

Life History Package

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Introduction

library(lh)

The Package contains various methods for working with life history traits, i.e. natural mortality, growth, maturity.

Data

There are several example datasets; life history parameters of pelagic species caught in the South Atlantic and Indian Ocean longline fisheries

data(lhPel)

names(lhPel)

```
[1] "lmax"      "l50"      "l50lmax"  "fec"
[5] "linf"      "k"        "a50"      "amax"
[9] "m"        "ocean"    "sp"       "name"
[13] "family"
```

and Atlantic bonito length frequency data.

data(bonLn)

library(ggplot2)

ggplot(bonLn)+

```
  geom_histogram(aes(len,weight=n,fill=month))+
  scale_y_continuous(breaks=c(1))+
  theme_bw()+
  xlab("Length")+ylab("Proportion")
```

Estimating Total Mortality

Beverton and Holt developed a method to estimate total mortality (Z) from length frequency data if the growth parameters are known. Powell and then Wetherall extended this method to estimate the growth parameters as well as mortality, by recognising that the right hand tail of a length frequency distribution is determined by the asymptotic length (L_{∞}) and the ratio between Z and the growth rate

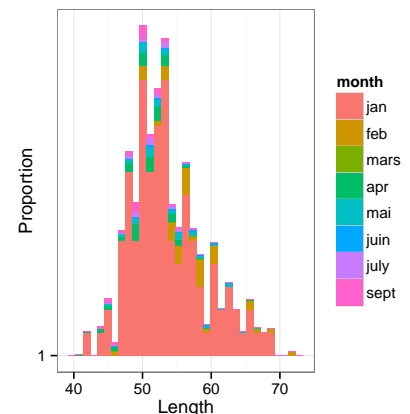


Figure 1: Length frequencies

(k) of the von Bertalanffy growth curve and that there is a linear relationship between $\bar{L} - L'$ and L' . Where L' can take any value between the smallest and largest sizes.

This allows Z and L_∞ to be derived from a regression analysis. While the Beverton and Holt method requires estimates for k and L_∞ , the Powell-Wetherall method only requires an estimate of k , since L_∞ is estimated as well as Z/k . The method therefore provides estimates for Z/k and Z if k is known.

A change in the slope also allows the selection patterns to be inferred. As well as assuming that growth follows the von Bertalanffy growth function, it is assumed that the population is in a steady state with constant exponential mortality, no changes in selection pattern of the fishery and constant recruitment. All of which are violated of course but the method has been shown to provide good indications of total mortality when compared to data rich methods.

Atlantic bonito example

Run the Powell-Wetherall method

```
rslt=with(bonLn, powh(len,n))
```

Estimates of L_∞ and Z/k

```
rslt$params
```

```
      linf      zk
71.612630  2.724911
```

Powell-Weatherall plot

```
ggplot(rslt$data)+
  geom_path(aes(len,diff),col="grey75")+
  geom_point(aes(len,diff),size=1)+
  geom_path(aes(len,hat),col="blue")+
  theme_bw()
```

Fish appear to be fully selected at length 47cm.

As a check compare estimate of L_{∞} with literature value

```
subset(lhPel,name=="Sarda sarda")[,c("name","linf","k")]
```

```
      name  linf    k
38 Sarda sarda 74.61 0.22
```

Estimate Z by multiplying by k

```
rslt$params["zk"]*subset(lhPel,name=="Sarda sarda")[,"k"]
```

```
      zk
0.5994804
```

$$Z = K \frac{L_\infty - \bar{L}}{\bar{L} - L'} \quad (1)$$

Relationship between total mortality and length

$$\bar{L} - L' = a + bL' \quad (2)$$

Powell and Weatheralls modification

$$Z/k = \frac{-1-b}{b} \quad (3)$$

Estimate of Z/k

$$L_\infty = -a/b \quad (4)$$

Estimate of L_∞

