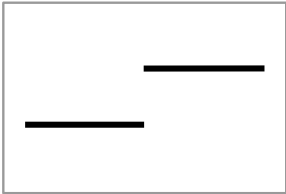


Evolutionary rates for the response trait



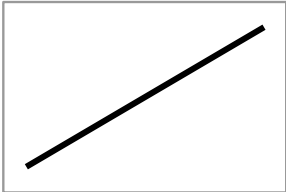
$$\sigma^2$$

A homogeneous rate throughout the tree.



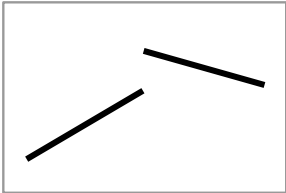
$$\sigma_{left}^2 \longrightarrow x \leq break$$
$$\sigma_{right}^2 \longrightarrow x > break$$

Two homogeneous rate regimes with shifts occurring at a threshold value of the predictor trait.



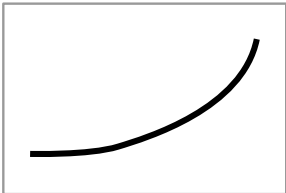
$$f(x) = \beta_1 x + \beta_2$$

A linear model. Rate changes linearly with the value of the predictor trait.



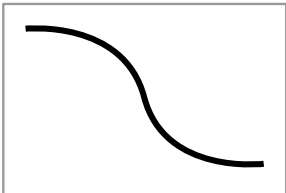
$$f(x) = \beta_{1a} x + \beta_{2a} \longrightarrow x \leq break$$
$$f(x) = \beta_{1b} x + \beta_{2b} \longrightarrow x > break$$

A two regimes linear model. Rate changes linearly with the value of the predictor trait, but the linear function shifts at a threshold



$$f(x) = c x^p$$

A power function model. Rate changes over a power function of the value of the predictor trait.



$$f(x) = c_1 + \frac{c_2}{1 + e^{\beta_1 (\beta_2 - x)}}$$

A sigmoid function model. This is the most flexible function implemented by default on the 'phylofix' package.

Predictor trait