An introduction to the model estimation of growth, mortality and gear / fishery selectivity and it's application to mesopelagic fish species

The TropFishR package

Ecologically and Economically Sustainable Mesopelagic Fisheries

Outline of e-learning material

- Background and motivation for a potential fishery targeting species in the mesopelagic layer

- Length-based methods for population dynamic parameters and stock assessment

- Estimation of growth and mortality parameters with the TropFishR model and software package

- Application of TropFishR to estimate life-history parameters of mesopelagic fish species

- Further steps: estimation of stock status with TropFishR

The H2020 MEESO project

Aim: filling in major knowledge gaps on mesopelagic organisms and at evaluating whether they can be exploited in an ecologically and economically sustainable way.

- New acoustic and trawling research survey technologies
- Development of new fishing and processing technologies
- Mapping of contaminant and nutrient content
- New tools for assessment of species and fisheries management
- Governance: trade-offs between exploitation and changes in ecosystem service values

TropFishR
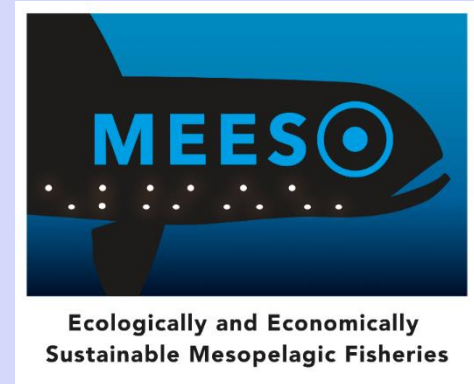
The mesopelagic zone

200-1000 m water depth layer

Mixed species:
- – Crustaceans
- – Cephalopods
- – Fish

Fish biomass estimates are high and variable:

~ 1 to 10 billion tonnes (e.g. Irigoien et al., 2014)

The mesopelagic zone & ecosystem services

Extensive diel vertical migrations
- Day: Hide from predators in deeper layers
- Night: Feed in epipelagic surface layers

- **Carbon transport** to deep ocean from atmosphere and surface layers
  - 2 - 6 billion metric tonnes annually

- **Resource** (prey) for higher trophic levels
  - E.g. marine mammals, tuna
  - More locally: e.g. blue whiting, saithe
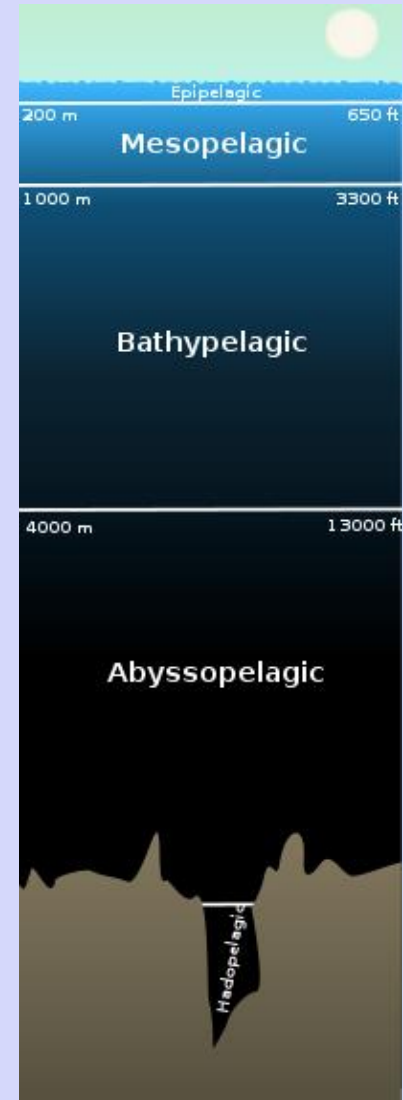
A mesopelagic fishery?

- Increasing demand for food

- FAO (2017):
  - Approx. 66% of exploited fish and shellfish stocks fished sustainably
  - Approx. 34% fished above biological sustainable limits

- Industrial fishery
  - Fish meal
  - Fish oil
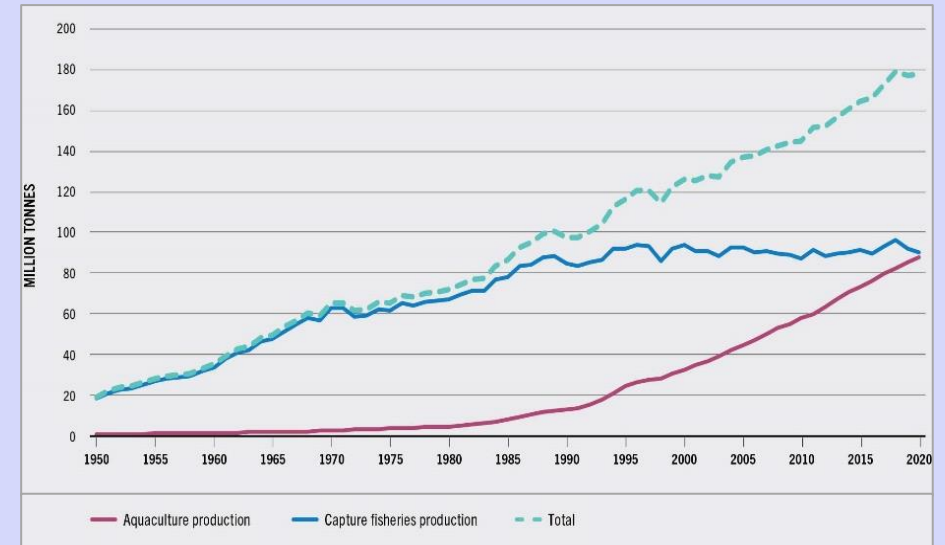
Source: FAO (2022)
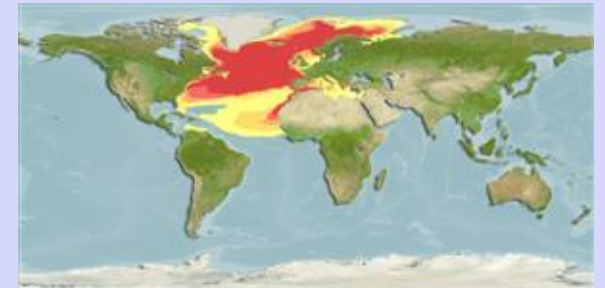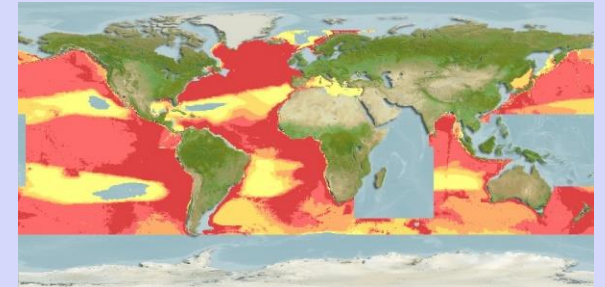
The selected case study species

*Maurolicus muelleri (*Mueller's pearlside)

- Max 3 years
- Max 7 cm
- Maturation after 1 year
- Global oceans (mainly temperate Atlantic and Pacific waters)

*Benthosema glaciale (*Glacier lantern fish)

- Max 8 years
- Max 10.3 cm
- Maturation after 2-3 years
- Atlantic Ocean

Source: Fishbase

The mesopelagic case study

Aim: Estimate robust individual growth and mortality parameters

– First step toward sustainable harvesting

– Required in stock assessments, estimation of reference points according to Maximum Sustainable Yield (MSY) and as input for other models

– Currently only limited estimates related to growth and mortality available

• Analysis of seasonal and regional differences and differences in fishery / gear selectivity to identify:

– **Sources of variability** in life-history characteristics that might influence stock assessments

– **Spatio-temporal variability**, possibly suggesting different stock units

The mesopelagic case study

Spatio-temporal variability in life history estimates of *Maurolicus muelleri* and *Benthosema glaciale* in the North Atlantic.

– Estimate **growth parameters and mortality rates and their uncertainties** for *Benthosema glaciale* and *Maurolicus muelleri* in the North Atlantic ocean.

– Identify **spatio-temporal variability** in population dynamic parameters taking into account (i) horizontal distribution patterns and (ii) temporal variability according to year and season.

– Evaluate and discuss the **management implications** considering (i) identification of the potential to manage each of the two species as a single stock and (ii) optimize sampling design and future perspectives.

Length-based methods for population dynamic parameters and stock assessment of data-limited stocks

Length-based methods allow to take into account the full variability of sizes at different times and places and from different gears

- Length-frequency data is easy to collect
  - On board of survey vessels, fishing vessels, landing sites or fish markets
  - Measurements can be made with reasonable precision.
- Fish lengths are directly related to vital rates, sexual maturity and fisheries / gear selectivity
- Age data is often constrained by interpretation
- Catch and effort data is constrained by operational limits of the commercial fishery

In the case of an unexploited situation (such as for mesopelagic species) there are challenges in relation to the use of common assessment methods and models:

- *Age-based methods*
  Age readings and / or time series are not available
- *No production models*
  Unexploited situation: no previous catches and/or landings i.e. no adequate catch time series
- *Acoustic surveys*
  Difficulties to distinguish between trophic levels and species (and stocks)

TropFishR Package

Mildenberger, T.K., Taylor, M.H., Wolff, M. (2017). TropFishR: an R package for fisheries analysis with length-frequency data. Methods in Ecology and Evolution, 8, pp.1520-1527

- TropFishR: R package compiling single-species stock assessment methods designed for data-limited fish / shellfish stock and fisheries analysis using length-frequency data for fish and shellfish

- Name derives also from the framework and model given by the FAO Manual on Tropical Fish stock Assessment (Sparre and Venema, 1988,1989) referring back to the ELEFAN Model (Pauly, 1981)

Installing TropFishR Software package

CRAN:

```
install.packages("TropFishR", repos = "https://cran.rstudio.com/")
```

GitHub:

```
install.packages("remotes")
remotes::install_github("tokami/TropFishR")
```

Length-based stock assessments with TropFishR

Includes methods for estimating:

– Estimating biological population dynamic parameters such as individual growth rate and mortality,

– Fishery related parameters such as exploitation rate and gear / fishery selectivity,

– Assessing stock size and status
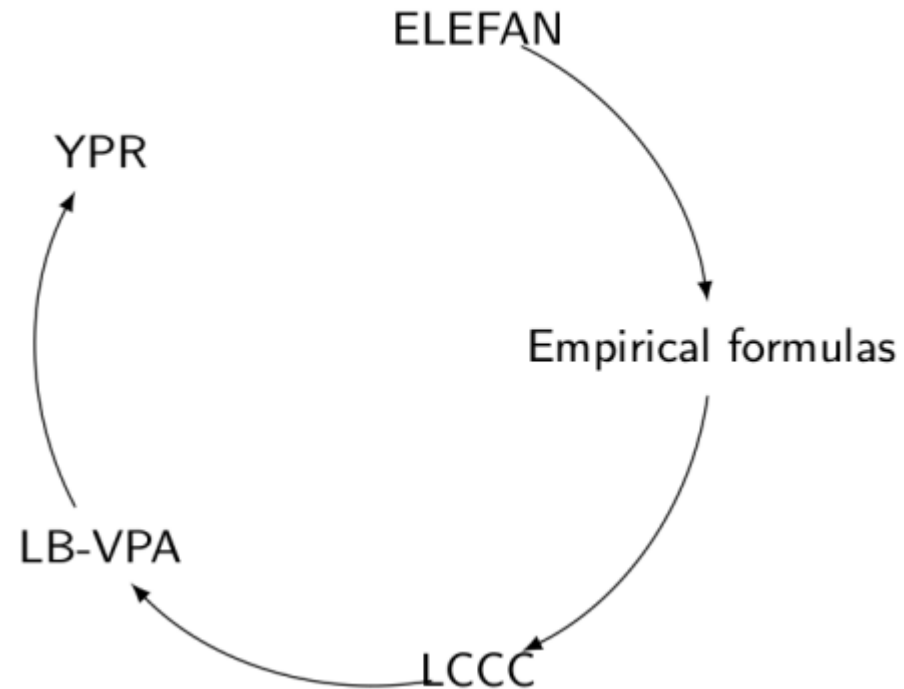
Individual Growth

Von Bertalanffy growth function, VBGF (Bertalanffy, 1938):
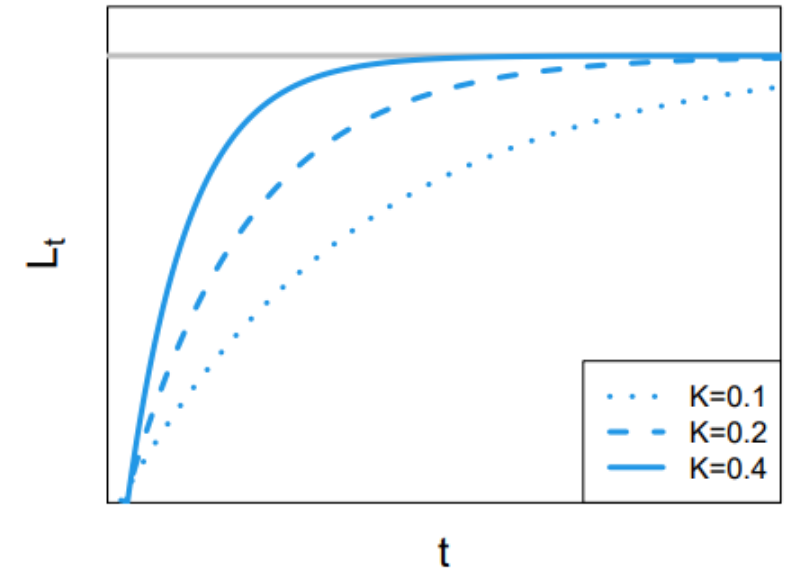
$$\frac{dL}{dt} = k(L_\infty - L)$$

With solution:

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

L : Length of an individual fish

K : Somatic growth rate

L_∞: The asymptotic length

t_0 : hypothetical age at length zero

Electronic Length Frequency Analysis (ELEFAN)

- Allows to estimate the growth of fish by following the increasing mean lengths of cohorts over time
- Assumes that peaks correspond to mean length of cohorts (year classes)
- Requires length measurements collected ideally throughout the year

ELEFAN consists of two steps:
  – Data restructuring to identify modes
  – Fitting of growth curves
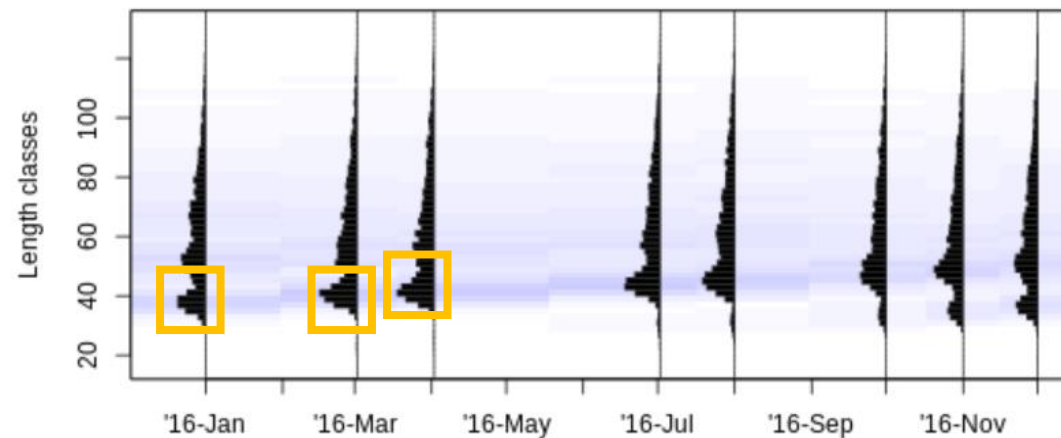
Data restructuring

Aim: Transform length frequency data to better identify potential cohorts (year classes)

1. Aggregate length measurements into length classes by choosing an appropriate bin size (as small as possible but still reducing noise)

2. Aggregate and sort data by some time unit (e.g. month, quarter or year)

3. Restructure length data

– Choose an appropriate Moving Average (MA; rule of thumb: equal to number of adjacent bins of the youngest cohorts)
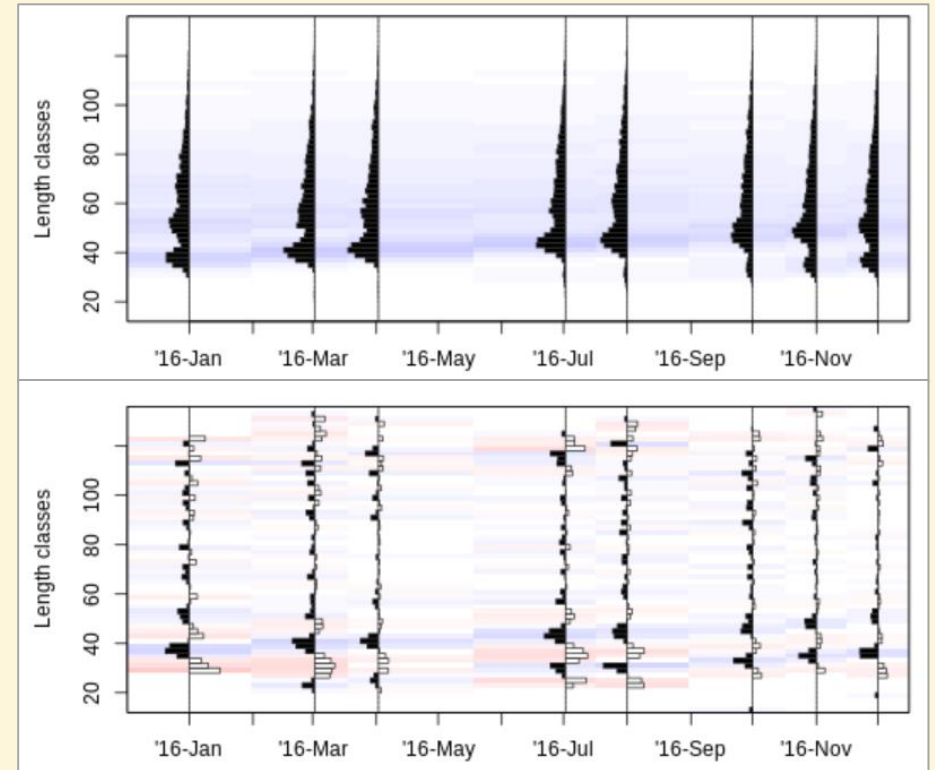
– Divide frequency in each length class by MA

Restructuring of data

```r
## adjust bin size
lfq_bin2 <- lfqModify(lfq, bin_size = 2)

## plot raw and restructured LFQ data
ma <- 7
lfq_bin2_res <- lfqRestructure(lfq_bin2, MA = 7, addl.sqrt = FALSE)

opar <- par(mfrow = c(2,1), mar = c(2,5,2,3), oma = c(2,0,0,0))
plot(lfq_bin2_res, Fname = "catch", date.axis = "modern")
plot(lfq_bin2_res, Fname = "rcounts", date.axis = "modern")
par(opar)
```
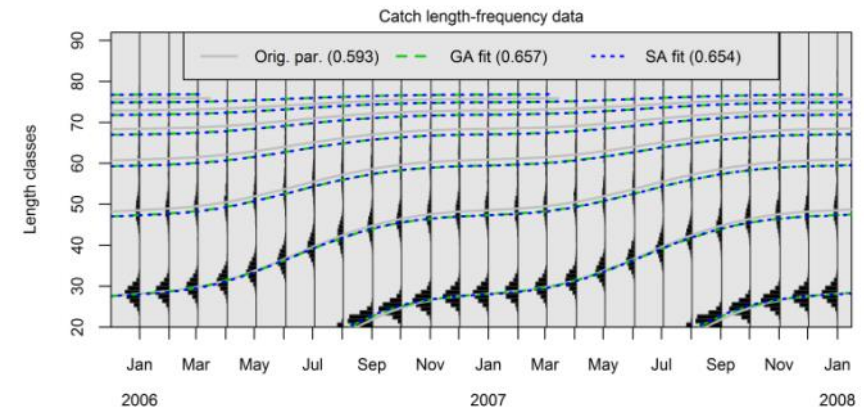
Estimation of growth

- Different growth curves are fitted through the score matrix
- Each set is scored by the number of peaks that are passed through by the curve
- The best fitting set is judged according to the explained sum of peaks (ESP) compared to the available sum of peaks (ASP)

- Maximize according to the value $R_n = \dfrac{10^{\frac{ESP}{ASP}}}{10}$

Catch length-frequency data

Different methods available in TropFishR, we here focus on ELEFAN with a genetic algorithm (ELEFAN_GA)

– Stochastic search algorithm inspired by the basic principles of biological evolution and natural selection

– Parameter combinations of individuals with higher score values are passed on to the next generation (iteration)
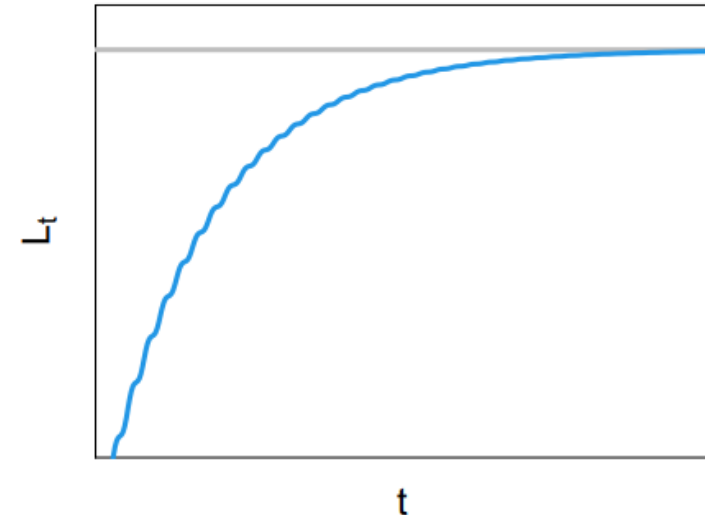
Estimation of growth

With ELEFAN_GA it is also possible to account for seasonal variation in growth using a seasonalised VBGF:

$$L_t = L_\infty(1 - e^{-K(t-t_0)+S(t)-S(t_0)} \text{ with } S(t) = \frac{CK}{2\pi}\sin(2\pi(t - t_s))$$

C : Constant indicating the amplitude of the oscillation

t_s : Fraction of the year where the sine wave begins

Estimation of growth

```
## run ELEFAN with genetic algorithm
res_GA <- ELEFAN_GA(lfq_bin2, MA = ma, seasonalised = TRUE,
                    maxiter = 50, addl.sqrt = FALSE,
                    low_par = low_par,
                    up_par = up_par,
                    monitor = FALSE)

## show results
res_GA$par
res_GA$Rn_max
```
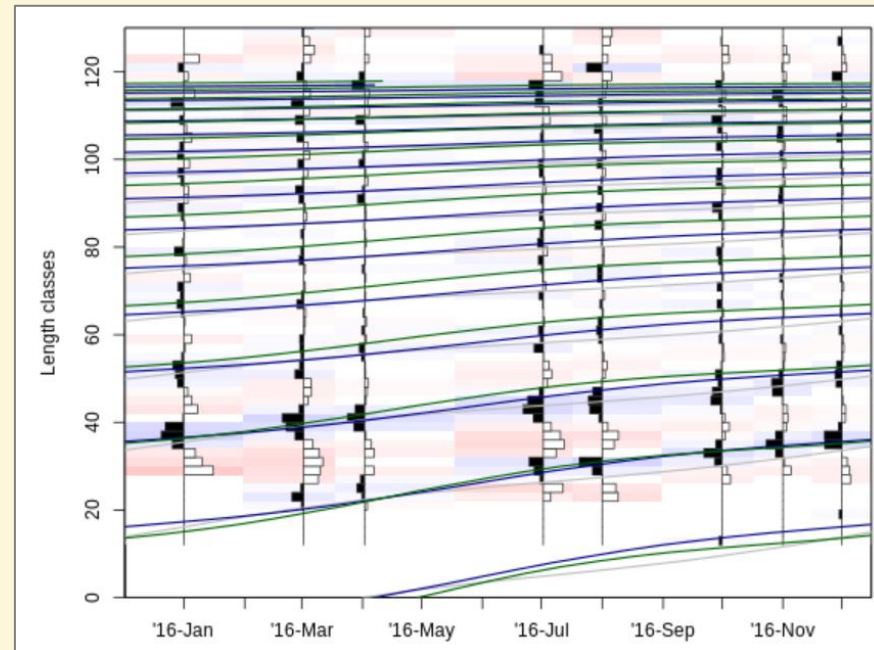
```
## coarse estimate of Linf
linf_guess <- max(lfq_bin2$midLengths) / 0.95

## lower search space bounds
low_par <- list(Linf = 0.8 * linf_guess,
                K = 0.01,
                t_anchor = 0,
                C = 0,
                ts = 0)

## upper search space bounds
up_par <- list(Linf = 1.2 * linf_guess,
               K = 1,
               t_anchor = 1,
               C = 1,
               ts = 1)
```

ELEFAN checklist

1. Find best bin size: amplify signal and reduce noise

2. Test different combinations of bin size and MA as a sensitivity analysis

3. Double check the settings of the genetic algorithm

4. Provide visual fit of the results

Estimation of natural mortality, M

- Caused by:
  - Starvation
  - Illness, parasites
  - Predation
  - Post-spawning mortality
  - Abiotic stressors

$$N_t = N_0 e^{-Mt}$$

- Estimated using empirical formulas (there are many)
  - Relying on life history parameters and/or environmental information
  - Example: equation based upon a meta-analysis of 201 fish species (Then et al., 2015) using the VBGF parameters L_∞ and K as input
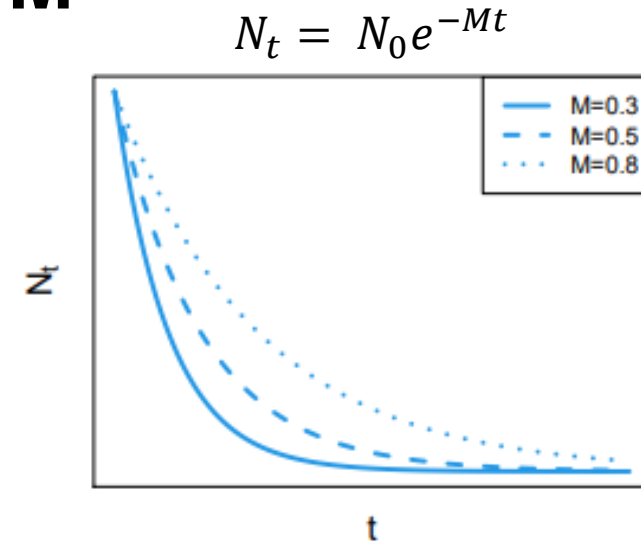
Estimation of natural mortality

```
## estimation of M
Ms <- M_empirical(Linf = lfq_bin2$par$Linf, K_l = lfq_bin2$par$K, method = "Then_growth")

## assign M to data set
lfq_bin2$par$M <- as.numeric(Ms)
```
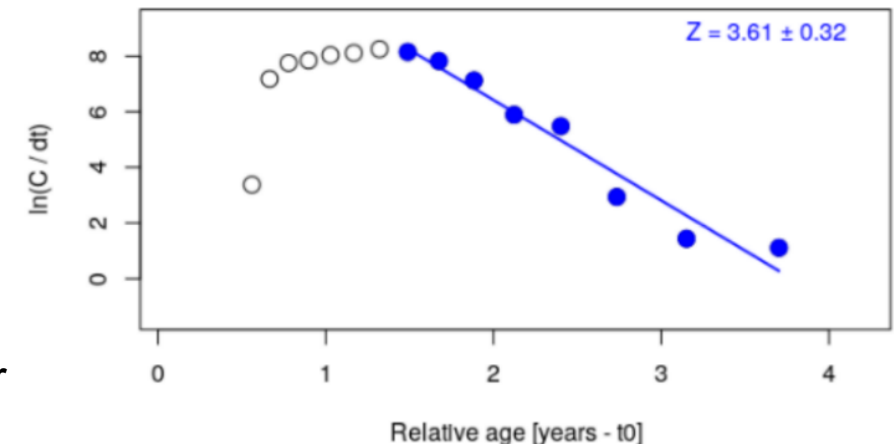
Estimation of total mortality, Z, and gear/fishery selectivity

Total mortality, Z, as the sum of natural and fishing mortality, (M + F), is estimated using the length-converted catch curve

- Length composition of a population says something about the mortality rate in a population, but the mortality signal is confounded with information about growth parameters and fishery / gear selectivity

- Input:
  – Length-frequency data by year
  – Growth parameters (L_∞, K, t_anchor)

- Assumes steady-state, with mortality and recruitment having been constant for a period prior to the time of observation

Approach:

- The natural logarithm of the numbers in each length-group are plotted against the relative age

- Correct the number of fish by dividing the time to grow through the length class

- Result should be a linear descending right-hand side, with slope Z

Z = 3.61 ± 0.32

ln(C / dt)

Relative age [years - t0]

Estimation of total mortality, Z, and gear / fishery selectivity

Selectivity is estimated based on a backwards extrapolation of the length-converted catch-curve

- Estimate of selectivity is given by the ratio between the observed frequency and that of the back-interpolation
- Important not to extrapolate too far beyond the range of good observations (three or four size groups smaller than the peak in the length-frequency)

Here a logistic selection ogive is assumed, typical for trawl-net selectivity
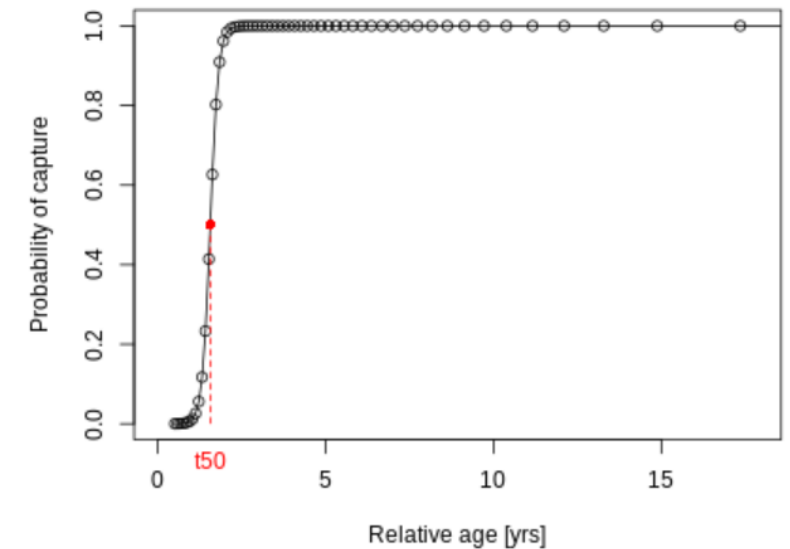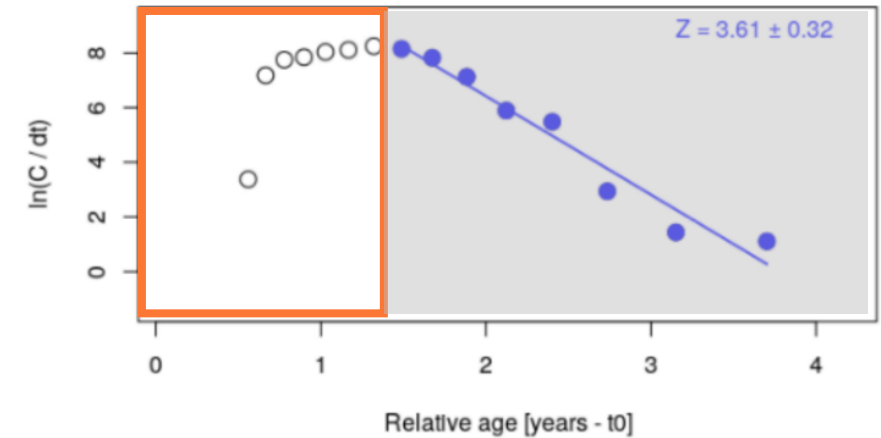
Estimation of total mortality, Z, and gear / fishery selectivity

```
## define plus group as largest length class smaller than Linf
plus_group <- lfq_bin2$midLengths[max(which(lfq_bin2$midLengths < lfq_bin2$par$Linf))]

## summarise catch matrix into vector and add plus group
lfq_catch_vec <- lfqModify(lfq_bin2, vectorise_catch = TRUE, plus_group = plus_group)
```

```
## run catch curve
res_cc <- catchCurve(lfq_catch_vec, reg_int = c(18,55), calc_ogive = TRUE)

## assign estimates to the data list
lfq_catch_vec$par$Z <- res_cc$Z
lfq_catch_vec$par$FM <- as.numeric(lfq_catch_vec$par$Z - lfq_catch_vec$par$M)
```

Parameter uncertainty

- Non-parametric bootstrapping
  - 500 random sub-samples of the Length Frequency (LFQ) data with replacement
  - Estimation of Maximum Density Estimate (MDE) and confidence intervals

- Available in TropFishR version 1.6
  - Can be downloaded trough **install_github("tokami/TropFishR", ref = "nojags")**
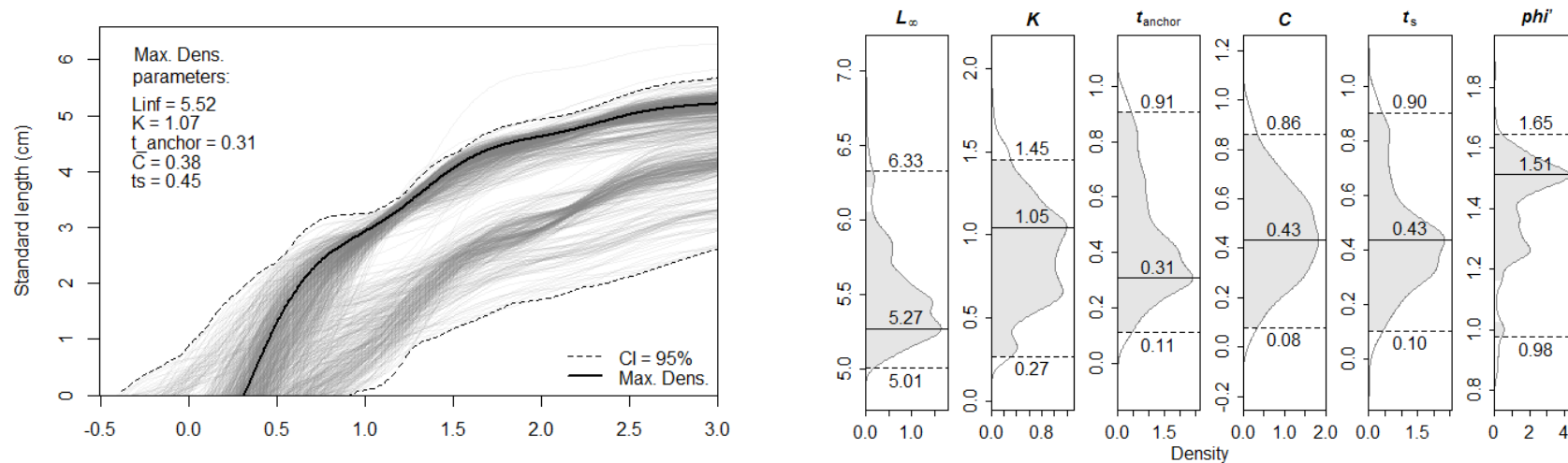
Data availability

Length-frequency data from:

- Norway (Surveys 2008-2020) – *Maurolicus muelleri and Benthosema glaciale*
- Iceland (2009-2011/2020)
  - Survey – *Maurolicus muelleri and Benthosema glaciale*
  - Commercial trial fishery – *Maurolicus muelleri*
- Spain (Surveys 2013-2020) – *Maurolicus muelleri*

Analyses by sea region:

- Different gear and mesh sizes
- Different sampling frequencies

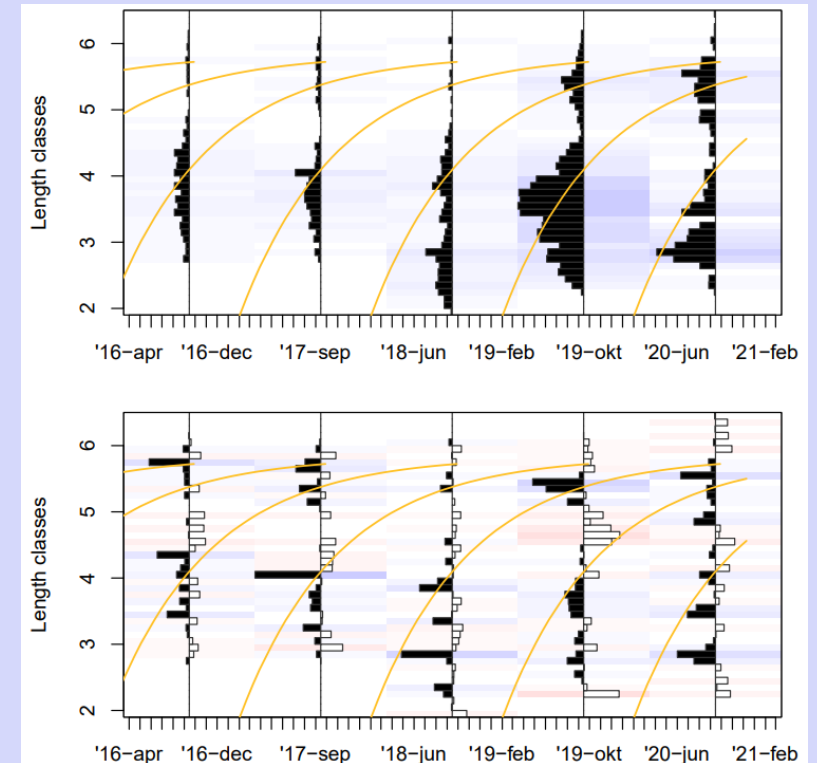*Maurolicus muelleri*
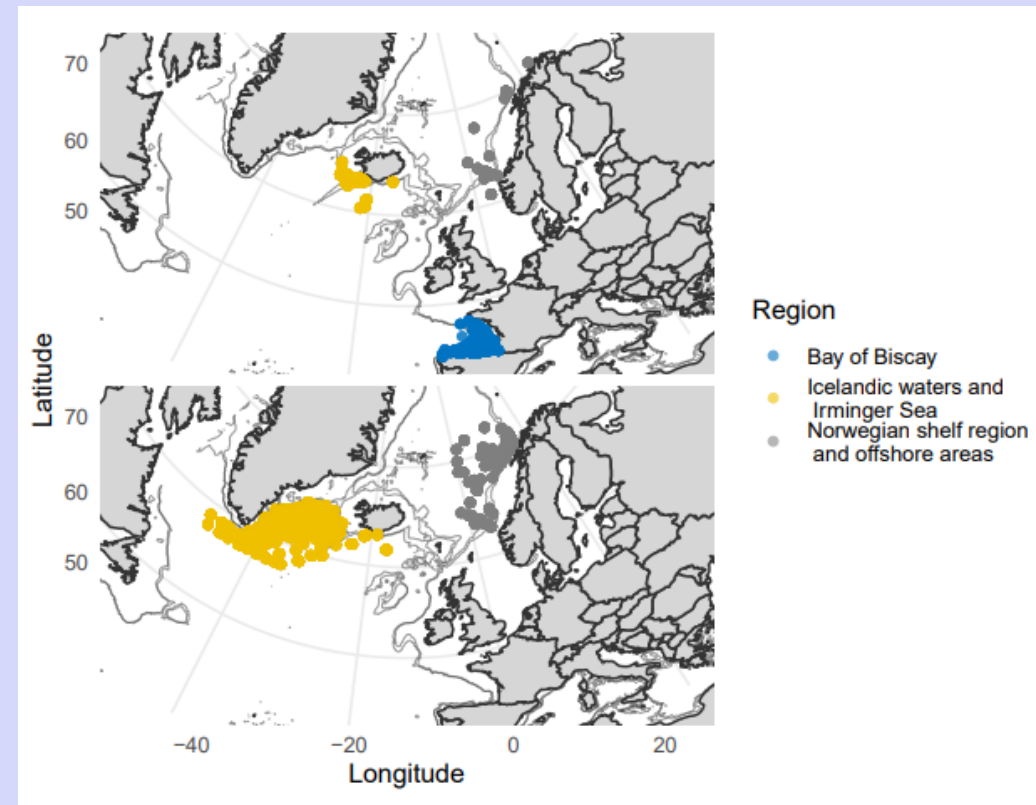
Benthosema glaciale

Data standardization

Data standardization

- Conversion of some samples from total length (TL) into standard length (SL)

- Raising of the numbers to the entire catch, if subsamples were measured

- Removal of outliers

Example: *Maurolicus muelleri* in the Bay of Biscay (September, 2016 – 2020)

Restructuring sensitivity

- Sensitivity analyses for each combination of bin and MA to assess differences

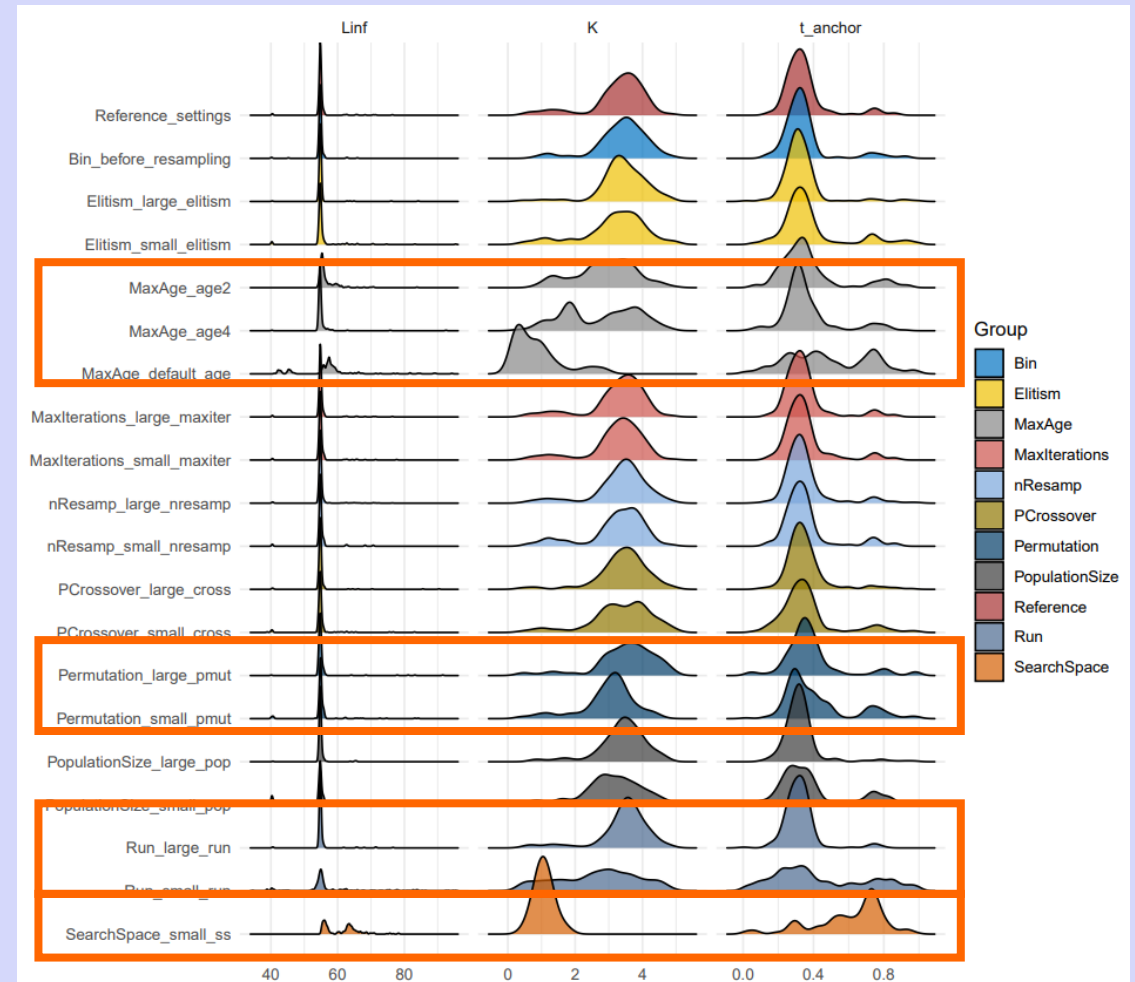- Example: *Maurolicus muelleri* in the Bay of Biscay
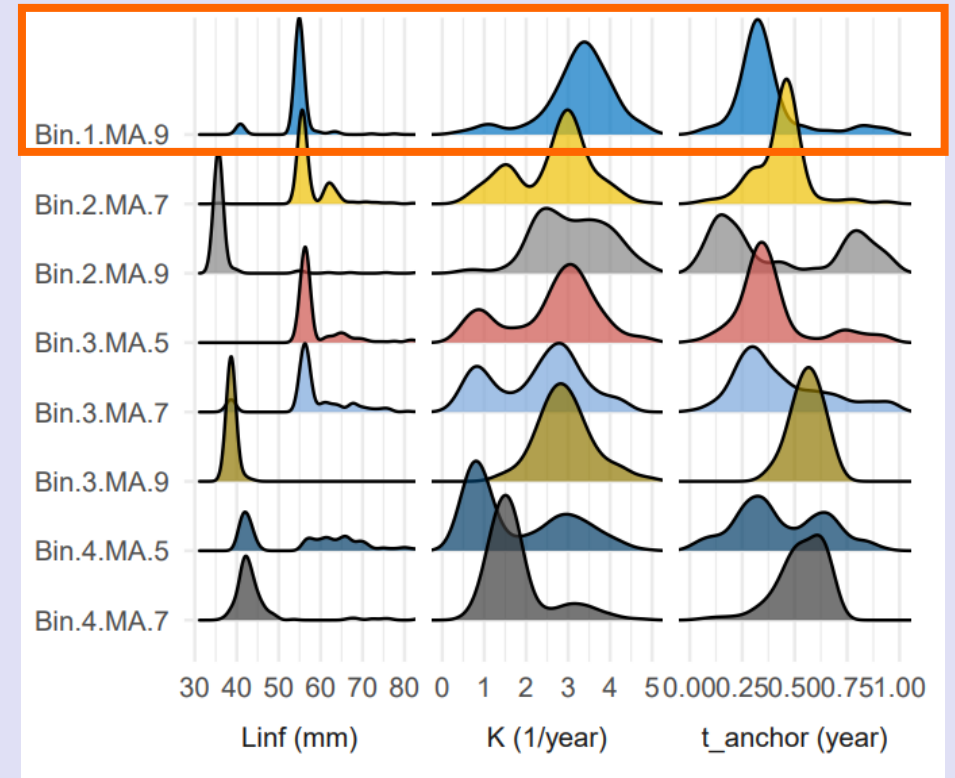
Sensitivity analyses regarding model settings

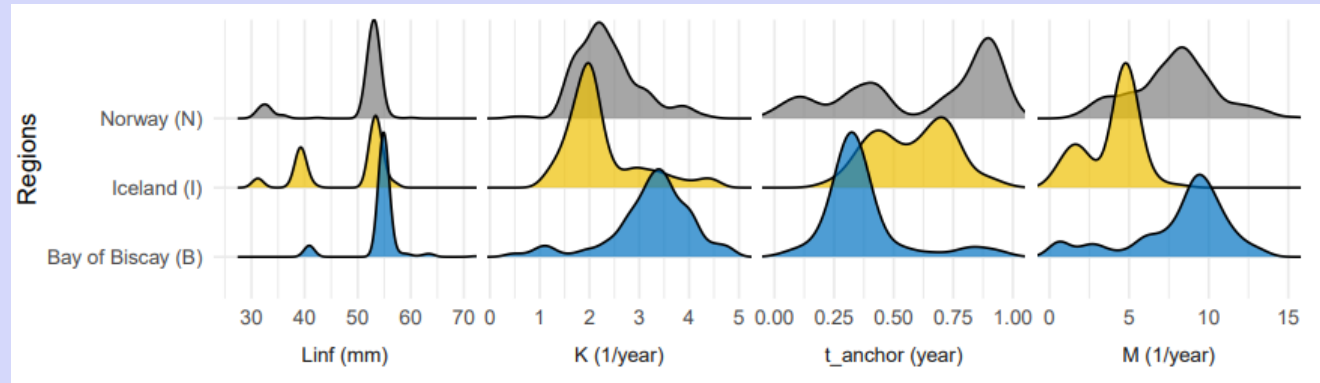Example: *Maurolicus muelleri*

Influential parameters:

- – Bootstrapping search space
- – Maximum age (number of peaks fitted)
- – Runtime
- – Number of permutations

Regional differences in estimates of growth and mortality parameters

ELEFAN_GA: Linf, K and t_anchor

Catch curve: Z = M in this case

Maximum density estimates (MDE) and the uncertainty range, given by the difference between the upper and the lower limit of the 95% CI, for each estimated parameter

ID	Linf, MDE (mm)	Linf, CI (mm)	K, MDE (1/year)	K, CI (1/year)	t_anchor, MDE (year)	t_anchor, CI (year)	M, MDE (1/year)	M, CI (1/year)
Regions								
Bay of Biscay (B)	54.8	23.4	3.4	3.9	0.3	0.9	9.4	12.1
Iceland (I)	52.8	26.5	1.9	3.5	0.4	0.7	4.8	6.0
Norway (N)	53.0	26.0	2.2	2.7	0.9	1.0	8.3	10.6

Gear / fishery selectivity parameters

L50 and L75: the lengths at which the fish have 50% and 75% probability to be caught

Bay of Biscay
- Pelagic trawl, 10 mm mesh size at cod end
  - L50: 34.3 mm (CI range: 3.7 mm)
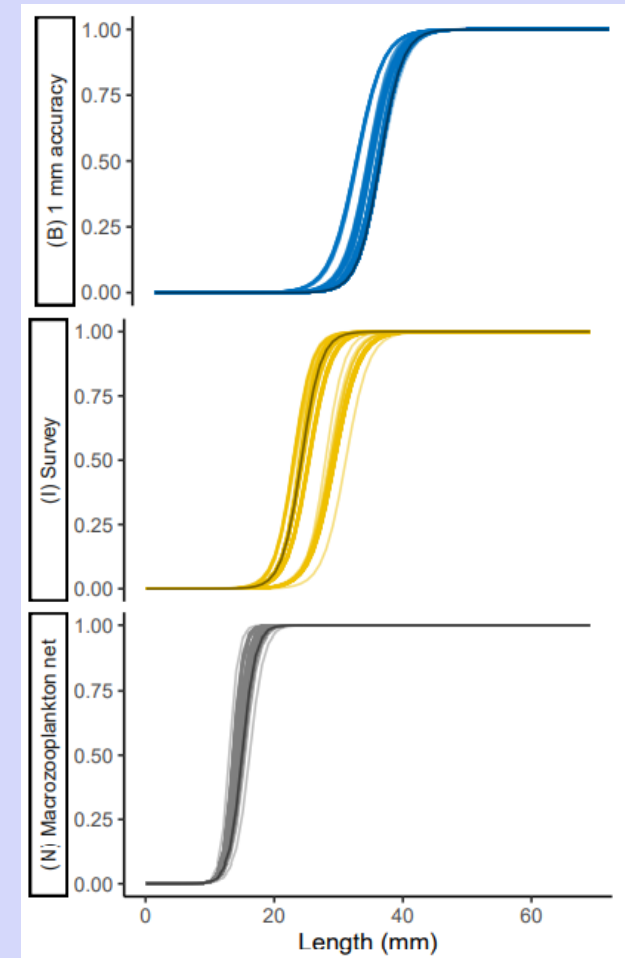 - L75: 36.2 mm (CI range: 3.3 mm)

- Icelandic offshore areas
  - Pelagic trawl, 9 mm mesh size at cod end
    - L50: 24.2 mm (CI range: 6.4 mm)
    - L75: 25.9 mm (CI range: 7.0 mm)

- Norwegian shelf region and offshore areas
  - Macrozooplankton net, 3 mm mesh size
    - L50: 15.0 mm (CI range: 1.5 mm)
    - L75: 16.1 mm (CI range: 1.8 mm)

Further steps: estimation of stock status with TropFishR

- Exploitation rate
  - E = F/Z

- Yield-per-recruit modelling
  - Predicts the theoretical yield and biomass per recruit for a range of fishing mortality and gear selectivity assumptions and thus allows to estimate biological reference points and stock status.
  - Assumes VBGF growth and equilibrium conditions
  - Requires length-frequency data, estimated growth and mortality parameters, selectivity information, and parameters of the length-weight relationship a and b. If maturity information is available reference points related to the Spawning Potential Ratio (SPR) can be estimated.

Further material

- Download the TropFishR Package (Version 1.6.3 and older) via CRAN:

  - https://cran.r-project.org/web/packages/TropFishR/index.html

- TropFishR Reference manual:

  - https://cran.r-project.org/web/packages/TropFishR/TropFishR.pdf

- Vignettes:

  - https://cran.r-project.org/web/packages/TropFishR/vignettes/lfqData.html
  - https://cran.r-project.org/web/packages/TropFishR/vignettes/tutorial.html
  - https://cran.r-project.org/web/packages/TropFishR/vignettes/Using_TropFishR_ELEFAN_functions.html

- FAO Manual by P. Sparre and S.C. Venema (1998, 1999), "Introduction to tropical fish stock assessment" http://www.fao.org/documents/card/en/c/9bb12a06-2f05-5dcb-a6ca-2d6dd3080f65

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References

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