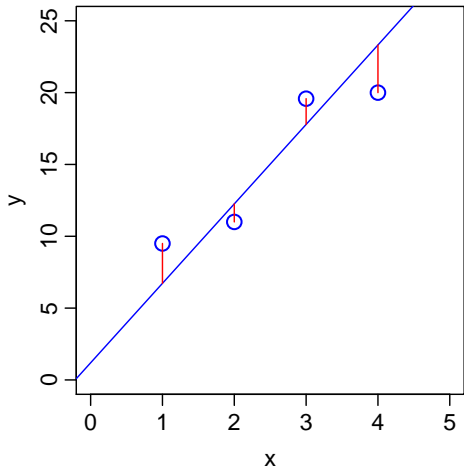


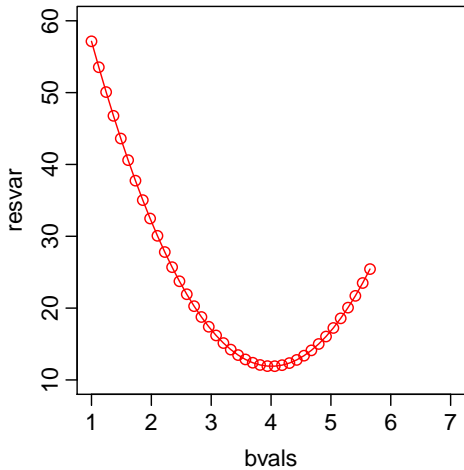
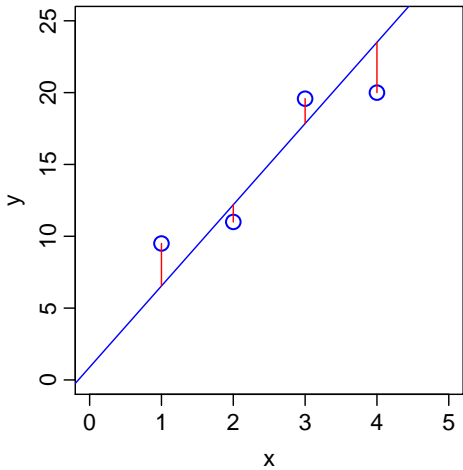




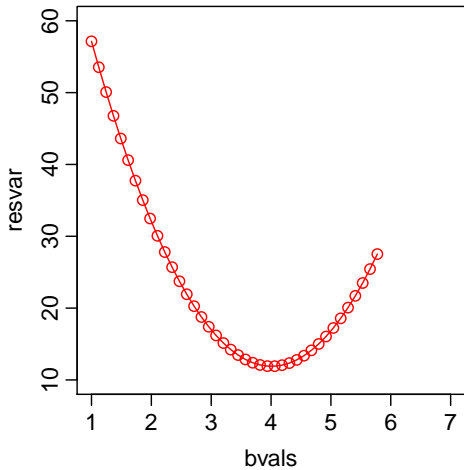
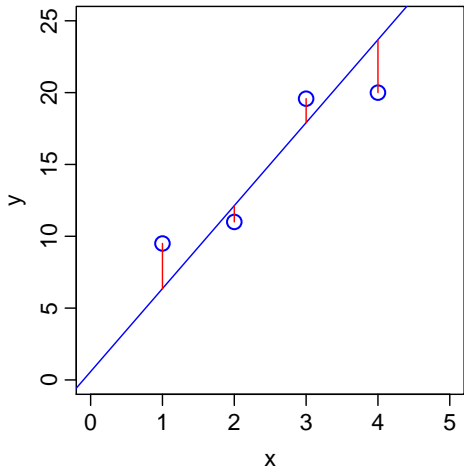


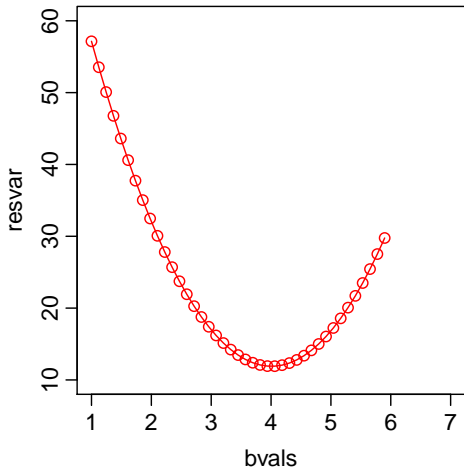
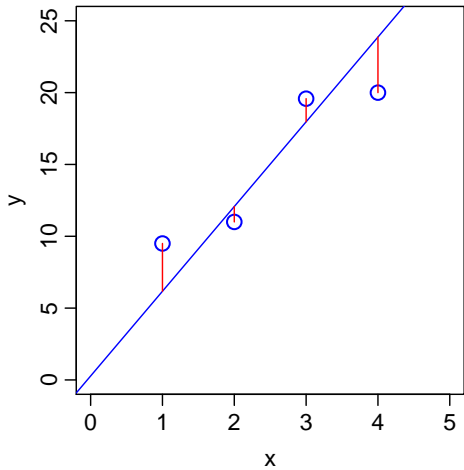


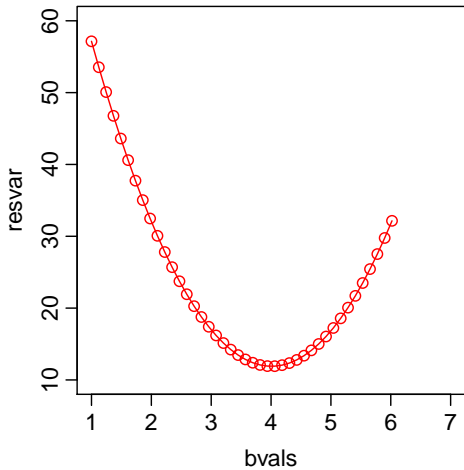
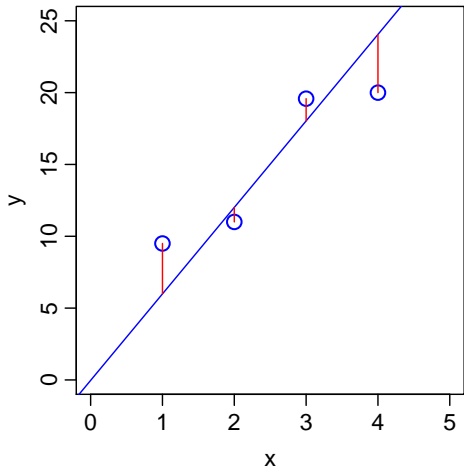


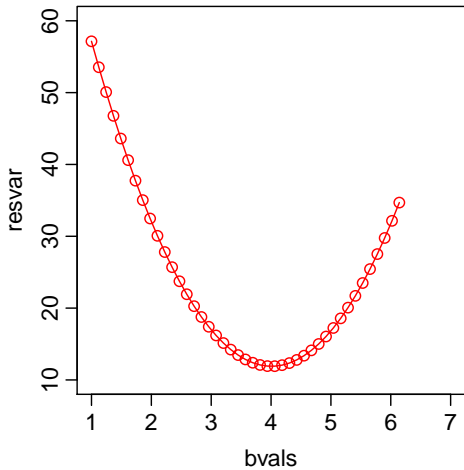
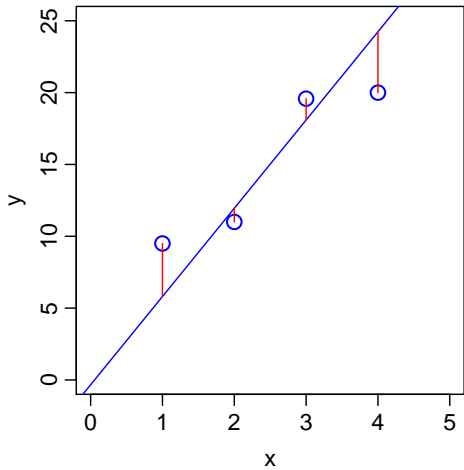


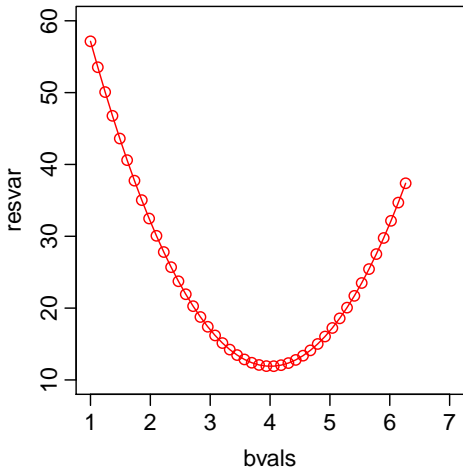
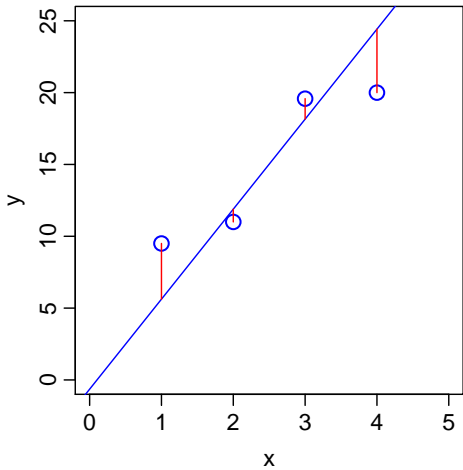


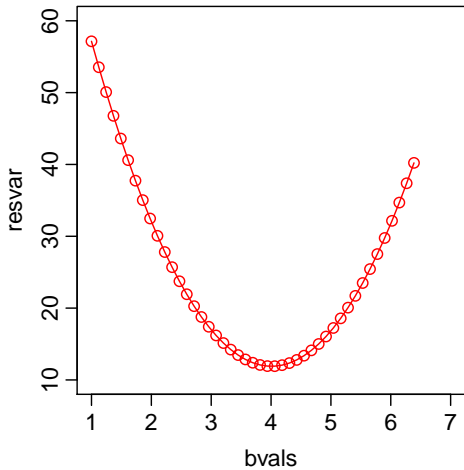
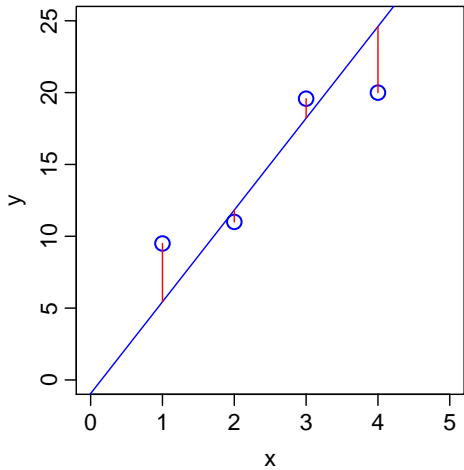


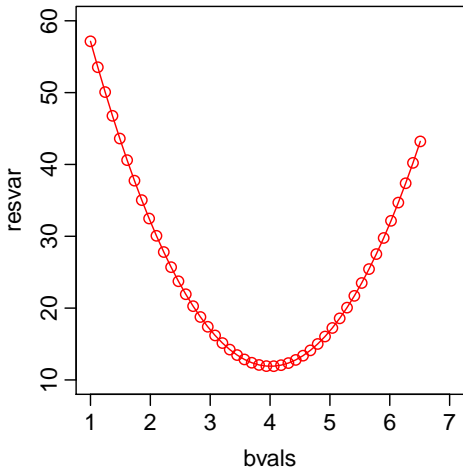
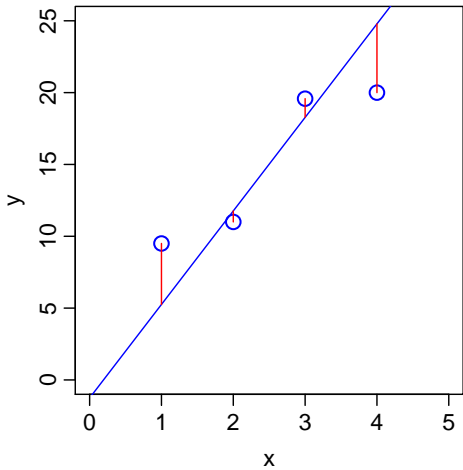


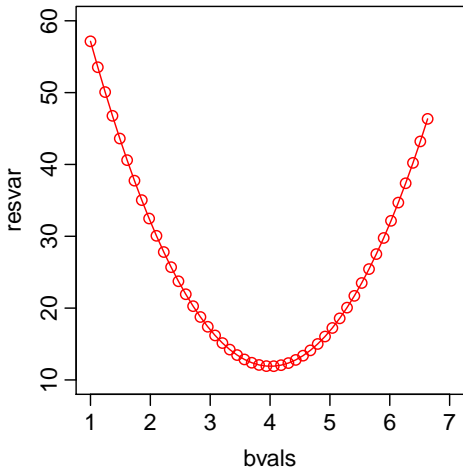
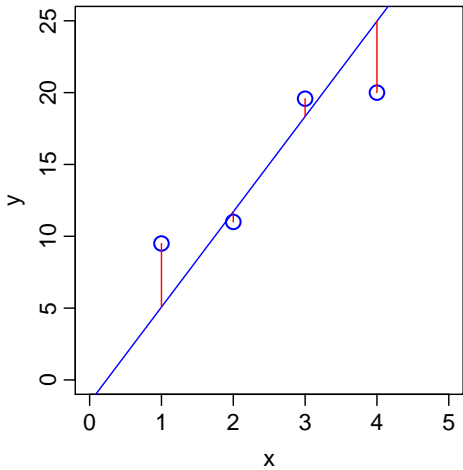




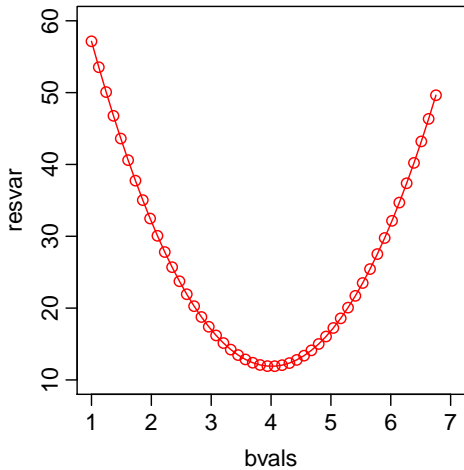
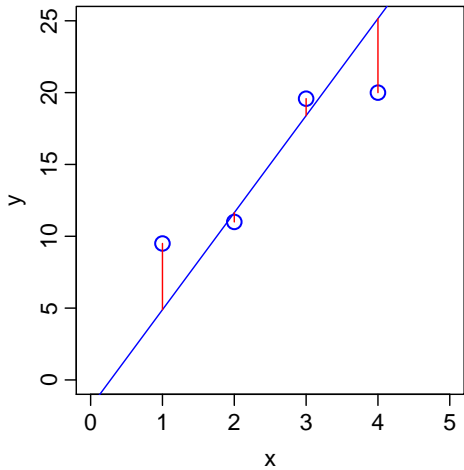


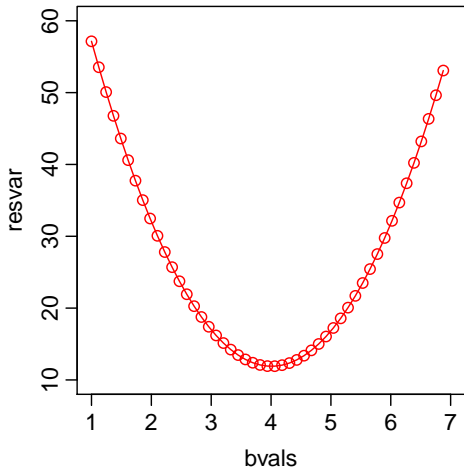
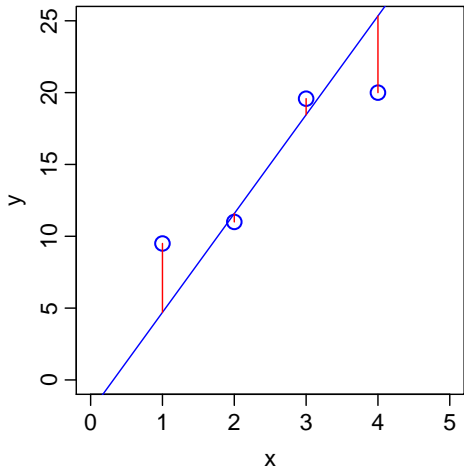


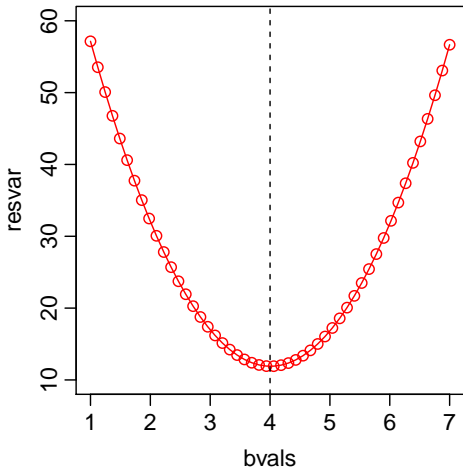
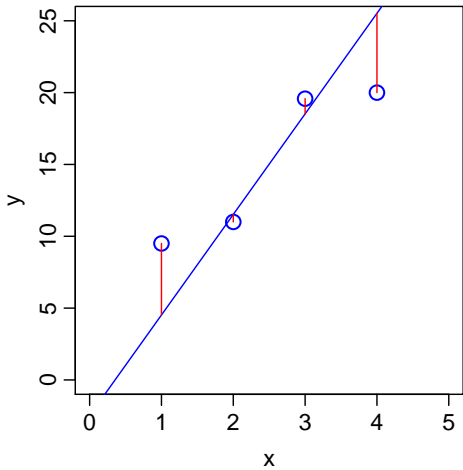




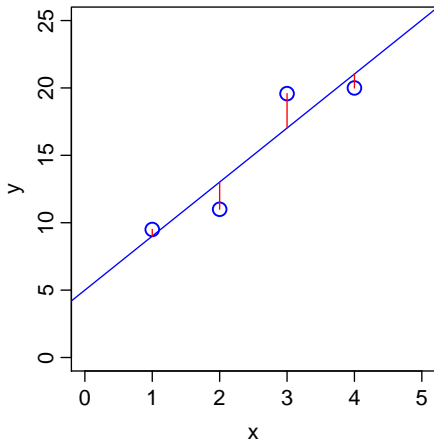








# IF THE MODEL IS LINEAR, THE LEAST-SQUARE SOLUTION IS EXACT



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

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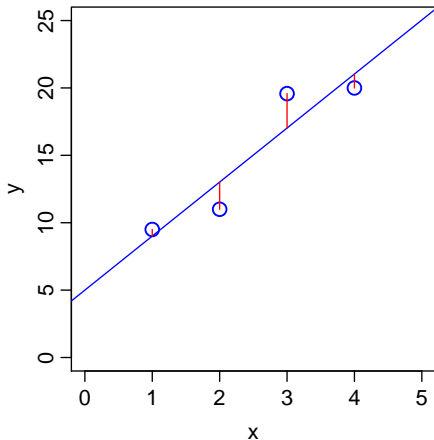
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The least squares solution here is:

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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-SQUARES MODEL FITTING DIFFICULT

- In an intrinsically non-linear model such as  $y_i = \beta_0 e^{\beta_2 x_i} + \varepsilon_i$ , the nice trick of solving  $\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$  *exactly* is impossible

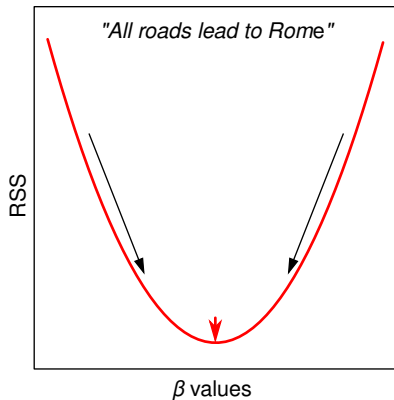
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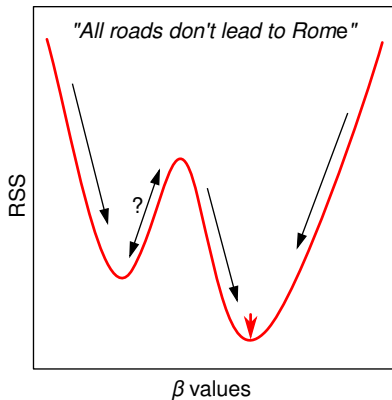
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**Linear Least-Squares  
Minimization**



**Non-Linear Least-Squares  
Minimization**





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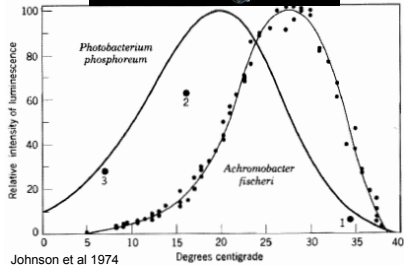
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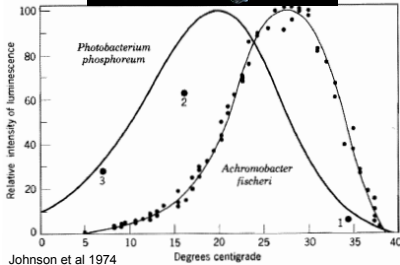
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- *Can you think of some examples?*

# NON-LINEAR MODEL EXAMPLE: TEMPERATURE AND METABOLISM

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

$T$  = temperature (K)

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

$E$  = 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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# THE NLLS METHOD: OVERVIEW

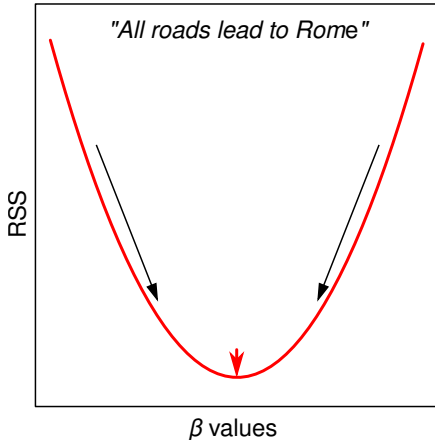
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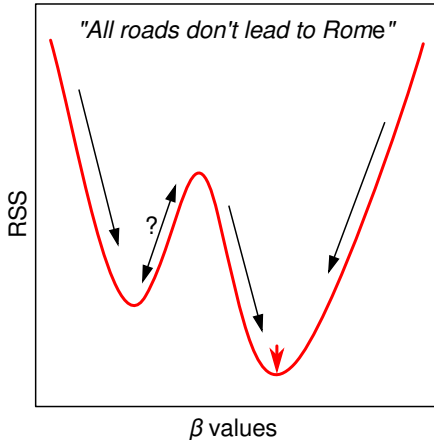
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  - Eventually, if it all goes well, a combination of  $\beta_j$ 's that is *very close* to the desired solution (where the RSS is *approximately* minimized) can be found

# THE NLLS FITTING / OPTIMIZATION PROCESS

## Linear Least-Squares Minimization



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- ➐ 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:

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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,  $R^2$  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

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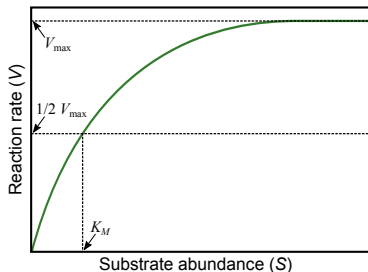
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  - It offers additional features like the ability to “bound” parameters to realistic values

# NLLS FITTING PRACTICALS

- 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 ( $= \frac{1}{2} V_{\max}$ )



- You will use NLLS fitting to obtain estimates of  $V_{\max}$  and  $K_M$
- Note that  $V_{\max} \leq 0$  and  $K_M \leq 0$  are physically impossible (useful for 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.