Growth models

fish5103growth Modelling length at age and length distributions

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Principles of mathematical modelling

A mathematical model of a biological process is, in its simplest form, just a formula used to describe the process.

Before attempting to fit complex statistical models, the procedure should be to envisage the biological processes, formulate them as mathematical models, and then study the behavior of the mathematical models.

Once the mathematical models appear to behave in accordance with the biological processes in question it is necessary to compare the models to data, which is where the statistics come in.

Part of the procedure is to plot and analyse data in order to verify which mathematical assumptions may reflect biological reality.

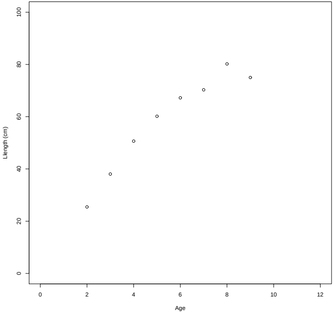
Example: If the age of a fish is stored in R as a vector,a, then one can use

```
lhat<-Linf*(1-exp(-K*(a-t0)))
```

to compute the predicted length at age.

Always first plot the data

First always plot the data - e.g. length against age.

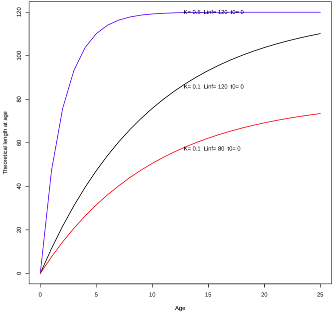


A model of fish growth

A model of growth - the von Bertalanffy growth equation

$$L_t = L_\infty \left(1 - e^{-Kt}\right)$$

$$L_t = L_\infty \left(1 - e^{-K(t-t_0)}\right)$$



Mathematical models as functions in R

The sum of squares

Need to define the sum of squares deviations based on

$$y_i - \hat{y}_i$$

so use

$$\sum_i (y_i - \hat{y}_i)^2$$

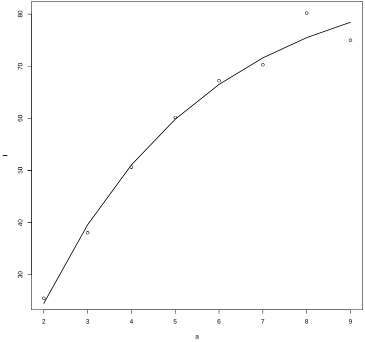
Example: Estimating a growth curve for a fish stock.
Define a new function which returns the sum of squared errors, for a given set of parameters.
The data is assumed to be available in the directory where the function is called.

```
sse<-function(b){
 lhat<-vonb(b)
 s<-sum((l-lhat)^2)
 return(s)
}
```

A better way of defining the function is to pass all the data as arguments:

```
sse<-function(b,a,l){
 lhat<-vonb(b,a)
```

Fitting a nonlinear growth model



Plot some of the results

```
plot(a,l)
K<-fm$estimate[2]
t0<-fm$estimate[3]
Linf<-fm$estimate[1]
lhat<-Linf*(1-exp(-K*(a-t0)))
lines(a,lhat)
```