Using information on Life History relationships

12 December, 2017

Life history traits include growth rate; age and size at sexual maturity; the temporal pattern or schedule of reproduction; the number, size, and sex ratio of offspring; the distribution of intrinsic or extrinsic mortality rates (e.g., patterns of senescence); and patterns of dormancy and dispersal. These traits contribute directly to age-specific survival and reproductive functions.[1] The **FLife** package has a variety of methods for modelling life history traits and functional forms for processes for use in fish stock assessment and for conducting Management Strategy Evaluation (MSE).

These relationships have many uses, for example in age-structured population models, functional relationships for these processes allow the calculation of the population growth rate and have been used to to develop priors in stock assesments and to parameterise ecological models.

The **FLife** package has methods for modelling functional forms, for simulating equilibrium `FLBRP` and dynamic stock objects `FLStock`.

Back to Top

Quick Start

This section provide a quick way to get running and overview of what functions are available, their potential use, and where to seek help. More details are given in later sections.

The simplest way to obtain **FLife** is to install it from the `FLR` repository via the R console:

```
install.packages("FLife", repos = "http://flr-project.org/R")
```

See help(install.packages) for more details.

After installing the **FLife** package, you need to load it

```
library(FLife)
```

There is an example teleost dataset used for illustration and as a test dataset, alternatively you can load your own data.

```
data(teleost)
```

The dataset contains life history parameters for a range of bony fish species and families, i.e. von Bertalanffy growth parameters (L_∞, k, t_0), length at 50% mature (L_{50}), and the length weight relationship (a, b).

When loading a new dataset it is always a good idea to run a sanity check e.g.

---

[1] http://www.oxfordbibliographies.com/view/document/obo-9780199830060/obo-9780199830060-0016.xml

```r
is(teleost)
```

```
[1] "FLPar"     "array"     "structure" "vector"
```

The `teleost` object can be used to create `vectors` or other 'objects with values by age using **FLife** methods, e.g. to construct a growth curve for hutchen (*Hucho hucho*)

```r
vonB(1:10,teleost[,"Hucho hucho"])
```

```
 [1]  29.0  40.8  51.5  61.1  69.9  77.8  84.9  91.4  97.3 102.6
```

Plotting

Plotting is done using **ggplot2** which provides a powerful alternative paradigm for creating both simple and complex plots in R using the *Grammar of Graphics*[2] The idea of the grammar is to specify the individual building blocks of a plot and then to combine them to create the desired graphic[3].

The **ggplot** methods expects a `data.frame` for its first argument, `data` (this has been overloaded by **ggplotFL** to also accept FLR objects); then a geometric object `geom` that specifies the actual marks put on to a plot and an aesthetic that is "something you can see" have to be provided. Examples of geometic Objects (geom) include points (geom_point, for scatter plots, dot plots, etc), lines (geom_line, for time series, trend lines, etc) and boxplot (geom_boxplot, for, well, boxplots!). Aesthetic mappings are set with the aes() function and, examples include, position (i.e., on the x and y axes), color ("outside" color), fill ("inside" color), shape (of points), linetype and size.

```r
age=FLQuant(1:20,dimnames=list(age=1:20))
len=vonB(age,teleost)

ggplot(as.data.frame(len))+
  geom_line(aes(age,data,col=iter))+
  theme(legend.position="none")
```

Back to Top

Methods

Life History Parameters

Growth

Consider the von Bertalanffy growth equation

$$L_t = L_\infty(1 - e^{(-kt-t_0)})$$

where L_t is length at time t, L_∞ the asymptotic maximum length, k the growth coefficient, and t_0 the time at which an individual would, if it possible, be of zero length.

As L_∞ increases k declines. in other words at a given length a large species will grow faster than a small species. for example Gislason, Pope, et al. (2008) proposed the relationship

$$k = 3.15 L_\infty^{-0.64}$$

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[2] Wilkinson, L. 1999. *The Grammar of Graphics*, Springer. doi 10.1007/978-3-642-21551-3_13.

[3] http://tutorials.iq.harvard.edu/R/Rgraphics/Rgraphics.html

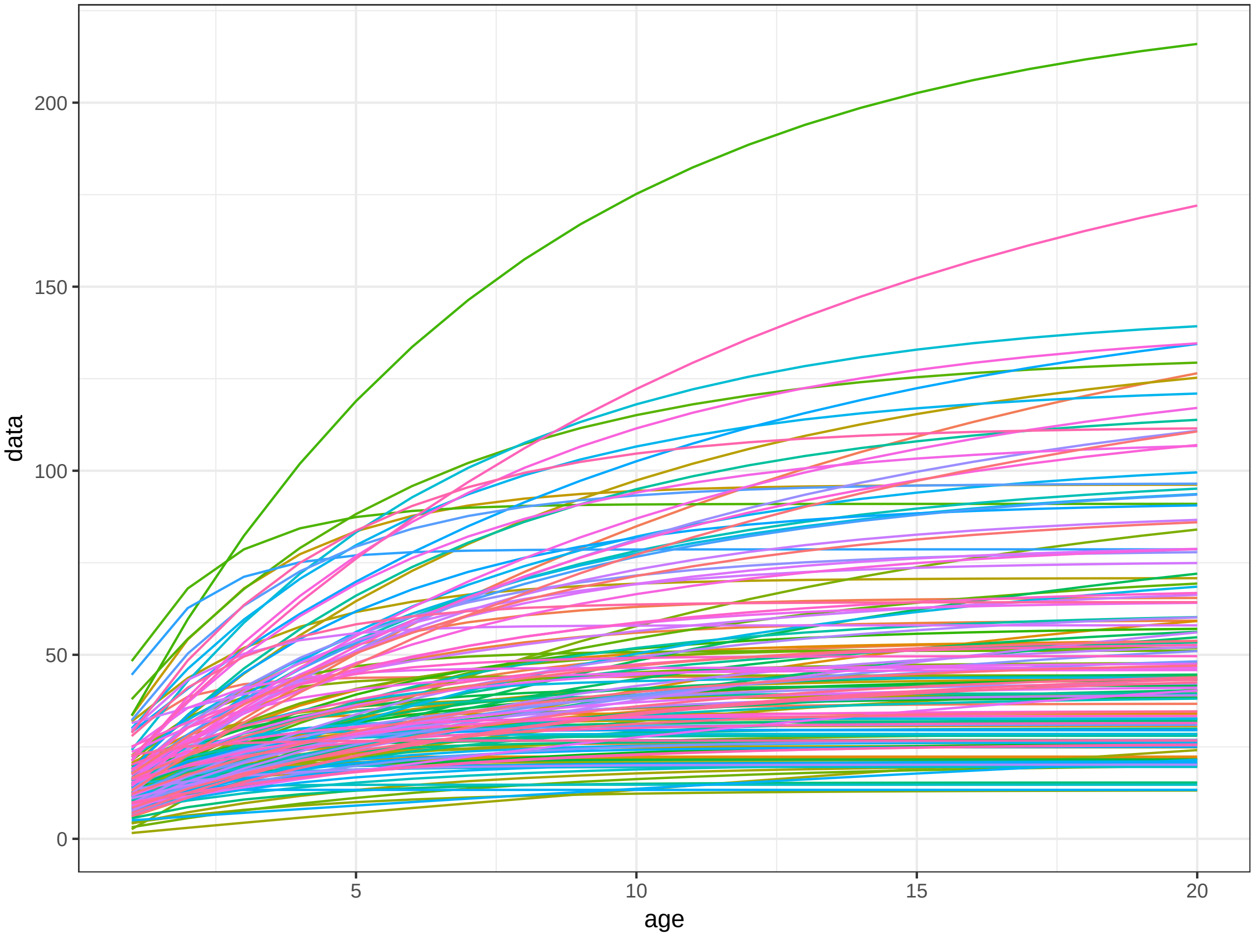


Figure 1: Von Bertalanffy growth curves.

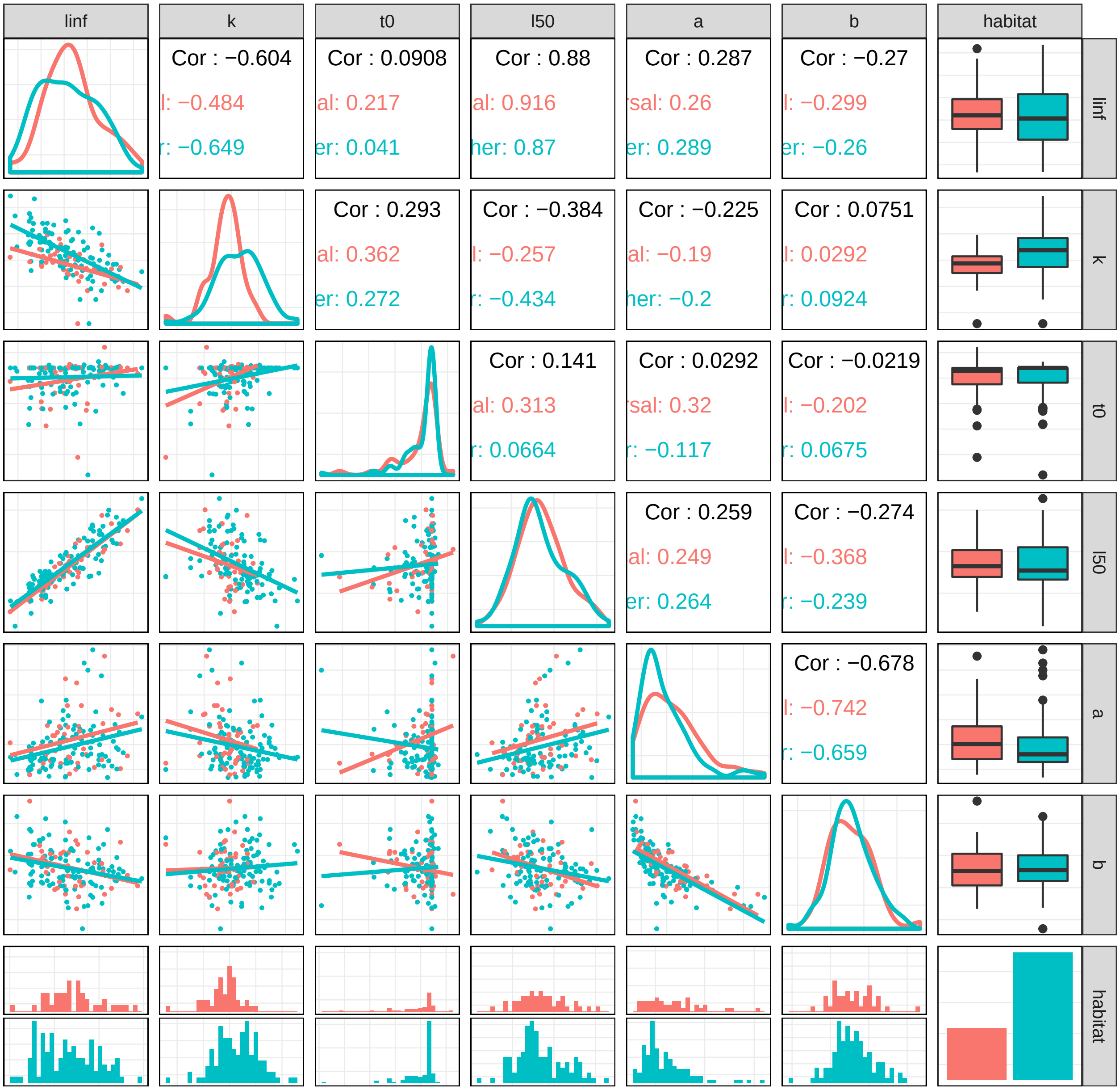


Figure 2: Relationship between life history parameters in the teleost dataset.

There also appears to be empirical relationship between t_0 and L_∞ and k i.e.

$$log(-t_0) = -0.3922 - 0.2752 log(L_\infty) - 1.038 log(k)$$

Therefore for a value of L_∞ or even L_{max} the maximum size observered as $L_\infty = 0.95L_{max}$ then all the growth parameters can be recovered.

Maturity

There is also a relationship between L_{50} the length at which 50% of individuals are mature

$$l_{50} = 0.72L_\infty^{0.93}$$

and even between the length weight relationship

$$W = aL^b$$

Natural Mortality

For larger species securing sufficient food to maintain a fast growth rate may entail exposure to a higher natural mortality Gislason, Daan, et al. (2008). While many small demersal species seem to be partly protected against predation by hiding, cryptic behaviour, being flat or by possessing spines have the lowest rates of natural mortality Griffiths and Harrod (2007). Hence, at a given length individuals belonging to species with a high L_∞ may generally be exposed to a higher M than individuals belonging to species with a low L_∞.

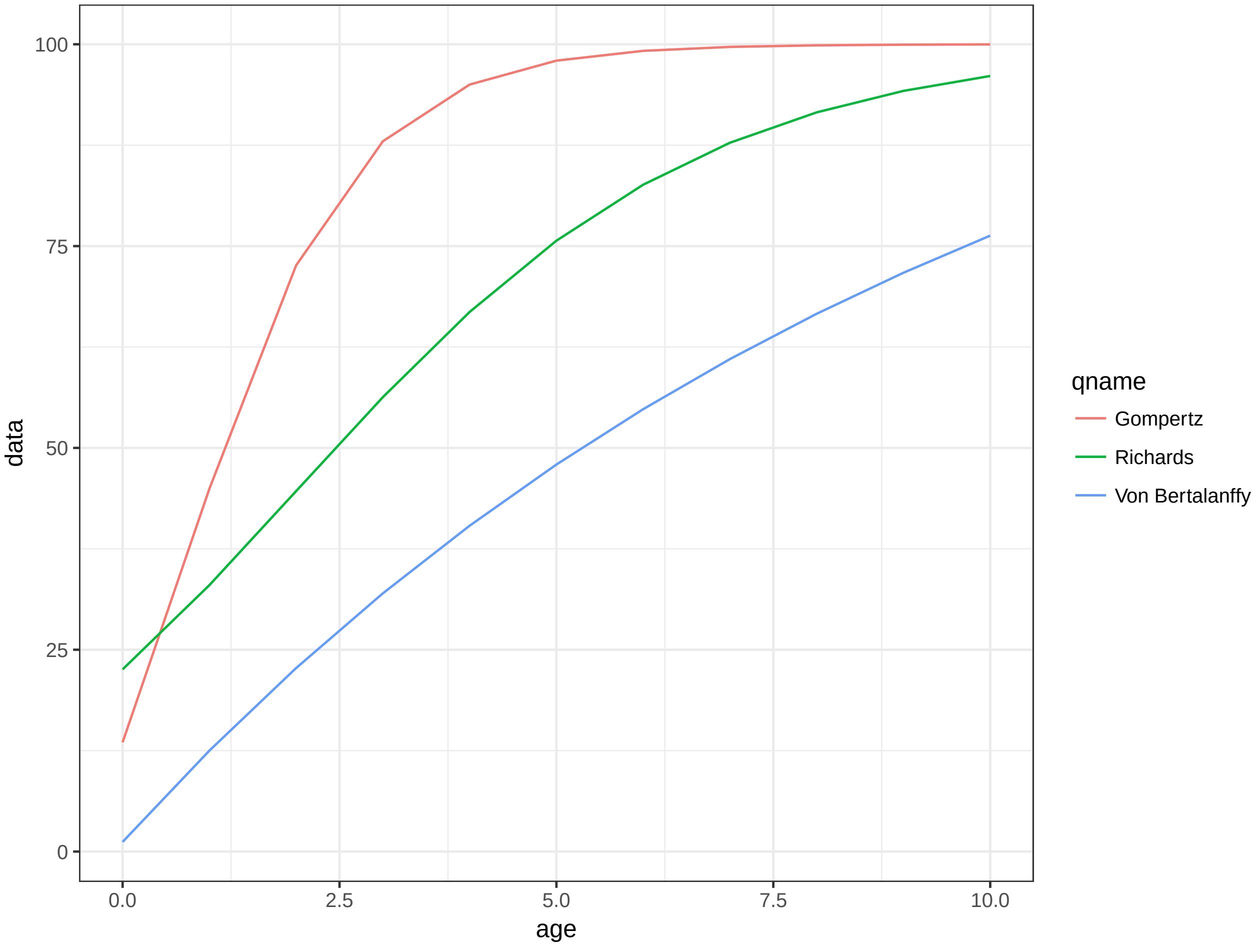
$$log(M) = 0.55 - 1.61 log(L) + 1.44 log(L_\infty) + log(k)$$

Functional forms

In **FLIfe** there are methods for creating growth curves, maturity ogives and natural mortality vectors, selection patterns, and other ogives. All these methods are used to create `FLQuant` objects.

Growth

gompertz, richards, vonB



Ogives

dnormal, knife, logistic, sigmoid

```
dnormal( age,FLPar(a1=4,sl=2,sr=5000))
knife(   age,FLPar(a1=4))
logistic(age,FLPar(a50=4,ato95=1,asym=1.0))
sigmoid( age,FLPar(a50=4,ato95=1))
```

Natural Mortality

Many estimators have been propose for M, based on growth and reproduction, see Kenchington (2014).

Natural Mortality

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Age at maturity a_{50}

Rikhter and Efanov

$$M = \frac{1.521}{a_{50}^{0.72}} - 0.155$$

Jensen

$$M = \frac{1.65}{a_{50}}$$

Growth

Jensen

$$M = 1.5k$$

Griffiths and Harrod

$$M = 1.406 W_{\infty}^{-0.096} k^{0.78}$$

where $W_{\infty} = \alpha L_{\infty}^{\beta}$

Djabali

$$M = 1.0661 L_{\infty}^{-0.1172} k^{0.5092}$$

Growth and length at maturity L_{50}

Roff

$$M = 3kL_{\infty}\frac{(1 - \frac{L_{50}}{L_{\infty}})}{L_{50}}$$

Rikhter and Efanov

$$M = \frac{\beta k}{e^{k(a_{50}-t_0)} - 1}$$

where $a_{50} = t_0 + \frac{log(1-\frac{L_{50}}{L_{\infty}})}{-k}$

Varing by length

Gislason

$$M_L = 1.73 L^{-1.61} L_{\infty}^{1.44} k$$

Charnov

$$M_L = k\frac{L_{\infty}}{L}^{1.5}$$

Varying by weight

Peterson and Wroblewsk

$$M_W = 1.28W^{-0.25}$$

Lorenzen

$$M_W = 3W^{-0.288}$$

Senescence

Conversions

ages, len2wt, wt2len

Generation of missing life history relationships

```
par=lhPar(FLPar(linf=100))
par
```

```
An object of class "FLPar"
params
     linf         k        t0         a         b     ato95       a50 
 100.0000    0.1653   -0.1000    0.0003    3.0000    1.0000    4.3600 
     asym        bg        m1        m2        a1        sl        sr 
   1.0000    3.0000  217.3564   -1.6100    4.3600    2.0000 5000.0000 
        s         v 
   0.9000 1000.0000 
units:  cm 
```

There are relationships between the life history parameters and size, growth, maturation, natural mortality and productivity, as seen in the following.

Simulation

lhPar, lhEql

Function Forms

Population dynamics

Ecological

leslie, r

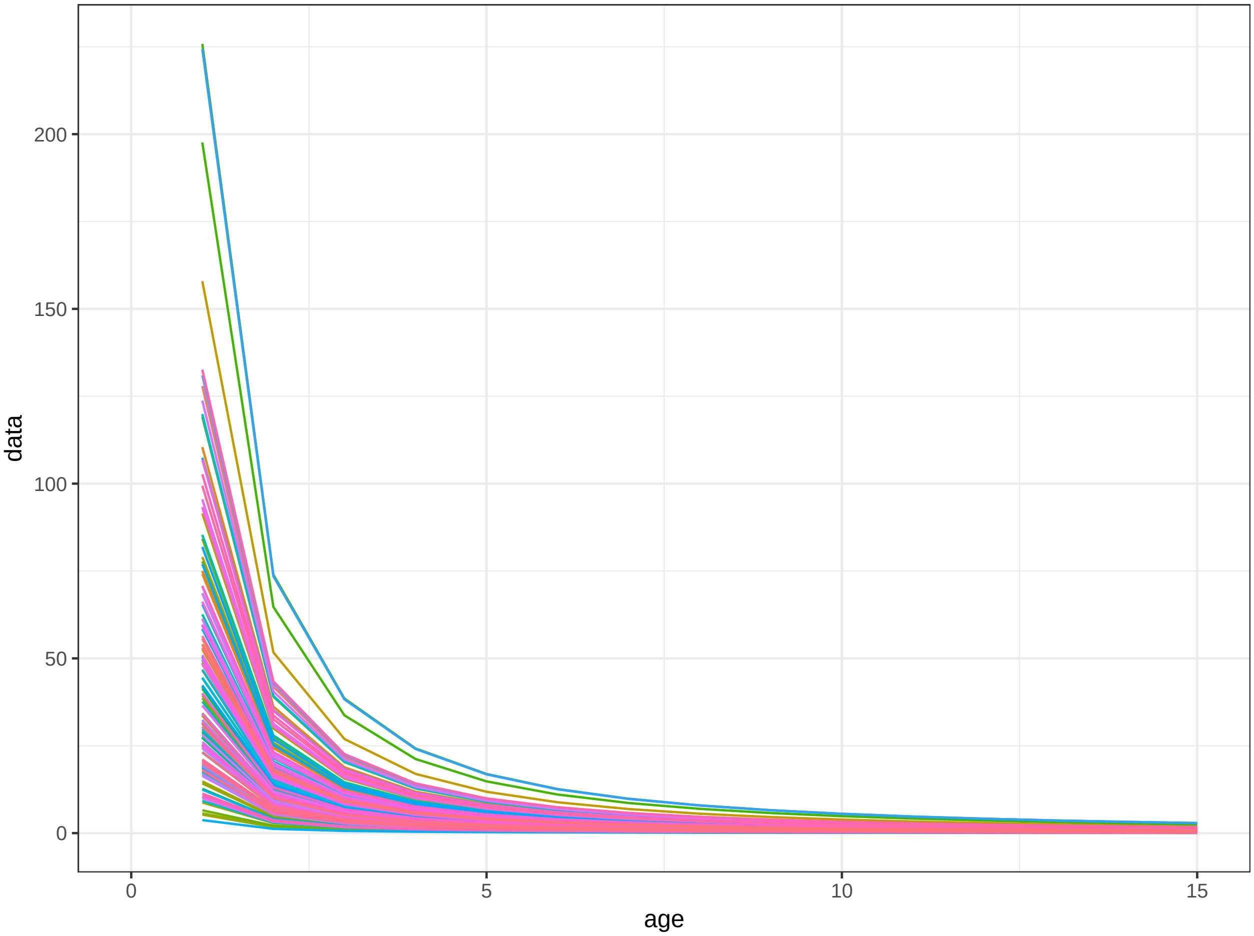
life history traits

```
An object of class "FLPar"
iters:  145

params
              linf                    k                   t0 
45.100000(28.02114)  0.246667( 0.17297) -0.143333( 0.13590) 
               l50                    a                    b 
22.100000(11.71254)  0.011865( 0.00776)  3.010000( 0.15271) 
units:  NA 
```

“‘

Natural Mortality



Stock recruitment

Fishery

Reference points

lopt, loptAge

Density Dependence

matdd, mdd

Parameter estination

moment, powh

Stationarity

rod

Random variables

rnoise

Refetrence points

```r
library(FLBRP)
data(ple4)
refs(ple4)
```

```
An object of class "FLPar"
params
     b.msy   b.virgin     b.f0.1     b.fmax   b.spr.30  b.spr.100
  1.76e+06   5.25e+06   2.56e+06   1.85e+06   1.89e+06   2.40e+06
   b.f0.1_    b.fmax_  b.spr.30_ b.spr.100_  b.current      s.msy
  2.12e+06   1.53e+06   1.56e+06   1.99e+06   3.20e+05   1.58e+06
  s.virgin     s.f0.1     s.fmax   s.spr.30  s.spr.100    s.f0.1_
  5.04e+06   2.34e+06   1.64e+06   1.68e+06   2.19e+06   1.94e+06
   s.fmax_  s.spr.30_ s.spr.100_  s.current      r.msy   r.virgin
  1.35e+06   1.39e+06   1.81e+06   2.06e+05   1.05e+06   1.13e+06
    r.f0.1     r.fmax   r.spr.30  r.spr.100    r.f0.1_    r.fmax_
  1.26e+06   1.26e+06   1.26e+06   1.26e+06   1.04e+06   1.04e+06
 r.spr.30_ r.spr.100_  r.current      f.msy    f.crash     f.f0.1
  1.04e+06   1.04e+06   8.44e+05   1.15e-01   6.44e-01   8.76e-02
    f.fmax   f.spr.30    f.f0.1_    f.fmax_  f.spr.30_  f.current
  1.35e-01   1.32e-01   8.76e-02   1.35e-01   1.32e-01   3.56e-01
     y.msy     y.f0.1     y.fmax   y.spr.30    y.f0.1_    y.fmax_
  1.43e+05   1.63e+05   1.72e+05   1.72e+05   1.35e+05   1.42e+05
 y.spr.30_ y.spr.100_  y.current          r         rc         rt
  1.42e+05   1.38e+05   9.60e+04   4.42e-01   9.38e-02   3.86e+00
units:
```

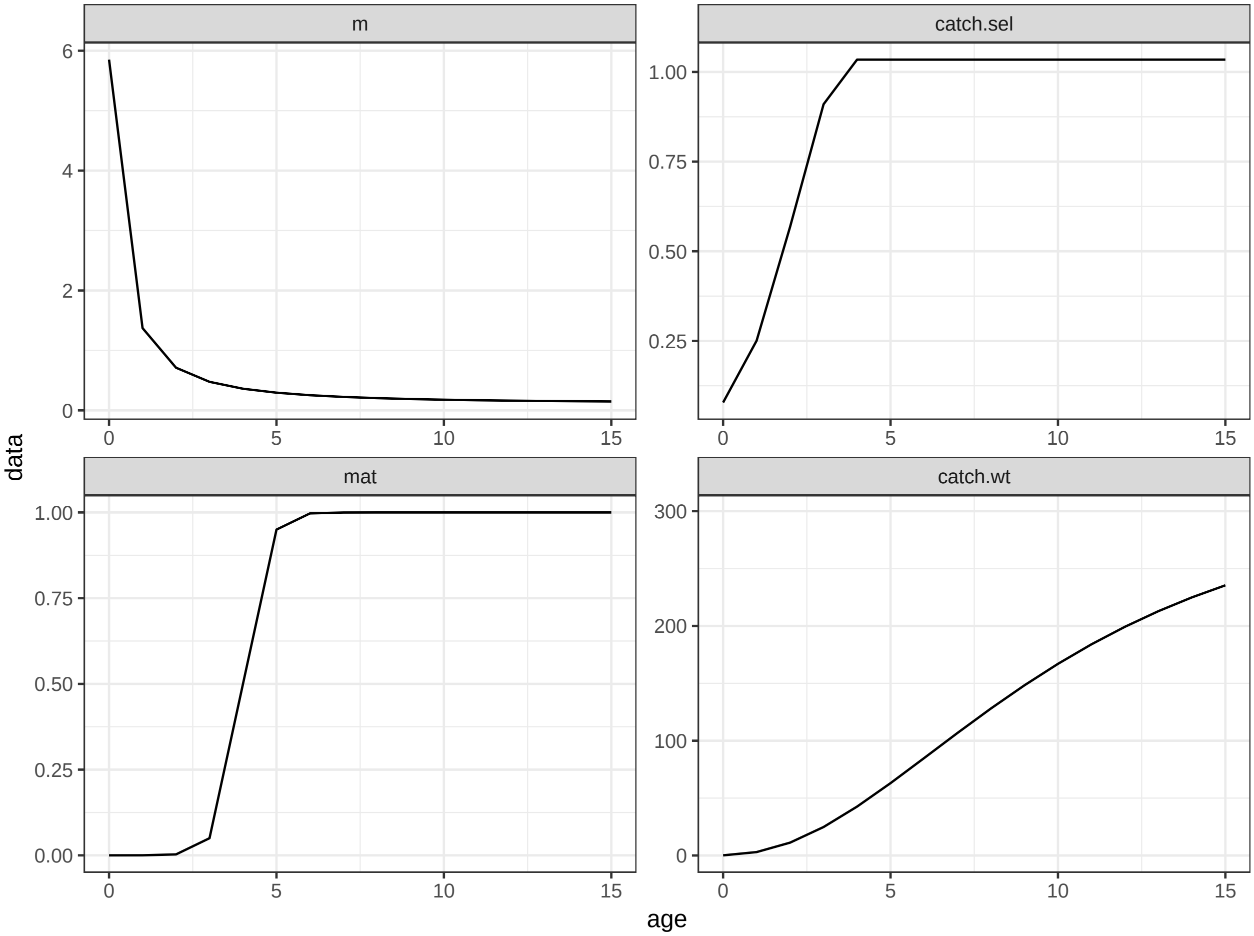


Figure 3: Age-vectors of growthm natural mortality, maturity and selection pattern

Simulation

Simulation of equilibrium values and reference points

```
library(FLBRP)
eql=lhEql(par)

ggplot(FLQuants(eql,"m","catch.sel","mat","catch.wt"))+
  geom_line(aes(age,data))+
  facet_wrap(~qname,scale="free")+
  scale_x_continuous(limits=c(0,15))
```

```
An object of class "FLPar"
params
      r      rc     msy    lopt      sk    spr0   sprmsy
 0.3943  0.1397 53.6441 63.5204  0.1954  0.1208  0.0263
units:  NA NA NA NA NA NA NA
```

Creation of FLBRP objects

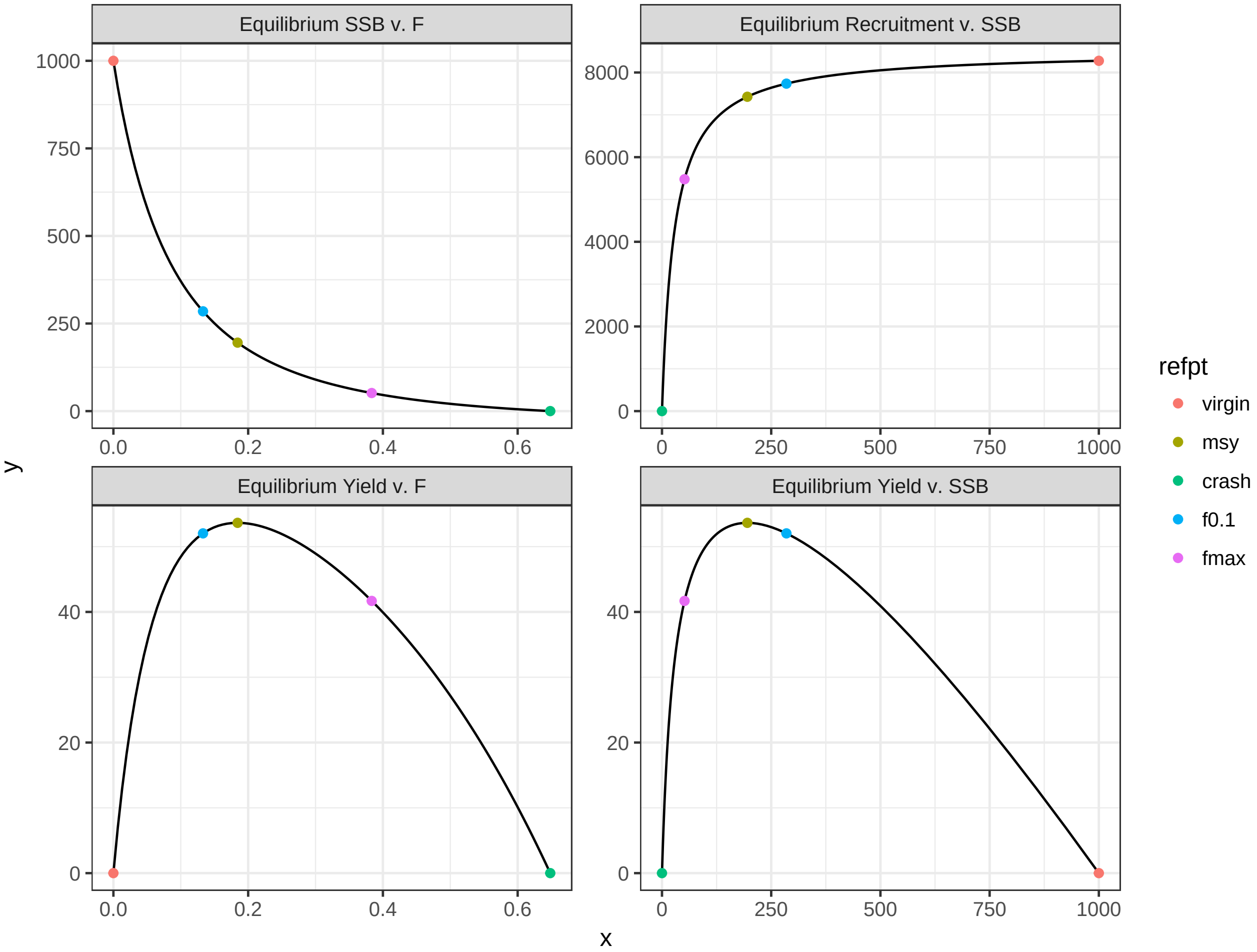


Figure 4: Equilibrium curves and reference points.

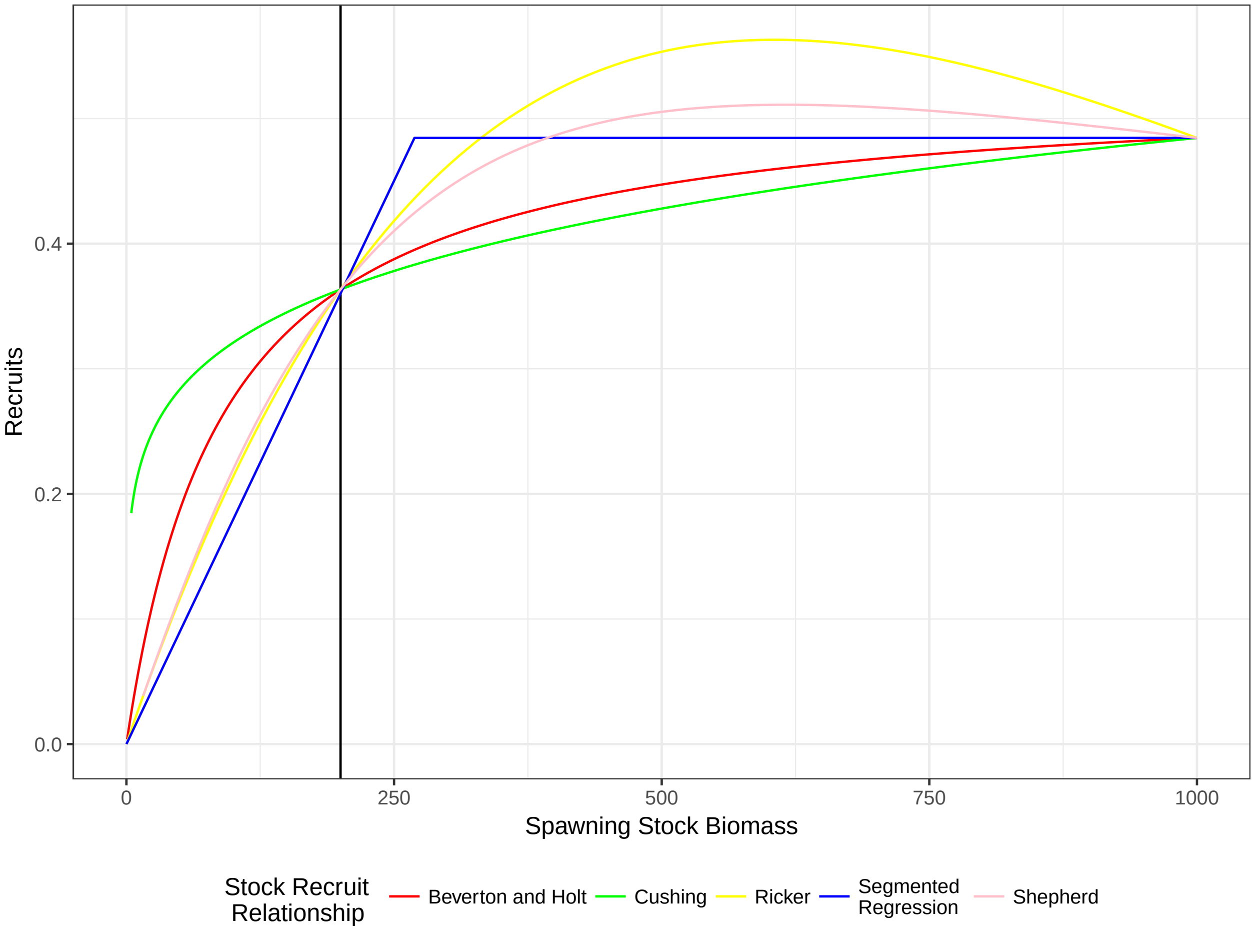


Figure 5: Stock recruitment relationships for a steepness of 0.75 and vigin biomass of 1000

Stock recruitment relationships

Density Dependence

Modelling density dependence in natural mortality and fecundity.

```
library(FLBRP)
library(FLife)

data(teleost)
par=teleost[,"Hucho hucho"]
par=lhPar(par)
hutchen=lhEql(par)

scale=stock.n(hutchen)[,25]%*%stock.wt(hutchen)
scale=(stock.n(hutchen)%*%stock.wt(hutchen)%-%scale)%/%scale

m=mdd(stock.wt(hutchen),par=FLPar(m1=.2,m2=-0.288),scale,k=.5)

ggplot(as.data.frame(m))+
   geom_line(aes(age,data,col=factor(year)))+
```

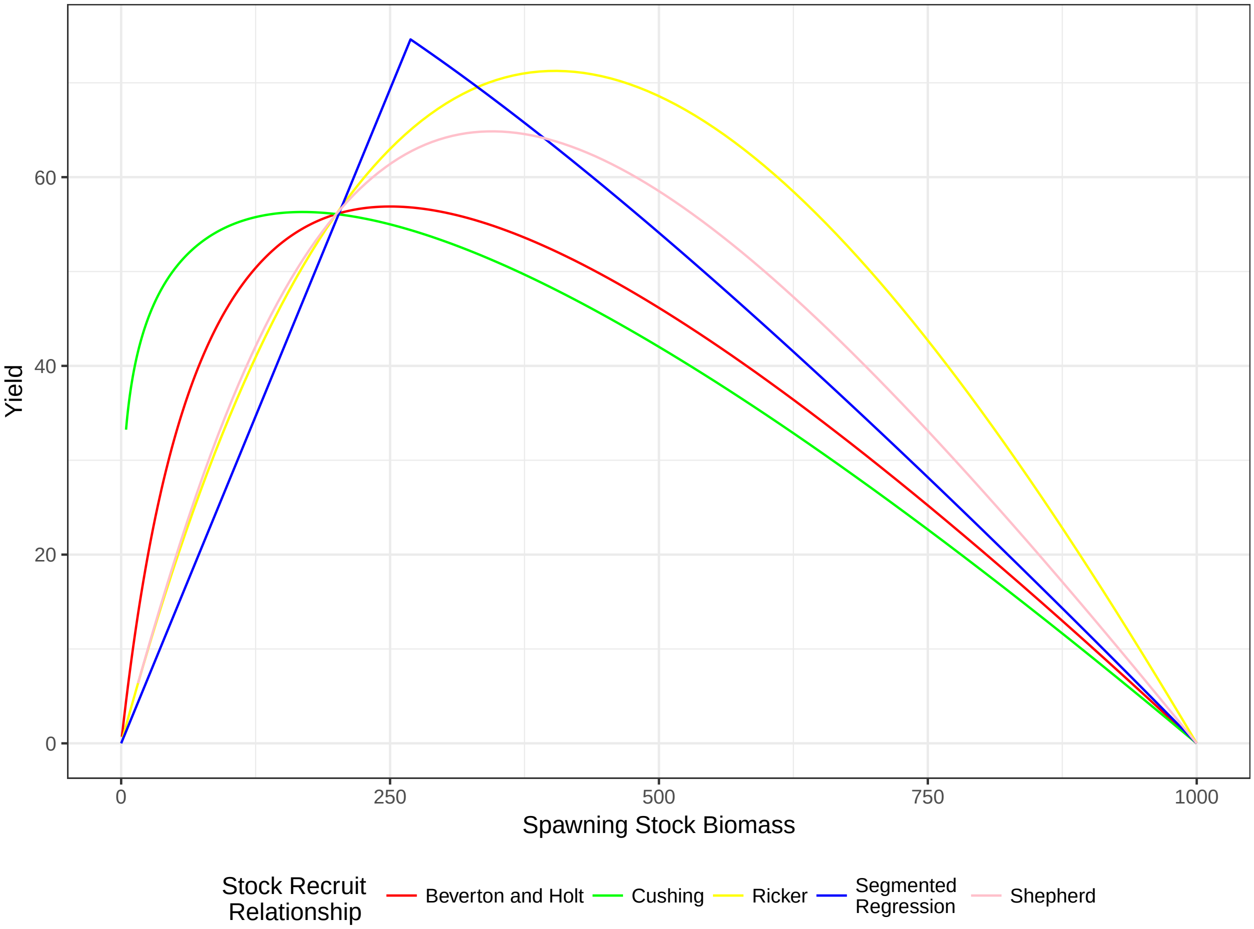


Figure 6: Production curves, Yield v SSB, for a steepness of 0.75 and vigin biomass of 1000.

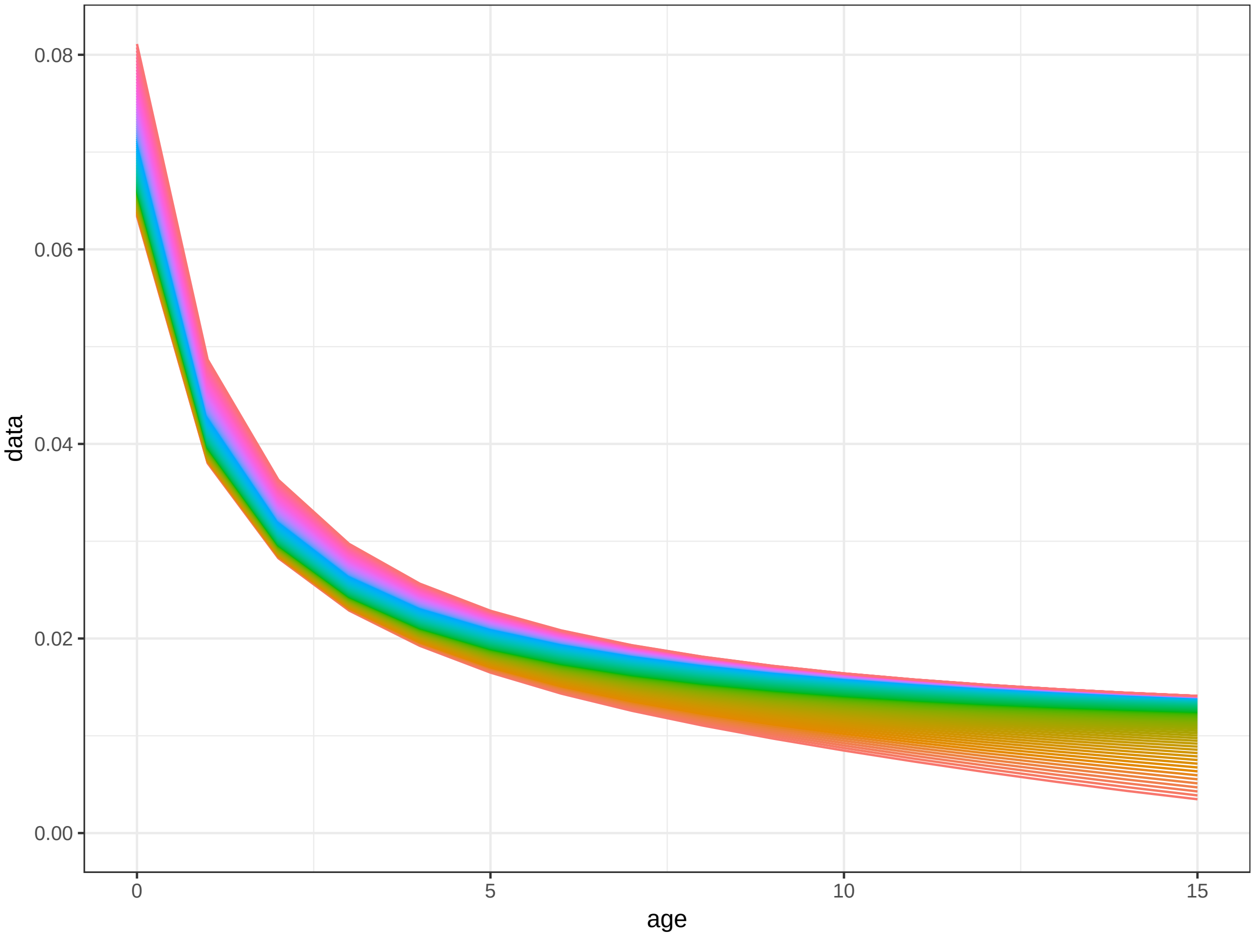


Figure 7: Density Dependence in M

```
   theme(legend.position="none")+
    scale_x_continuous(limits=c(0,15))
```

```
scale=stock.n(hutchen)[,25]%*%stock.wt(hutchen)
scale=(stock.n(hutchen)%*%stock.wt(hutchen)%-%scale)%/%scale

mat=matdd(ages(scale),par,scale,k=.5)

ggplot(as.data.frame(mat))+
    geom_line(aes(age,data,col=factor(year)))+
    theme(legend.position="none")+
    scale_x_continuous(limits=c(0,15))
```

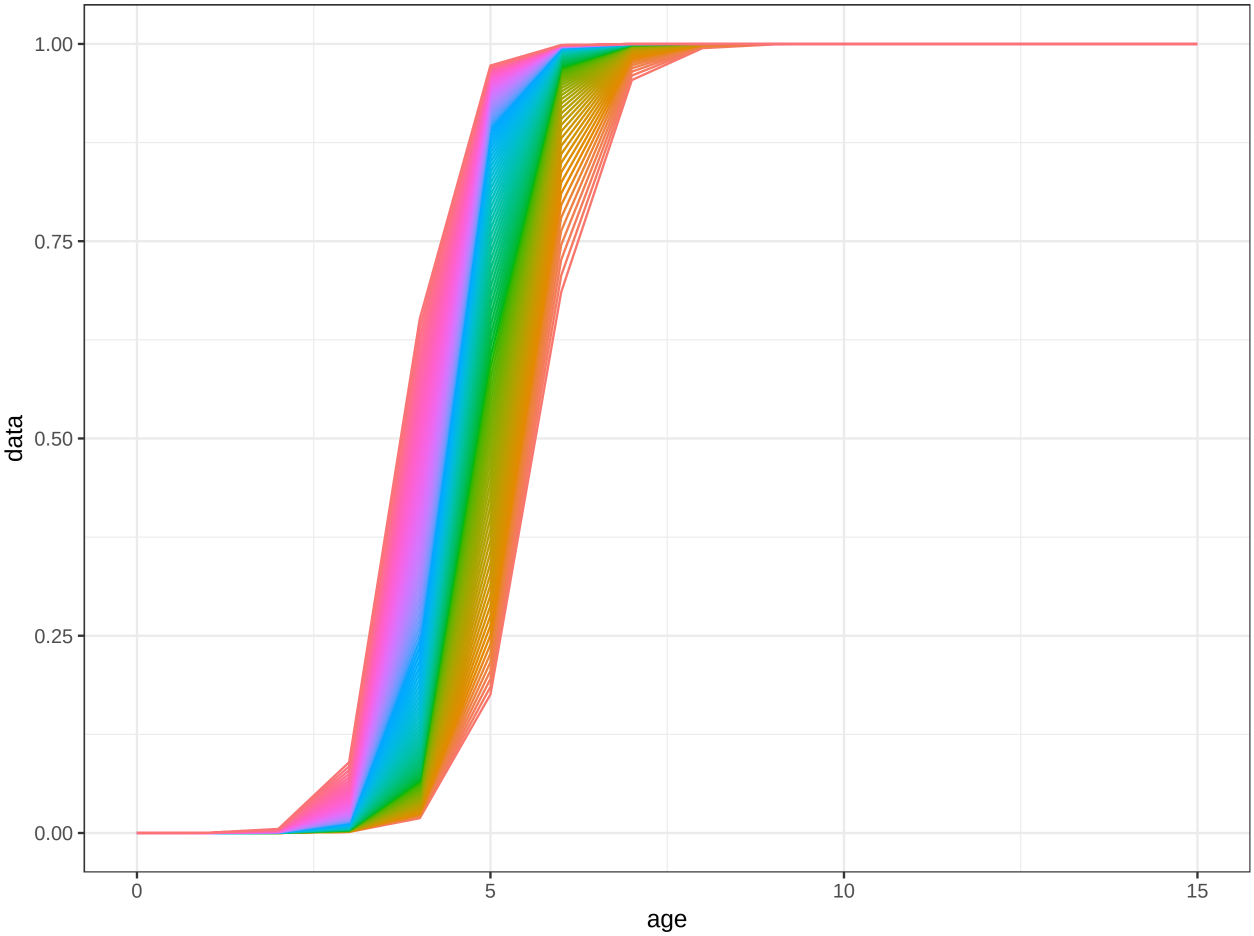
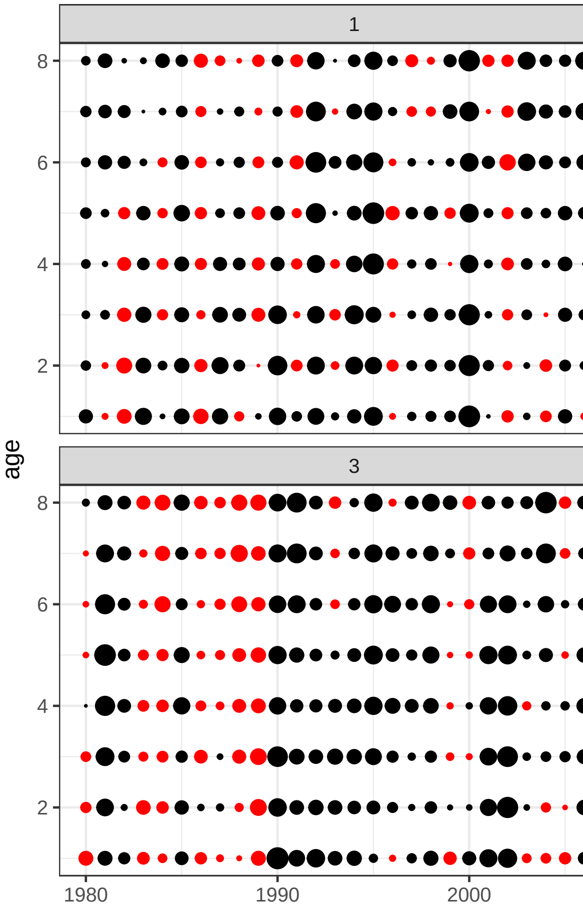
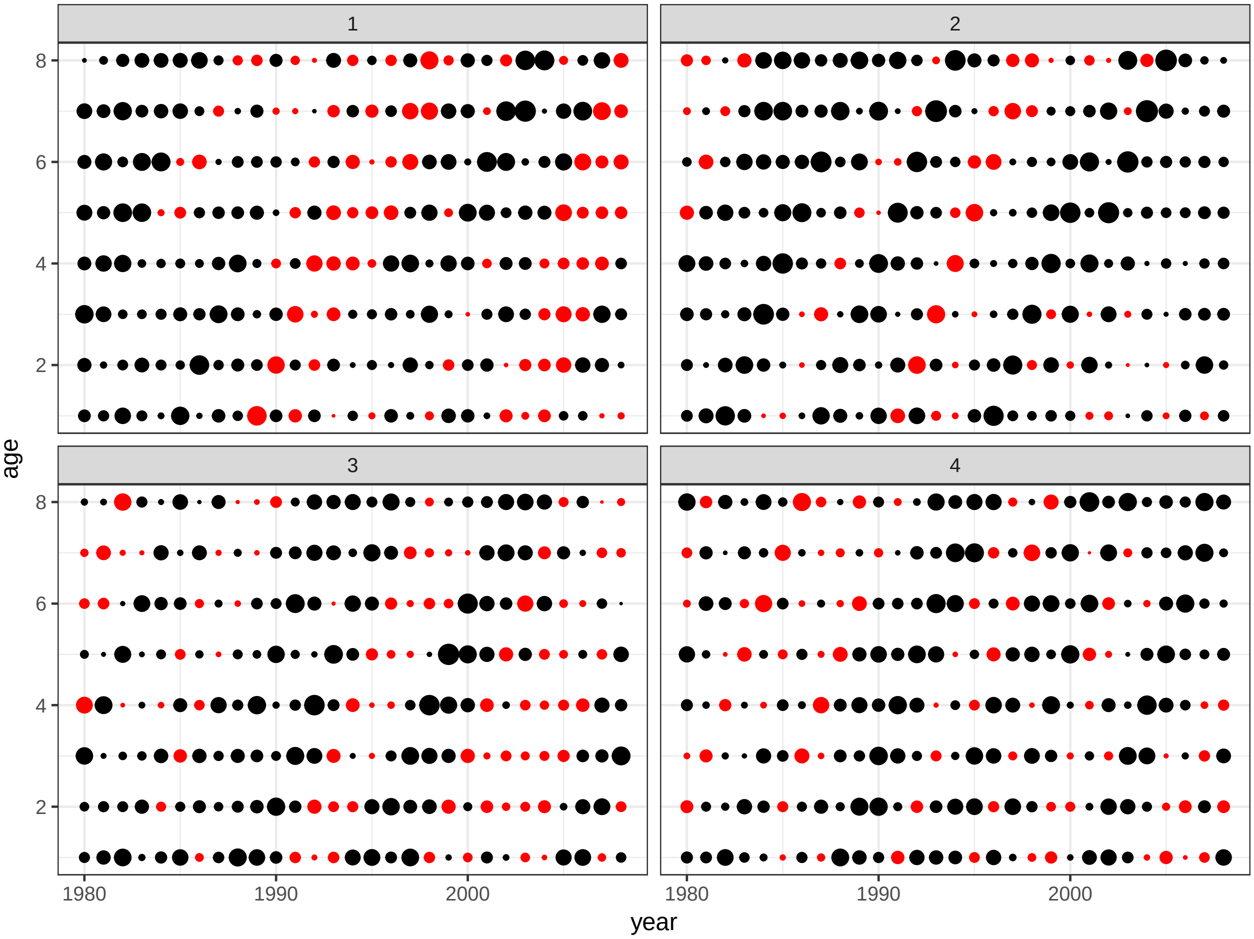


Figure 8: Density Dependence in M

Noise



Methods to simulate random noise with autocorrelation, e.g. by age or cohort



MSE using empirical HCR

Back to Top

Estimation

Life history parameters can also be used to estimate quantities of use in stock assessment

Beverton and Holt (1956) developed a method to estimate life history and population parameters length data. e.g.

$$Z = K\frac{L_\infty - \overline{L}}{\overline{L} - L'} \tag{1}$$

Based on which Powell (1979) developed a method, extended by Wetherall, Polovina, and Ralston (1987), to estimate growth and mortality parameters. This assumes that the right hand tail of a length frequency distribution was determined by the asymptotic length L_∞ and the ratio between Z and the growth rate k.

The Beverton and Holt methods assumes good estimates for K and L_∞, while the Powell-Wetherall method only requires an estimate of K, since L_∞ is estimated by the method as well as Z/K.These method therefore provide estimates for each distribution of Z/K, if K is unknown and Z if K is known.
%As well as assuming that growth follows the von Bertalanffy growth function, it is also assumed that the

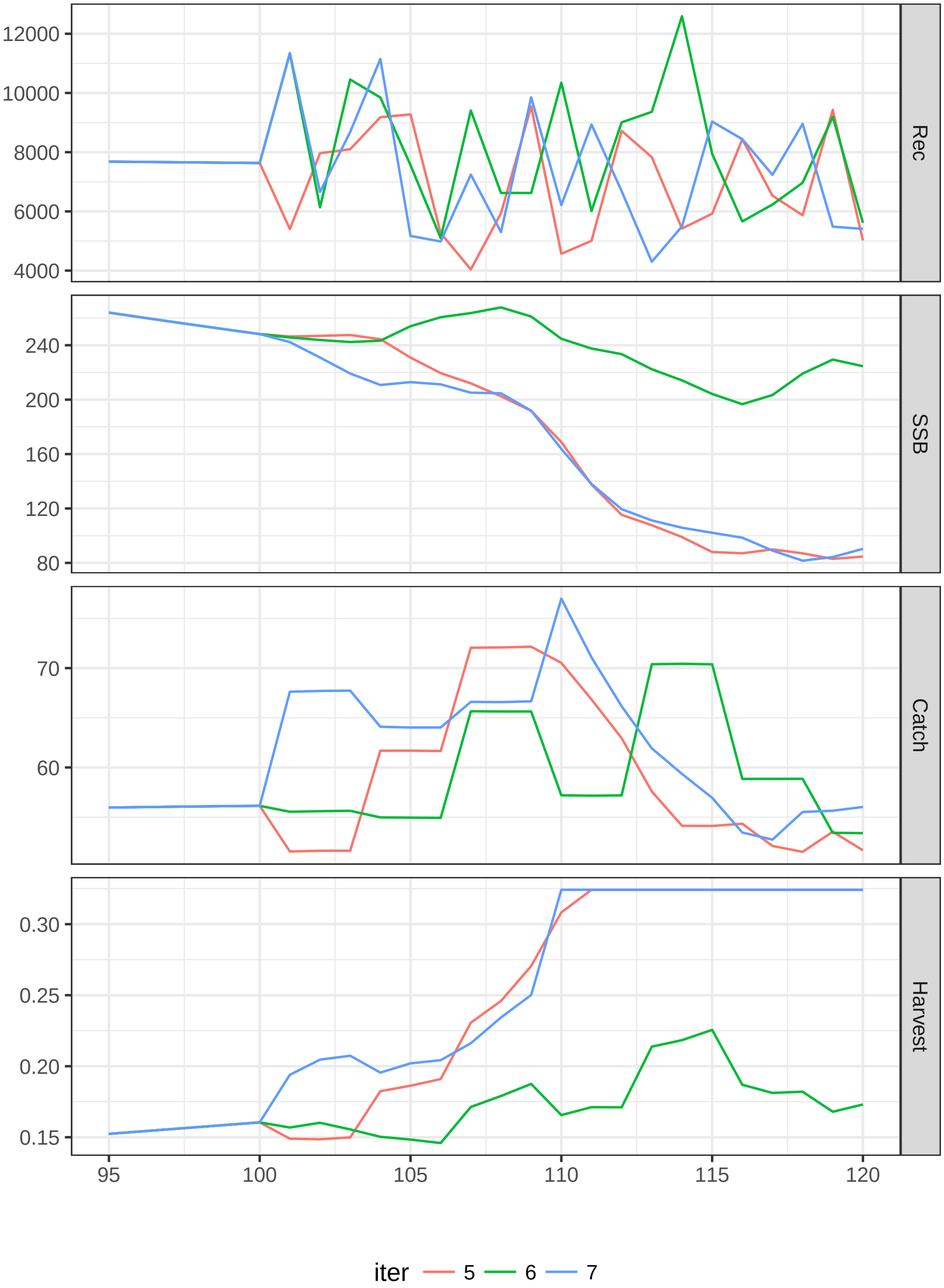


Figure 9: MSE using empirical HCR

population is in a steady state with constant exponential mortality, no changes in selection pattern of the fishery and constant recruitment. In the Powell-Wetherall method L' can take any value between the smallest and largest sizes. Equation 1 then provides a series of estimates of Z and since

$$\overline{L} - L' = a + bL' \tag{2}$$

a and b can be estimated by a regression analysis where

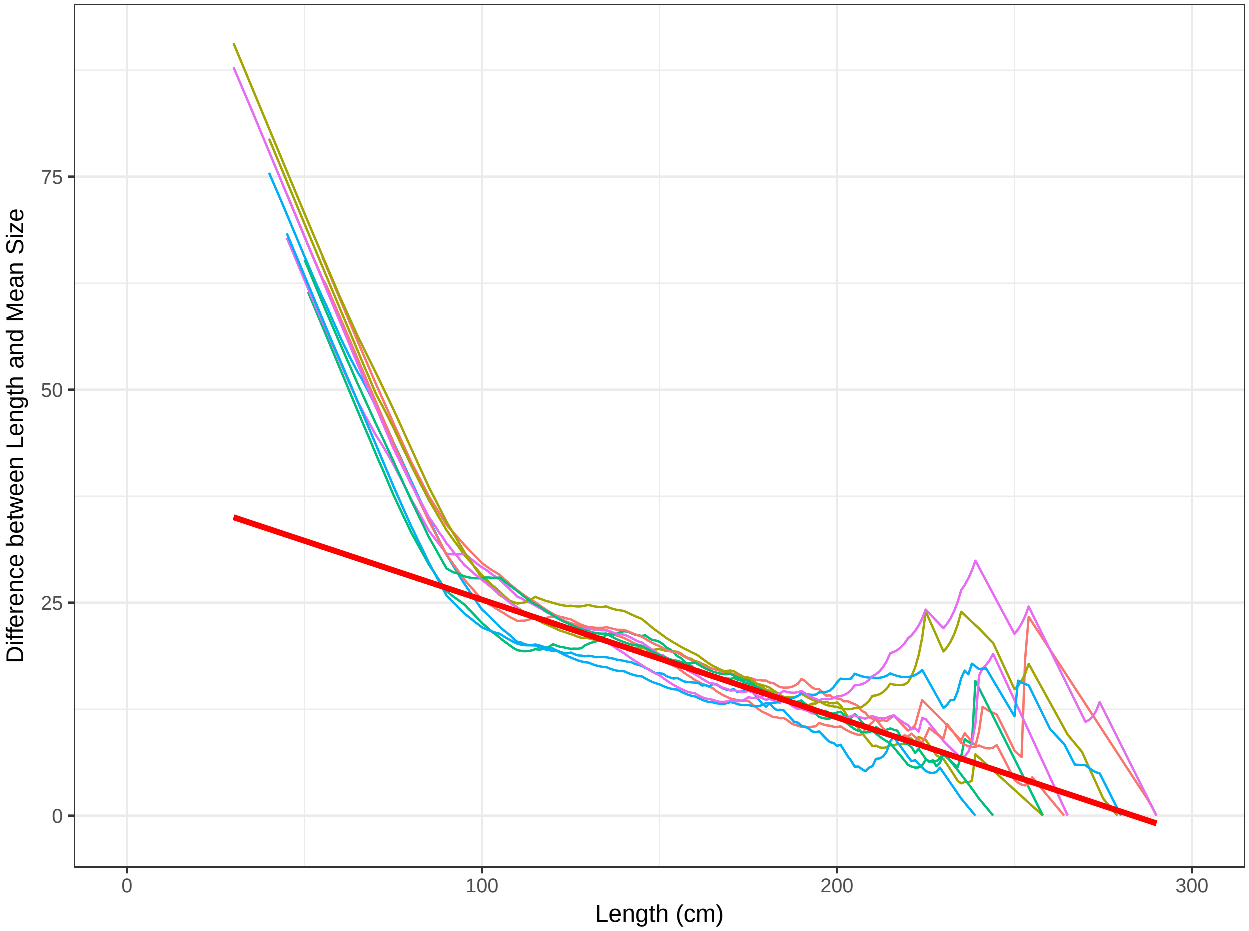
$$b = \frac{-K}{Z+K} \tag{3}$$

$$a = -bL_\infty \tag{4}$$

Therefore plotting $\overline{L} - L'$ against L' therefore provides an estimate of L_∞ and Z/K

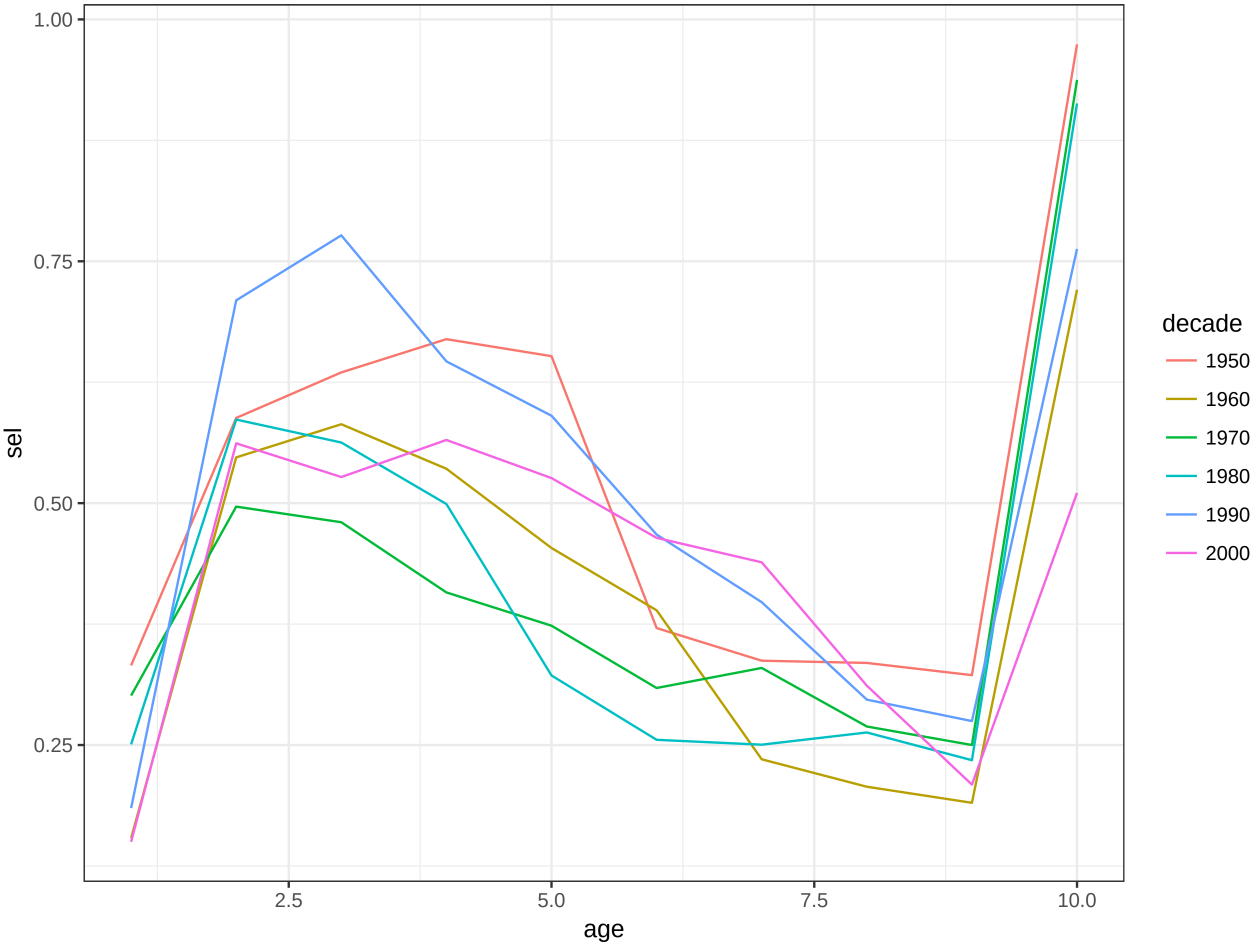
Plotting $\overline{L} - L'$ against L' provides an estimate of L_∞ and Z/k, since $L_\infty = -a/b$ and $Z/k = \frac{-1-b}{b}$. If k is known then it also provides an estimate of Z (**Figure ??**).

```
  age   obs    hat    sel
1   1 32356 249252 0.0136
2   2 49911 152624 0.0342
3   3 69038  93457 0.0773
4   4 45627  57226 0.0834
5   5 32732  35041 0.0977
6   6  8910  21457 0.0434
```



Catch curve analysis

```
data(ple4)
ctc=as.data.frame(catch.n(ple4))
ctc=ddply(ctc,.(year), with, cc(age=age,n=data))
ctc=ddply(transform(ctc,decade=factor(10*(year%/%10))),.(decade,age),with,data.frame(sel=mean(sel)))
ggplot(ctc)+
  geom_line(aes(age,sel,colour=decade))
```



Back to Top

More Information

- You can submit bug reports, questions or suggestions on `FLife` at the `FLife` issue page,[4] or on the *FLR* mailing list.
- Or send a pull request to https://github.com/flr/FLife/
- For more information on the FLR Project for Quantitative Fisheries Science in R, visit the FLR webpage.[5]
- The latest version of `FLife` can always be installed using the `devtools` package, by calling

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[4] https://github.com/flr/FLife/issues

[5] http://flr-project.org

```
library(devtools)
install_github("flr/FLife")
```

Software Versions

- R version 3.4.3 (2017-11-30)
- FLCore: 2.6.5
- FLPKG:
- **Compiled**: Tue Dec 12 16:10:12 2017
- **Git Hash**: bdd94ea

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Acknowledgements

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References

Back to Top

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