

FISH 104

von Bertalanffy

When estimating parameters using a non-linear minimiser it is preferable to provide 'reasonable' starting values. A way to do this for the von Bertalanffy equations is as follows:

$$L_t = L_\infty(1 - \exp(-K[t - t_0]))$$

Assume $t_0 = 0$, then,

$$L_t = L_\infty(1 - \exp(-Kt)) \quad (1)$$

$$L_t = L_\infty - L_\infty \exp(-Kt) \quad (2)$$

$$L_\infty - L_t = L_\infty \exp(-Kt) \quad (3)$$

Substitute L_{t+1} for L_t in equation 2.

$$L_{t+1} - L_t = L_\infty \exp(-K(t+1)) - L_\infty \exp(-Kt) \quad (4)$$

Which can be written as:

$$L_{t+1} - L_t = -L_\infty \exp(-Kt)(1 - \exp(-K)) \quad (5)$$

Substitute equation 4 into equation 5.

$$L_{t+1} - L_t = (L_\infty - L_t)(1 - \exp(-K))$$

L_{t+1} can be written as a function of L_t .

$$L_{t+1} = L_\infty(1 - \exp(-K)) + L_t \exp(-K) \quad (6)$$

L_{t+1} can be plotted against L_t and a linear regression model fitted.

$$L_{t+1} = a + bL_t$$

where $a = L_\infty(1 - \exp(-K))$ and $b = \exp(-K)$.

K and L_∞ can then be estimated from:

$$K = -\ln(b)$$

$$L_\infty = a/(1 - b).$$

von Bertalanffy — predicting

R can be used to calculate the predicted length at age (`lhat`) from the von Bertalanffy equation:

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

where `Linf`, `K` and `t0` are constants and `a` is the age (and can be a vector).

The equation can also be stored as a function:

```
vonb <- function(b) {  
  Linf <- b[1]  
  K <- b[2]  
  t0 <- b[3]  
  lhat <- Linf*(1-exp(-K*(a-t0)))  
  return(lhat)  
}
```

where `b` is a vector containing L_∞, K, t_0 . The required ages a are in another predefined vector.

- Write a function in R to predict length at age with $L_\infty = 160$, $K = 0.09$ and $t_0 = 0$ for fish aged 2 to 14.
- Plot the predicted lengths at age.
- Calculate the growth curves for different parameters and compare on the same plot.

von Bertalanffy — estimating

Given data on meanlength at age, the von Bertalanffy parameters can be estimated by finding the parameters which minimise the difference between the observed mean lengths at age and those predicted from the von Bertalanffy equation.

To calculate the sum of squared errors for a set of parameters use a function like this:

```
vb.sse <- function(b){  
  lhat <- vonb(b)  
  sse <- sum((1-lhat)^2)  
  return(sse)  
}
```

This function combines the function to predict the von Bertalanffy growth curve (`vonb`) with the calculation of the difference between the observed growth curve and predicted growth curve `sse`.

The best fit to the data is from the parameters giving the lowest sum of squared errors. To estimate these parameters there is an R function `nlm` which is used like this:

```
est <- nlm(vb.sse, c(100, 0.1, 0))
```

It is better to use:

```
est <- nlm(vb.sse, c(100, 0.1, 0), typsize = c(100, 0.1, 0.001))
```

where `typsize` is an estimate of the order of magnitude of the optimised parameters. Using this should reduce the number of iterations required, increase the chance an optimum will be

found and make the optimisation more robust. There are many other options in `nlm` which are explained in `help`.

The output of `nlm` includes

```
est$estimate      # the parameter estimates
est$minimum       # the minimum sse
est$code          # a code which tells you the status
                  # (i.e. whether an optimum has been found)
```

To see the search being done by `nlm` add
`lines(a, lhat, col=2)`
to `vb.sse` and set up a plot before running `nlm` e.g.
`plot(a, vonb(c(Linf,K,to)), type="n")`.

von Bertalanffy – fitting to data

- Given these data:

```
L <- c(18, 24, 29, 32, 35)
t <- c(1.5, 2.5, 3.5, 4.5, 5.5)
```

estimate the von Bertalanffy parameters.

Plot L_t against L_{t+1} , fit a linear regression line using `lm`. Use the estimates of K and L_∞ from the linear regression to start the non-linear minimisation.

- A dataset including haddock age and length is available from:
www.hafro.is/~lorna/haddockage
- Using these data, calculate mean length at age (`tapply` and fit a von Bertalanffy growth curve assuming age 1 is equivalent to $t = 1$ etc.
- Add the fitted growth curve to a plot of the observed data.
- How many fish are there at each age? Does eliminating from the analysis ages with a very small number of fish affect the estimated growth curve?

Models of length distribution

A single age

- If the length distribution of an ageclass has a Gaussian (Normal) distribution with mean length $\mu = 23$ and $\sigma = 1.4$ then it could look like this:

```
# estimating a point value for every cm
le <- seq(15,30,1)
plot(le, dnorm(le, 23, 1.4), lwd=2)
lines(le, dnorm(le, 23, 1.4))
```

- If a length group is assumed to go from -0.5 to +0.5 then it is more appropriate to sum the distribution within this region rather than use the density of the mid-point. The *cumulative distribution* is then used:

```
# the cumulative distribution is
# a continual sum of the density distribution
le <- seq(15,30,1)
plot(le, pnorm((le-23)/1.4), type="o")
# the density distn from the cumulative
leA <- seq(15.5,30.5,1) # upper point
leB <- seq(14.5,29.5,1) # lower point
# to check leA and leB are correct
rbind(leA,leB)
d2 <- pnorm((leA-23)/1.4) - pnorm((leB-23)/1.4)
# the values from the cumulative distn
plot(le, d2, type="o")
# the values from the density distn
points(le, dnorm(le, 23, 1.4), col=2)
```

Several ages

To model several ages, the mean length at each age can be defined in a vector eg `mu <- c(23, 34, 42, 50)` or a growth model can be used to define the mean length at age.

- A population containing several length distributions can be simulated like this:
The mean length at age is predicted using the von Bertalanffy model.
The standard deviation of length at age is fixed.
The number at age is predicted using the stock equation.

```
# estimate mean length from von Bertalanffy
a <- 1:8 # 8 age groups
mu <- vonb(c(60,0.18,0))
sdev <- rep(2.4,length(a))
le <- 1:60
leA <- seq(1.5,60.5,1) # upper point
leB <- seq(0.5,59.5,1) # lower point
```

```

# the proportion at age assuming no fishing and M = 0.3
N <- 1
M <- 0.3
for(i in a){
  N <- c(N, exp(-M)*N[i])
}

Ntot <- sum(N)
p <- N/Ntot

# use a loop to calculate length distribution for each age
# and store in rows

# the length distribution * proportion at age

ldist <- NULL
for(i in a) {
  d2 <- (pnorm((leA-mu[i])/sdev[i]) - pnorm((leB-mu[i])/sdev[i]))*p[i]
  ldist <- rbind(ldist, d2)
}

# these can be plotted individually
matplot(le, t(ldist), type="l")
# and the length distribution would look like
plot(le, apply(ldist, 2, sum), type="l")

```

- Plot the length distributions for different von Bertalanffy growth curves and with different patterns of mortality at age (eg with only natural mortality on younger fish but fishing mortality on older fish).