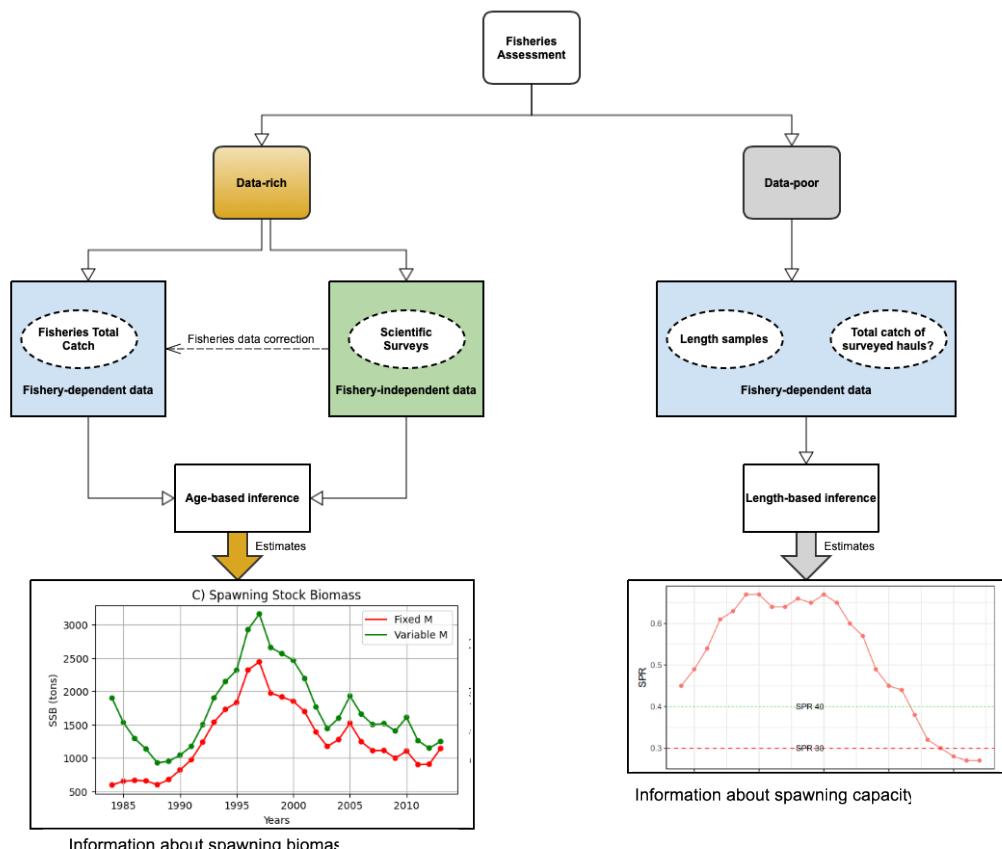


1. Data Rich vs Data Poor

According to the nature of the data available for fisheries assessments there are two scenarios, those with plenty of data or data-rich and those with very limited details about the underlying stock to study, so-called data-poor or data-limited assessments.



1.1 Data-rich assessments

1. **Total catch** of the fisheries under study
2. Fish's hard-part analysis such as otoliths to estimate age, therefore an **age-based evaluation model** is possible.
3. Ability to identify and follow cohorts
4. In some occasions, **scientific surveys** are available to correct potential vias arising from fishery-dependent data. For example, large parts of the stocks could be confined in a specific area given the impression that there is much more fish available to catch than what there is actually.

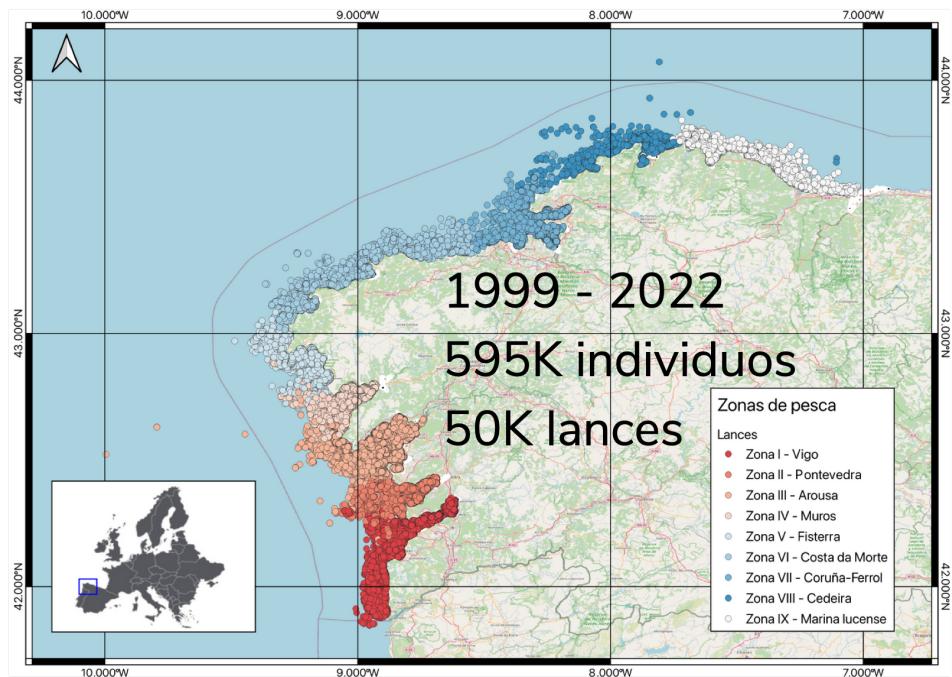
The return on investement (ROI) is that results are **at scale** and are representative of the stock per se. For example, the **total spawning stock biomass** available year after year would be in tons.

1.2 Data-poor assessments

1. **Individual lengths** obtained from random surveys taking place on board of vessels or at port.
2. Sometimes total catch of the **surveyed hauls** are available, so a **relative index of abundance** may be constructed.
3. knowledge of the parameters of the **growth equations**, usually Von Bertalanffy.

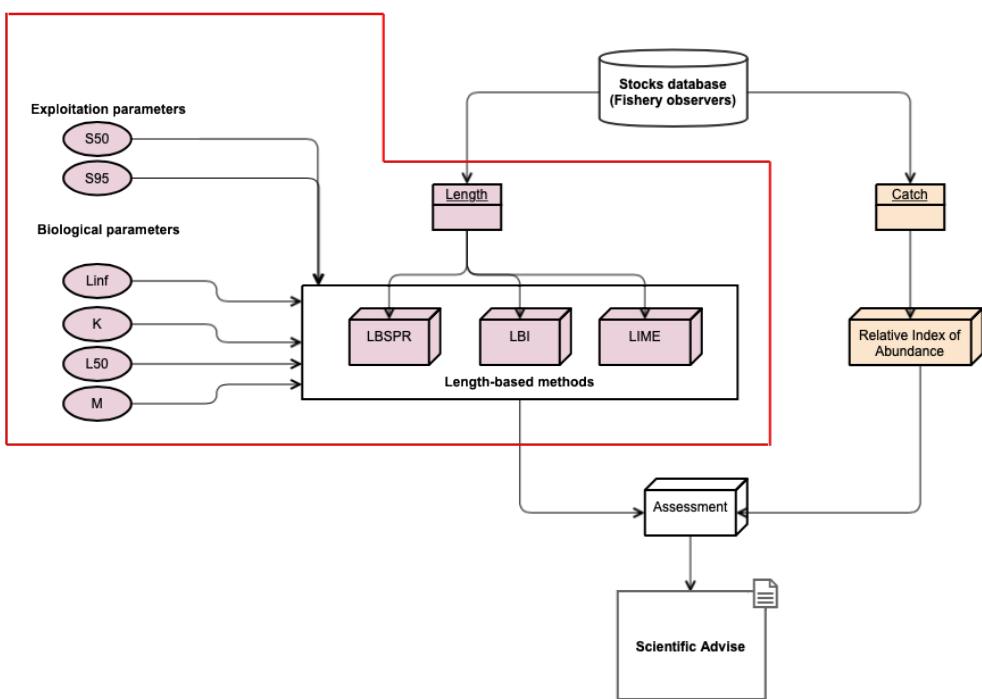
Such a lack of data allows only to establish a series of indicators to evaluate the health of stock. We do not have information at scale but **indicative ratios**

2. Study case: small-scale fisheries in Galicia within a data-poor context



2.1 Small-scale fishery highlights

1. **~4K** vessels < 12m
2. **Great variety of fishing gears:** drifting nets, surface and bottom long lines, creels and some artisanal trawling
3. **20 different species** (teleosts, elasmobranchs, molusks and crustaceans)
4. **Fishery-dependent data:** fisheries observers taken note of lengths and weight of some individuals of the random haul assigned to them as well as the total catch



2.2 Pipeline developed for the assessments fisheries

1. With total catches per hauls => A relative index of abundance
2. With lengths and weights of individuals => Length Based Methods (**LBMs**)
 - WKLIFE ICES recommendation: Length Based Indicators (**LBI**) and Length-Based Spawning Potential Ratio (**LBSPR**), both assuming *equilibrium conditions* (Recruitment and Z are constant)
 - Non equilibrium conditions: Length-based Integrated Mixed Effects (**LIME**)

3. Overview of LBMs

The three methods have some requirements and assumptions and yield different indicators from which we have selected only the few we have an interest in, as shown in the table below:

3.1 Details of parameters

METHODS	REQUIREMENTS	SOUGHT ESTIMATES	ASUMPTIONS(*)
LBSPR ¹	<ul style="list-style-type: none"> L_{inf} L_{50} y L_{95} M/K L_{wa}, L_{wb} Length frequency matrix 	<ul style="list-style-type: none"> SPR F/M 	<ul style="list-style-type: none"> Equilibrium condition Asymptotic selectivity (lengths) Known LHTs
LIME ²	<ul style="list-style-type: none"> L_{inf}, k, t_0, L_{50} y L_{95} M, R_{var} y F_{var} L_{wa}, L_{wb} Length frequency matrix 	<ul style="list-style-type: none"> SPR F Recruitment variability 	<ul style="list-style-type: none"> No equilibrium conditions Constant and asymptotic selectivity (lengths) Known LHTs
LBI ³	<ul style="list-style-type: none"> L_{inf} y L_{50} M/K Length frequency matrix 	<ul style="list-style-type: none"> Juvenile conservation Adult conservation Optimum Yield 	<ul style="list-style-type: none"> Equilibrium condition Asymptotic selectivity

- (*) Von Bertalanffy growth model for LBSPR and LIME is assumed and Life History Traits (LHTs) must be representative of the socks being studied
- 1: Hordyk et al. (2015) ICES Journal of Marine Science, 72; 2: Rudd, n.d. (2017) Accounting for Variability and Biases in Data-limited Fisheries Stock Assessment (dissertation); 3: ICES WKLIFE V REPORT 2015

1. **L_{inf}** : asymptotic length assuming Von Bertalanffy equation (
$$L_t = L_{inf}(1 - \exp^{(-k(t-t_0))})$$
).
2. **k** : growth coefficient rate of the Von Bertalanffy equation.
3. **t_0** : intercept of the Von Bertalanffy curve with the 'y' axis. Theoretical age at size 0.
4. **L_{50}** : length of first sexual maturity assuming a logistic curve.
5. **L_{95}** : length at which 95% of individuals are mature.
6. **L_{wa}** : parameter 'a' in the Length-Weight relationship equation (
$$W = aL^b$$
).
7. **L_{wb}** : parameter 'b' in the Length-Weight relationship equation.
8. **M** : constant natural mortality across all cohorts and years.
9. **R_{var}** : recruitment variability.
10. **F_{var}** : fishing mortality variability to cap inter-annual variation.
11. **M/K** : Beverton-Holt Life History Invariant (BH-LHIs) that Pauly defined as ~ 1.5 as a rule of thumb for teleosts (Prince et al., 2015).

Likewise, an explanation for the outputs of each algorithm is as follows:

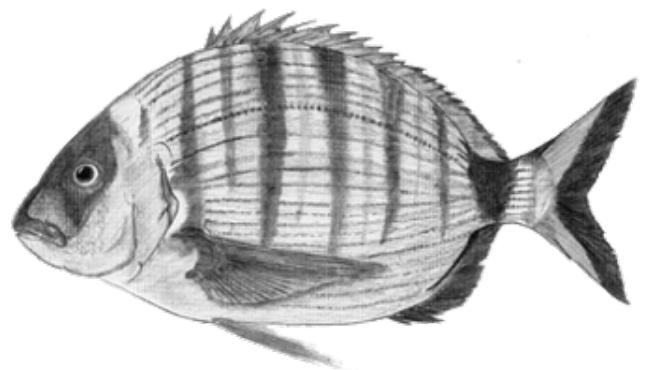
- **F/M (LBSPR)**: ratio between F over M, where F is understood as the highest fishing mortality experienced by any size

class. M though, is the adult natural mortality.

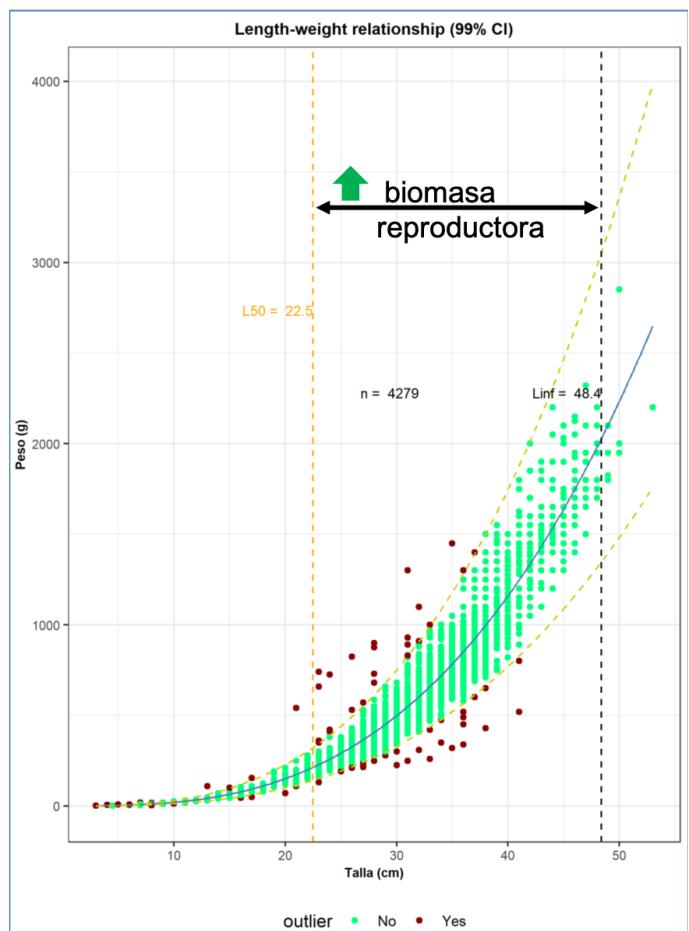
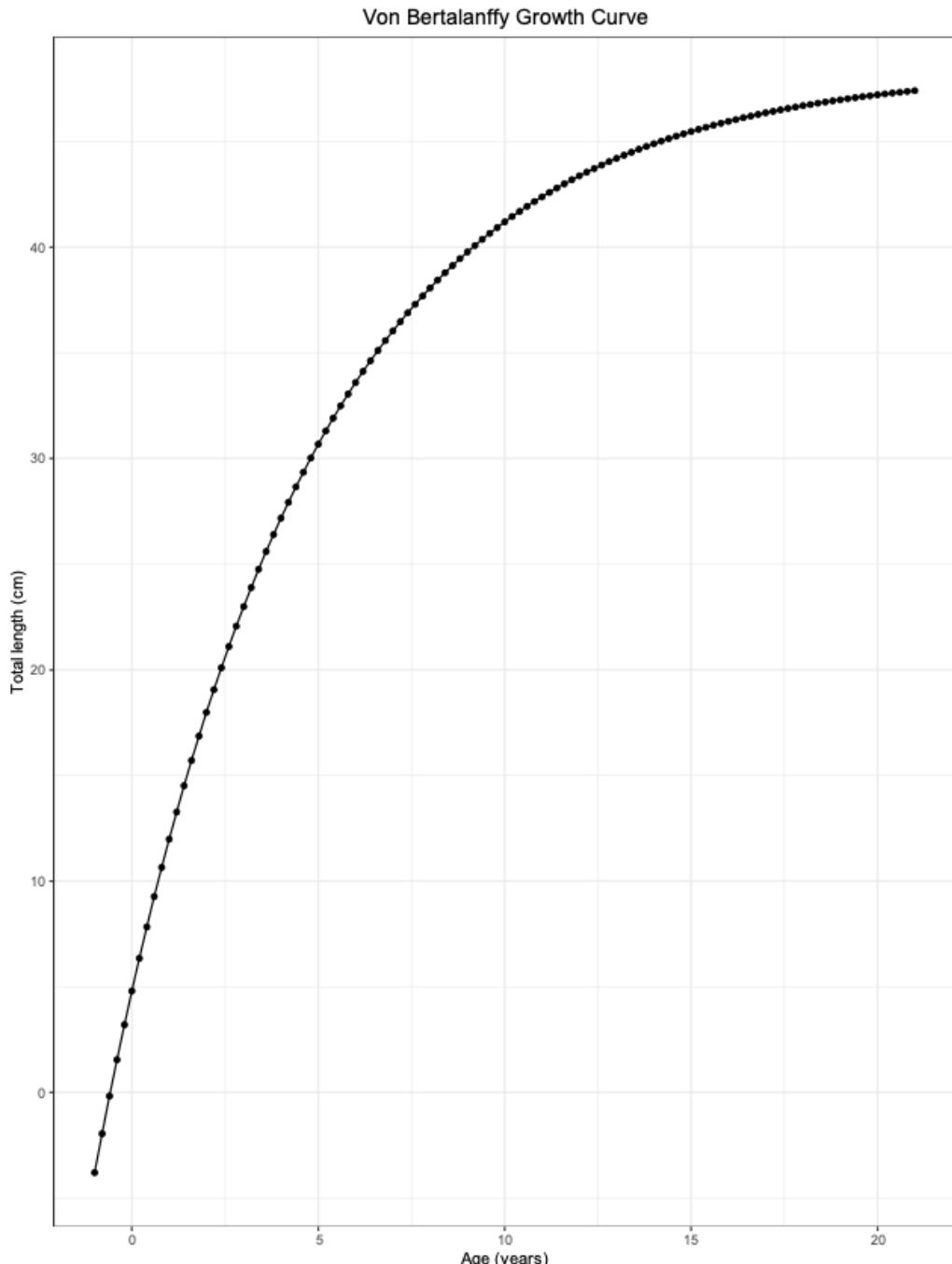
- **SPR (LBSPR and LIME):** the ratio between the average of unfished lifetime egg production per individual over the same average in an exploited situation. In short, reproductive capacity of the stock nowadays compare to that when the stock was unexploited.
- **LBI indicators:** how fisheries are preserving juvenile and adults and keeping in mind the performance of the fisheries.

4. Fish case study: *Diplodus sargus* (White Seabream)

This workshop will apply LBSPR, LIME and LBI to *Diplodus sargus*, a omnivorous bottom-dwelling species which growth parameters were taken from the **Cantabrian Sea (Benchalel and Kara, 2013)** and natural mortality from the **Mediterranean (M Al-Beak, 2015)**. The timeseries stretches from **1999** all the way to **2022**. In addition, details about the recruitment variability were fetched from a meta-analysis study conducted for a database of 154 species. Data however for this particular species did not emerge so the unobserved order-level distribution was used instead (Thorson et al., 2014):



- **Max Age:** 21 years
- **Mim legal size:** 22 cm
- **L_{inf} :** 48.4 cm
- **k:** 0.18
- **t_0 :** -0.58 years old
- **L_{50} :** 22.5 cm
- **L_{95} :** 23.115 cm (calculated as $1.15 * L_{50}$)
- **L_{wa} :** 0.021
- **L_{wb} :** 2.955
- **M:** 0.315
- **M/k:** 1.725
- **Recruitment Standard Deviation:** 0.737
- **Recruitment Mean:** 0.353
- **Fishing Mortality Interannual Standard Deviation:** 0.2
- **Main gears:** Vetas, Miños, Trasmallos y Palangrillo



5. Where to find the source code of this workshop

1. This workshop can be found here: https://github.com/d2gex/lbm_seminary.git
2. Lime library: <https://github.com/merrillrudd/LIME.git>
3. LBSPR library: <https://github.com/AdrianHordyk/LBSPR.git>
4. LBI library (ICES): https://raw.githubusercontent.com/ices-tools-dev/LBIndicator_shiny/master/utilities.R
5. LBI library (d2gex): https://github.com/d2gex/lbm_seminary/blob/main/R/lbi_library.R (Fixed bug with multiple length classes having the same highest biomass and thin down the required dependencies, i.e, *java*, *reportjars*, etc... is no longer required as *lb_tableSH* function is not used)

6. Installation of algorithms and required libraries

```
In [1]: # # ---> Install devtools
# install.packages("devtools", repos='http://cran.us.r-project.org')
# # ---> Install LIME
# devtools::install_github("merrillrudd/LIME")
# # ---> Install rest of supporting packages
# packages <- c("LBSPR", "tidyverse", "R6", "ggpubr", "openxlsx")

# # Install packages not yet installed
# installed_packages <- packages %in% rownames(installed.packages())
# if (any(installed_packages == FALSE)) {
#   install.packages(packages[!installed_packages])
# }
```

7. Include all libraries required for the workshop

```
In [7]: source("R/config.R")
source("R/utils.R")
source("R/plot_utils.R")
source("R/lbm_data_holder.R")
```

```
source("R/lbspr.R")
source("R/lime.R")
source("R/lbi.R")
source("R/algo_plotter.R")
```

8. Data fetching and exploring

```
In [8]: diplodus_data <- read_sheets_from_excel(FREQUENCY_DATA_PATH)
catch_weight_data <- CatchWeightMatrices$new(catch = diplodus_data$catch,
                                              catch_long = diplodus_data$catch_long,
                                              weight = diplodus_data$weight,
                                              weight_long = diplodus_data$weight_long)
```

8.1 Length Frequency Matrix

```
In [23]: head(catch_weight_data$catch)
```

	MeanLength	X1999	X2000	X2001	X2002	X2003	X2004	X2005	X2006	X2007	...	X2013	X2014	X2015	X2016
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	...	<dbl>	<dbl>	<dbl>	<dbl>
1	10.5	1	0	0	0	0	0	0	0	0	...	0	0	0	0
2	11.5	0	0	0	0	0	0	0	0	0	...	0	0	0	0
3	12.5	0	0	0	0	0	0	1	0	0	...	0	0	0	0
4	13.5	4	0	1	0	0	0	0	0	0	...	0	0	0	0
5	14.5	4	2	7	0	0	0	0	0	0	...	0	0	0	0
6	15.5	2	0	6	1	0	1	0	0	1	...	0	0	0	0

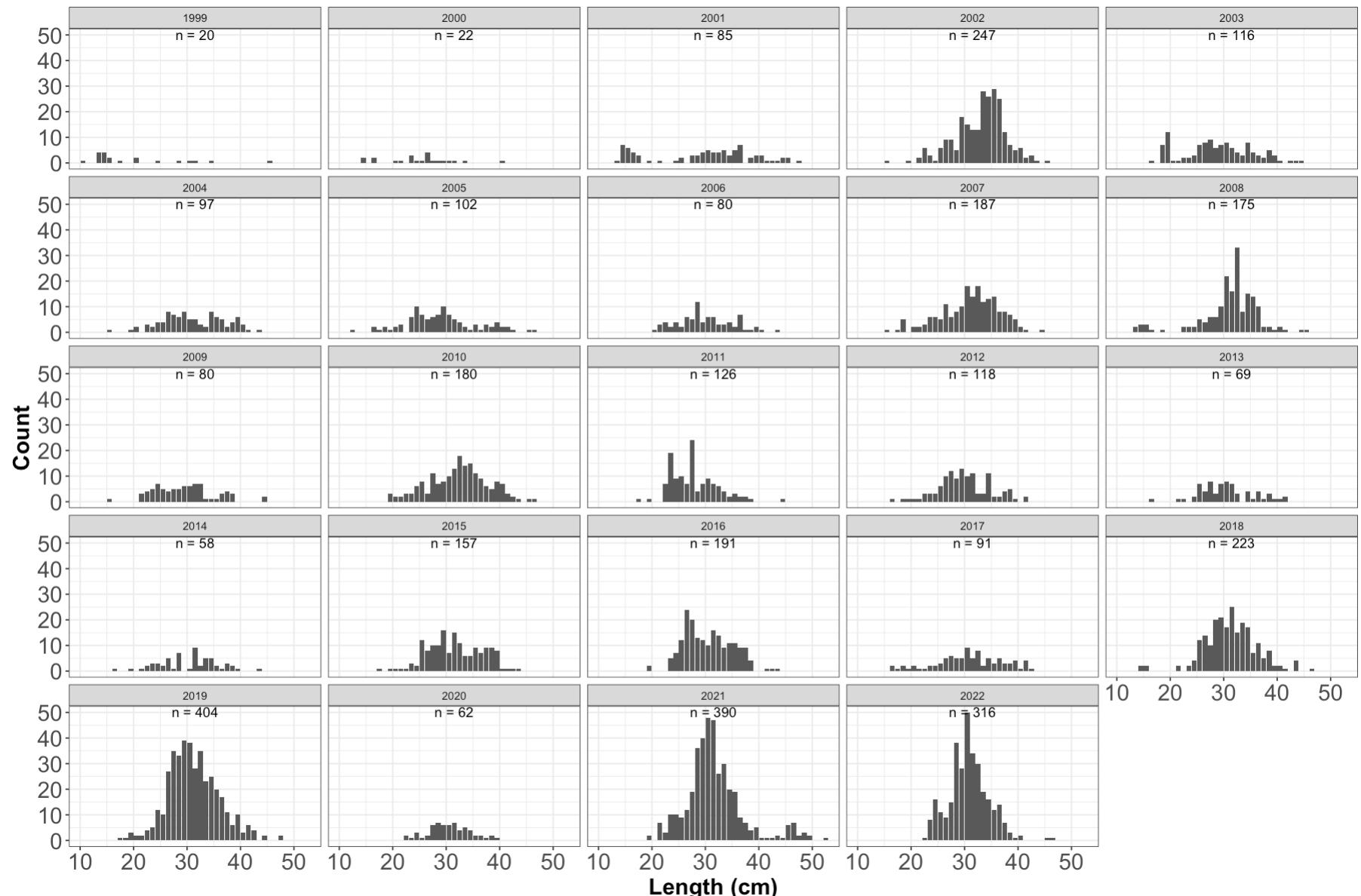
- Years are shown in the columns and length classes in the rows. In addition the first column must contain the mean lengths and must be named **MeanLength**

- **Number on individuals** caught in a length class for a particular year.
- Classes span out to **1cm**.
- i.e, class [15.5cm, 16.5cm] for year 2001 fishermen caught **6** individuals.

8.3 Plotting the annual length frequency matrices from 1999 - 2022.

```
In [9]: # Object (think about it as a list) that keeps the context details of the plot about to be visualised
options(repr.plot.width = 15, repr.plot.height = 10)
plot_context <- PlotContext$new()
plot_context <- PlotContext$new()
plot_context$title_size <- 10
plot_context$face_text_size <- 2
plot_context$x_text_size <- 18
plot_context$y_text_size <- 18
plot_context$x_lab <- "Length (cm)"
plot_context$y_lab <- "Count"

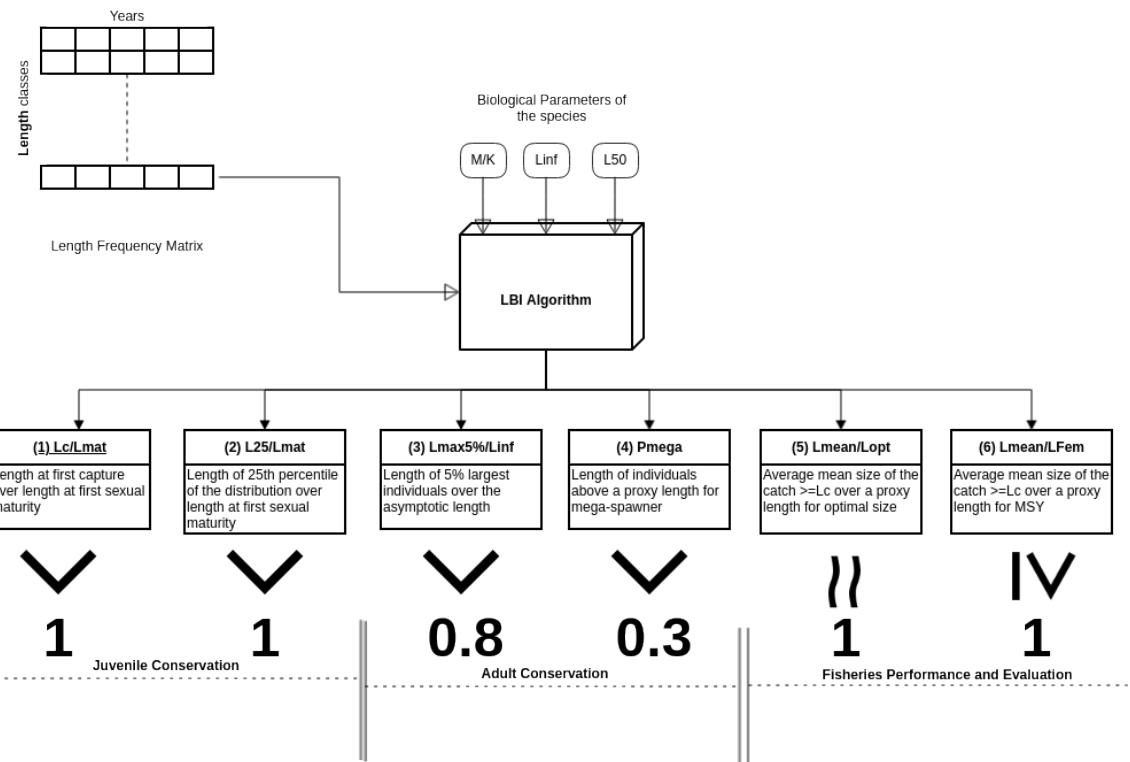
g <- generate_yearly_length_distribution (catch_weight_data$catch_long,
                                           'MeanLength',
                                           'catch',
                                           plot_context)
g
```



- a) The **first two years** of the series have a very low representativeness with an average of **n=21** individuals
- b) The first **two/three** years do not conform an unimodal distribution. Instead it stretches out along the x-axis.

9. LBI Algorithm

9.1 LBI overview



1. Inputs:

- A length frequency matrix
- Biological parameters

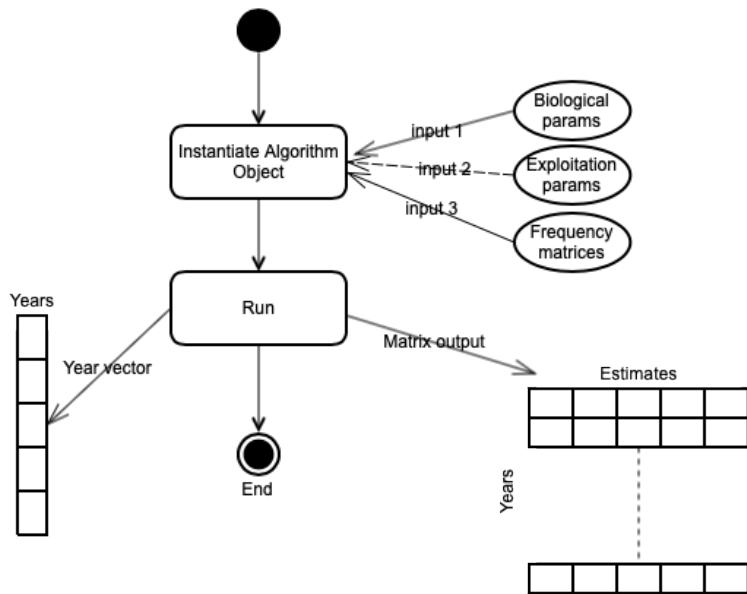
2. Outputs: (indicators need to be above a threshold)

- *Juvenile conservation (1,2)*: how does our length frequency matrix looks like with regards to the length of first sexual maturity?
- *Adult conservation (3,4)*: How representative is our length frequency matrix when it comes to adults? Pmega less important
- *Fisheries performance and MSY (4,5)*: all based on proxy lengths, it looks at the state of the fisheries by comparing the mean length above L_c to L_{inf}

9.2 Biological parameters loading

```
In [12]: bio_params <- BiologyParameters$new(  
  linf = 48.4,  
  k = 0.18,  
  t0 = -0.58,  
  l50 = 22.5,  
  l95 = 23.115,  
  M = 0.3105,  
  M_K = 1.725,  
  lwa = 0.021,  
  lwb = 2.955,  
  rec_variability_mean = 0.737, # Prior recruitment variability obtained from meta-analysis study  
  rec_variability_sd = 0.353 # Prior fishing penalisation obtained from meta-analysis study  
)  
  
exp_params <- ExplotationParameters$new()
```

9.3 Run LBI algorithm



9.3.1 Common structure to run all algorithms

1. Create three lists or parameters, each containing data about biological, exploitation and matrices data
 2. Not all list of parameters are required for all algorithms
 3. The outputs are a vector of the years analised and a matrix where columns have the indicators and in the rows their values

```
In [13]: lbi_algo <- Lbi$new(bio_params, exp_params, catch_weight_data)
lbi_results <- lbi_algo$run()
data <- lbi_results$estimates
data$years <- lbi_results$years
head(data)
```

```
Warning message in melt(newDat[, -1], id.var = "lmidp", value.name = "number", variable.name = "year"):  
"The melt generic in data.table has been passed a data.frame and will attempt to redirect to the relevant reshape2 m  
ethod; please note that reshape2 is deprecated, and this redirection is now deprecated as well. To continue using me  
lt methods from reshape2 while both libraries are attached, e.g. melt.list, you can prepend the namespace like resha  
pe2::melt(newDat[, -1]). In the next version, this warning will become an error."
```

A data.frame: 6 × 7

	Lc_Lmat	L25_Lmat	Lmax5_Linf	Pmega	Lmean_Lopt	Lmean_Lfem	years
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<int>
1	0.6000000	0.6000000	0.9400826	0.10000000	0.6790860	0.9777781	1999
2	0.6444444	0.9555556	0.8236169	0.04545455	0.8164914	1.1344125	2000
3	0.6444444	0.8666667	0.9437267	0.36470588	0.9684917	1.3455979	2001
4	1.3111111	1.3555556	0.8635443	0.47368421	1.1257064	1.0250672	2002
5	0.8222222	1.0888889	0.8624226	0.25000000	0.9435569	1.1497496	2003
6	1.0888889	1.1777778	0.8538175	0.37113402	1.0464993	1.0766068	2004

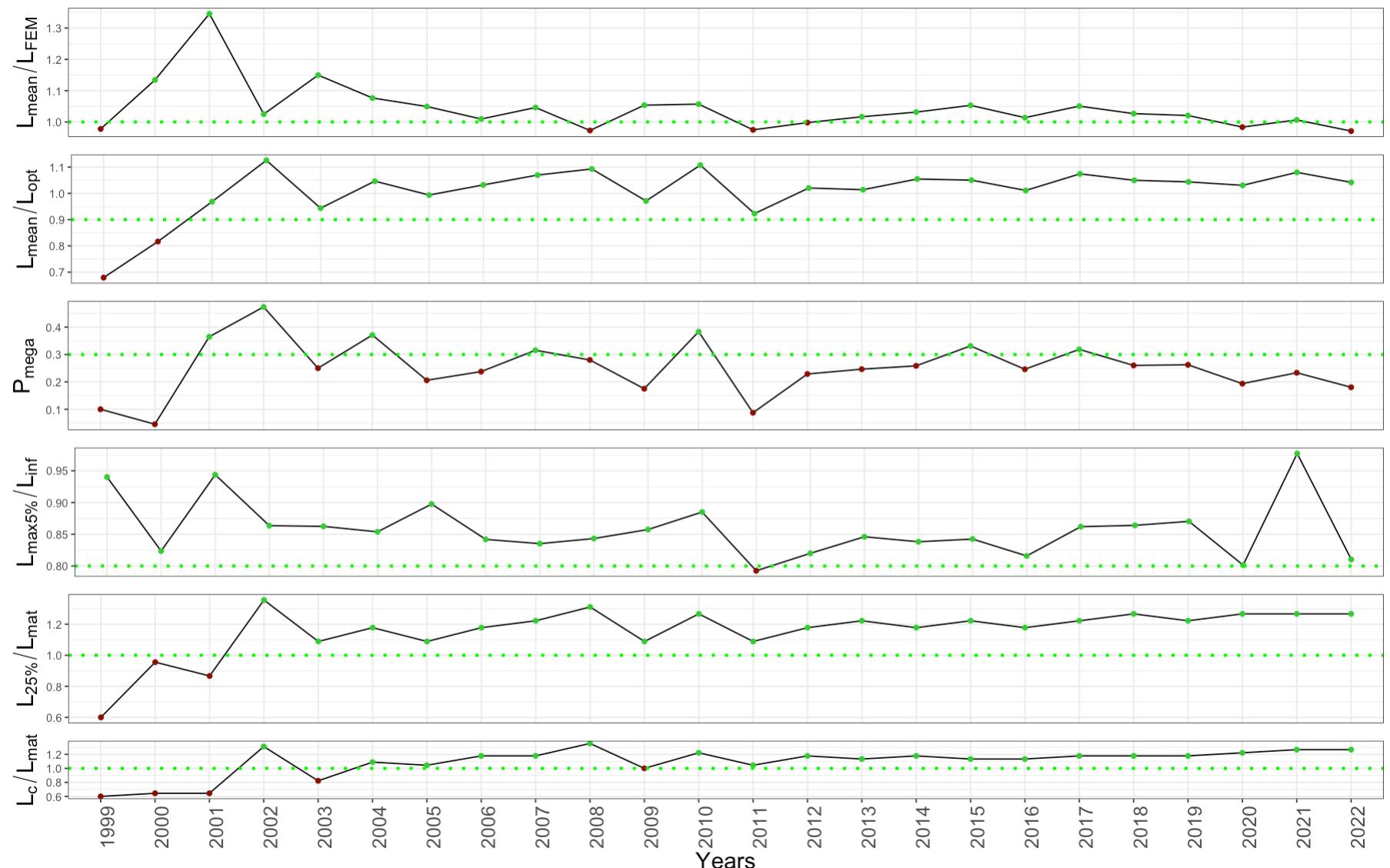
- **Along the columns** are laid the **indicators estimated**.
- **Each cell** for each row provides the value for a **single indicator per year**.

9.4 Plotting LBI estimates

The green dotted horizontal line show the threshold above which indicators are in good health. Then each yearly value showed as a dot is as well in green if it is above such line and red if it is under it.

```
In [14]: # Threshold above which the corresponding indicators are showing a healthy status
options(repr.plot.width = 15, repr.plot.height = 10)
thresholds <- list(
  Lc_Lmat = 1,
  L25_Lmat = 1,
  Lmax5_Linf = 0.8,
  Pmega = 0.3,
  Lmean_Lopt = 0.9,
  Lmean_Lfem = 1)
lbi_plotter <- LbiOutputPlotter$new(data, thresholds)
grid <- lbi_plotter$generate_outputs(title_size = 22, title = "Lbi scores")
grid
```

Lbi scores



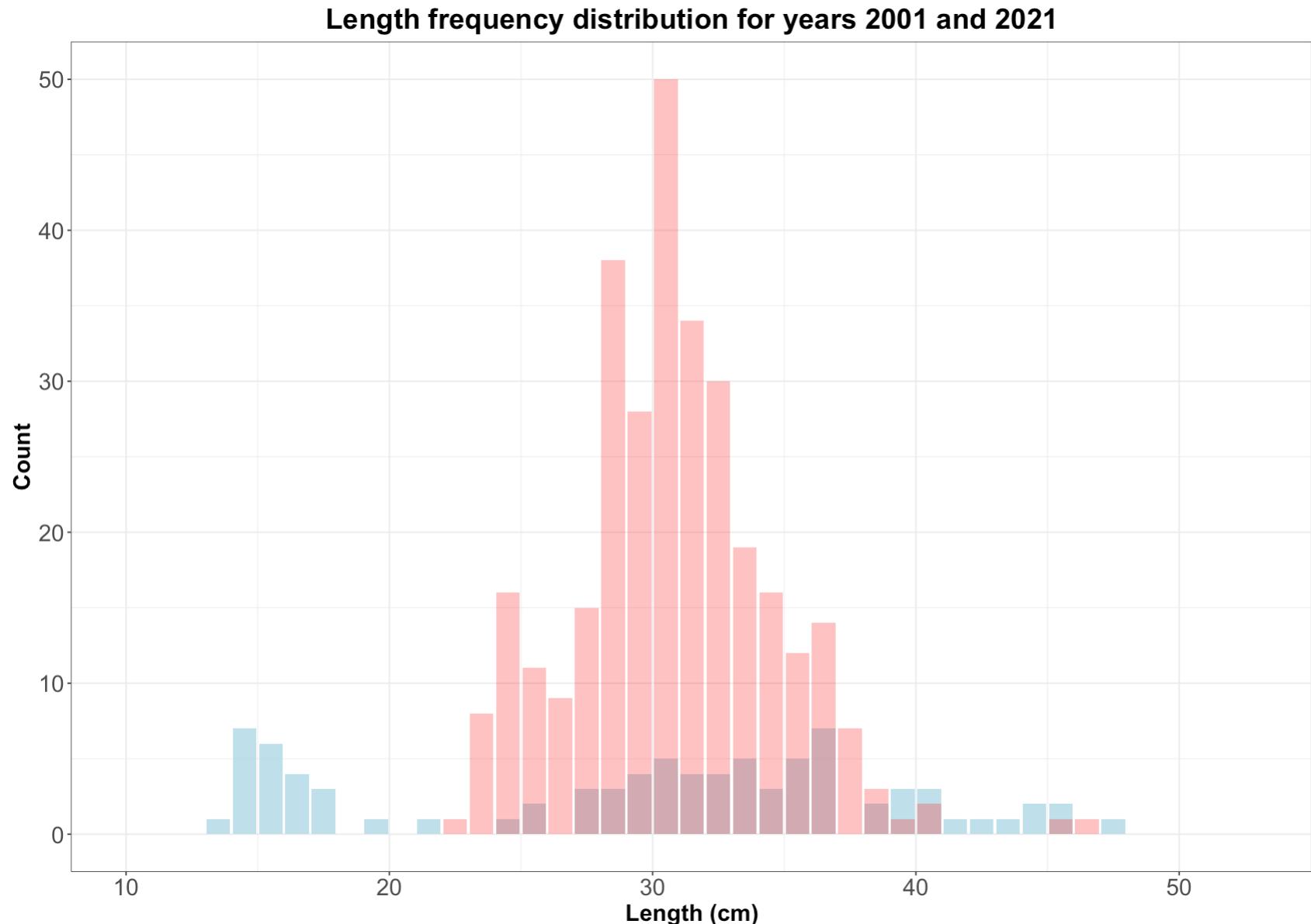
Looking at the results, it seems that:

- a) In **1999 and 2000** the indicators about *juvenile conservation* seem to not doign well.
- b) Between **2001 and 2002** best indicators about *adult conservation*.

- c) Likewise between **2001 and 2003** best indicators about *fisheries performance*.

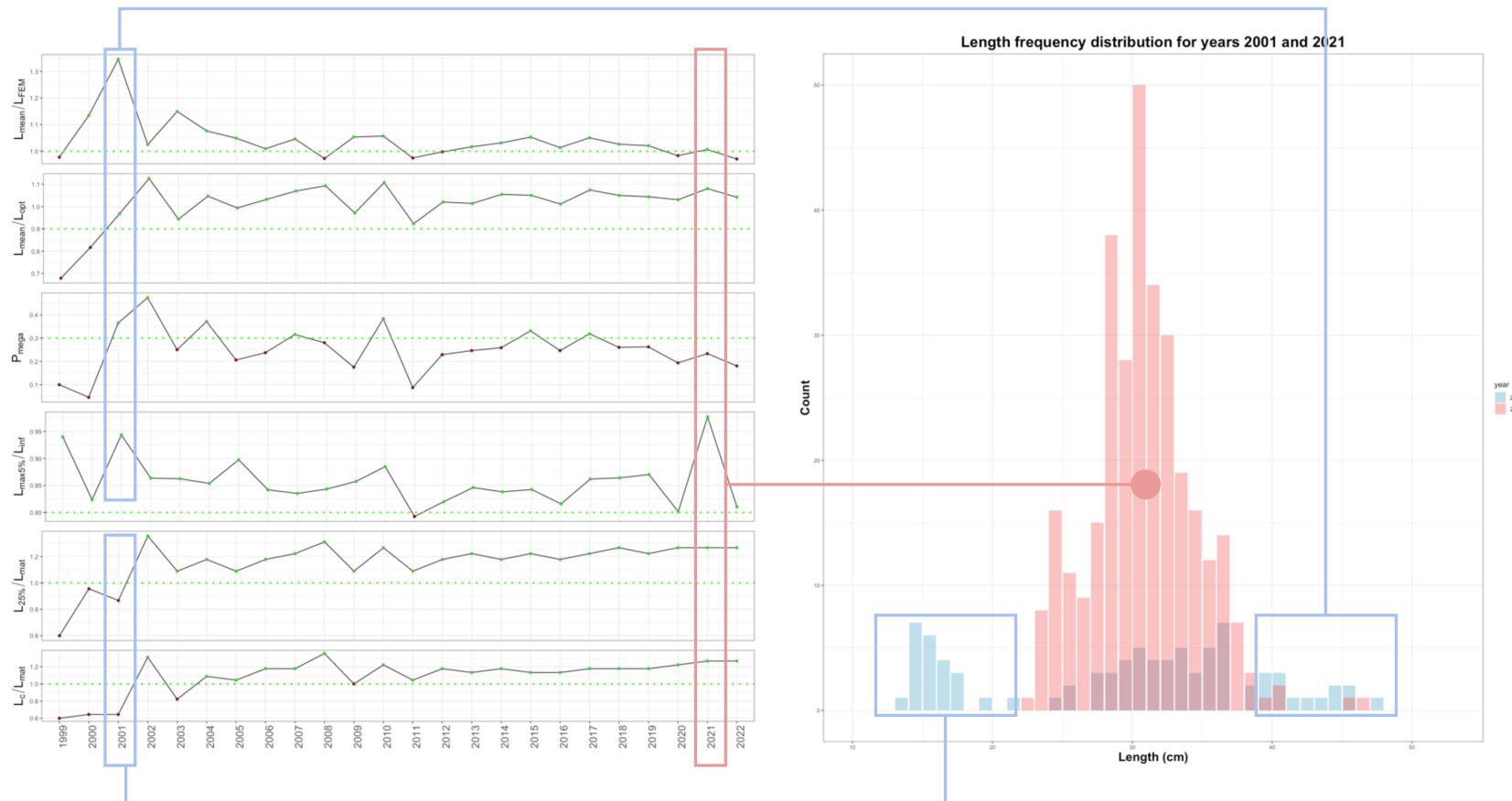
9.5 Superimposed 2001 and 2021 length frequencies

```
In [15]: options(repr.plot.width = 15, repr.plot.height = 10)
plot_context$title <- "Length frequency distribution for years 2001 and 2021"
plot_context$title_size <- 22
plot_context$x_title_size <- 18
plot_context$y_title_size <- 18
g <- generate_biannual_distribution(catch_weight_data$catch_long,
                                      'MeanLength',
                                      'catch',
                                      plot_context,
                                      2001,
                                      2022,
                                      bar_filled_colours = c("lightblue4", "red"),
                                      alpha_values = c(.8, .3))
g
```



- Length frequency distribution for 2001 **stretches out** along the x-axis
- However, the one for 2021 is **more centered**

9.6 An explanation of the indicators by looking at the length frequency distribution



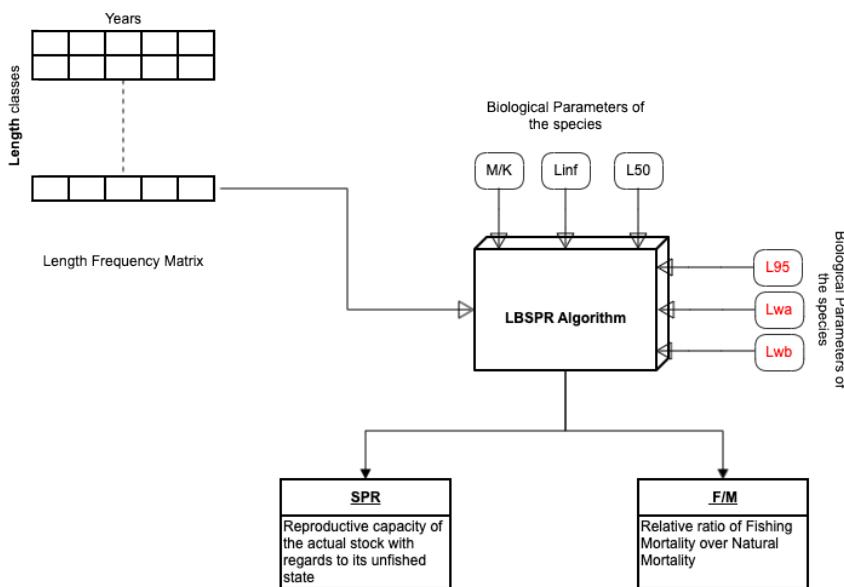
By looking at the distribution and the indicators in parallel, it seems that:

- a) The **left thick tale of 2001** may be the cause that **juveniles did not do very well** over that period. Compare the overall catch for that year the number of undersize individual caught is not negligible at all.
- b) At the same time, the **thick right tale** tell us quite another story. It may have helped boosting the indicators that show a **good conservation of adults**. The two indicators are not mutually exclusive.
- c) Lastly, the distribution for **2021 seems to be more centered**, therefore all indicators across seem to have more **moderate values**. Juveniles are not doing that bad and adults are doing more or less fine, with MSY for 2001 being notably better.

How representative is the 2001 distribution with just ~14% of the average annual representation and 0.5% of the overall sampled individuals along 24 years?

10. LBSPR algorithm

10.1 LBSPR Overview (Population dynamics model)



Minimum threshold: > 0.3

$\uparrow F/M \rightarrow \downarrow SPR$

Desired threshold: > 0.4

Lbspr is the first of the two algorithms that try to **simulate the population dynamics**.

- Unlike the LBI, it also requires three other parameters **L95**, **Lwa** and **Lwb**.
- The main output is the **SPR**: "actual reproductive capacity of the stocks compared to that in its unfished state".
- Desired values of SPR should be above 0.4. Below 0.3 the stock spawning biomass is in danger.
- Given **M/K**, **L_{inf}** and the **frequency matrix** ==> **selectivity at length** and **F/M** are estimated.
- Given **selectivity at length** and **F/M** ==> SPR is calculated
- As F/M determines the level of SPR we are at any given point, the larger F/M the lower the score of SPR and vice-versa.
- **Lwa** and **Lwb** are required to calculate the matrix of weight, which is necessary to calculate the spawning biomass different between the unfished and fished states

10.2 Run LBSPR

```
In [ ]: lbspr_algo <- Lbspr$new(bio_params, exp_params, catch_weight_data)
lbspr_results <- lbspr_algo$run()
data <- lbspr_results$estimates
data$years <- lbspr_results$years
```

```
In [15]: data
```

A data.frame: 24 × 5

SL50	SL95	FM	SPR	years
<dbl>	<dbl>	<dbl>	<dbl>	<int>
20.95	26.57	1.29	0.44	1999
21.92	27.88	1.36	0.46	2000
22.73	28.68	1.37	0.50	2001
24.47	30.99	1.52	0.49	2002
25.08	31.93	1.45	0.48	2003
25.71	32.66	1.44	0.47	2004
26.25	33.29	1.51	0.46	2005
27.06	34.17	1.67	0.44	2006
27.97	35.30	1.89	0.43	2007
28.21	35.42	1.93	0.42	2008
27.85	34.75	1.76	0.42	2009
27.89	34.68	1.67	0.42	2010
27.55	34.00	1.61	0.40	2011
27.63	34.09	1.57	0.40	2012
27.75	34.23	1.52	0.41	2013
27.98	34.62	1.50	0.41	2014
28.02	34.56	1.45	0.42	2015
28.08	34.51	1.45	0.42	2016
28.37	35.01	1.49	0.42	2017
28.44	34.88	1.55	0.42	2018
28.42	34.61	1.59	0.41	2019

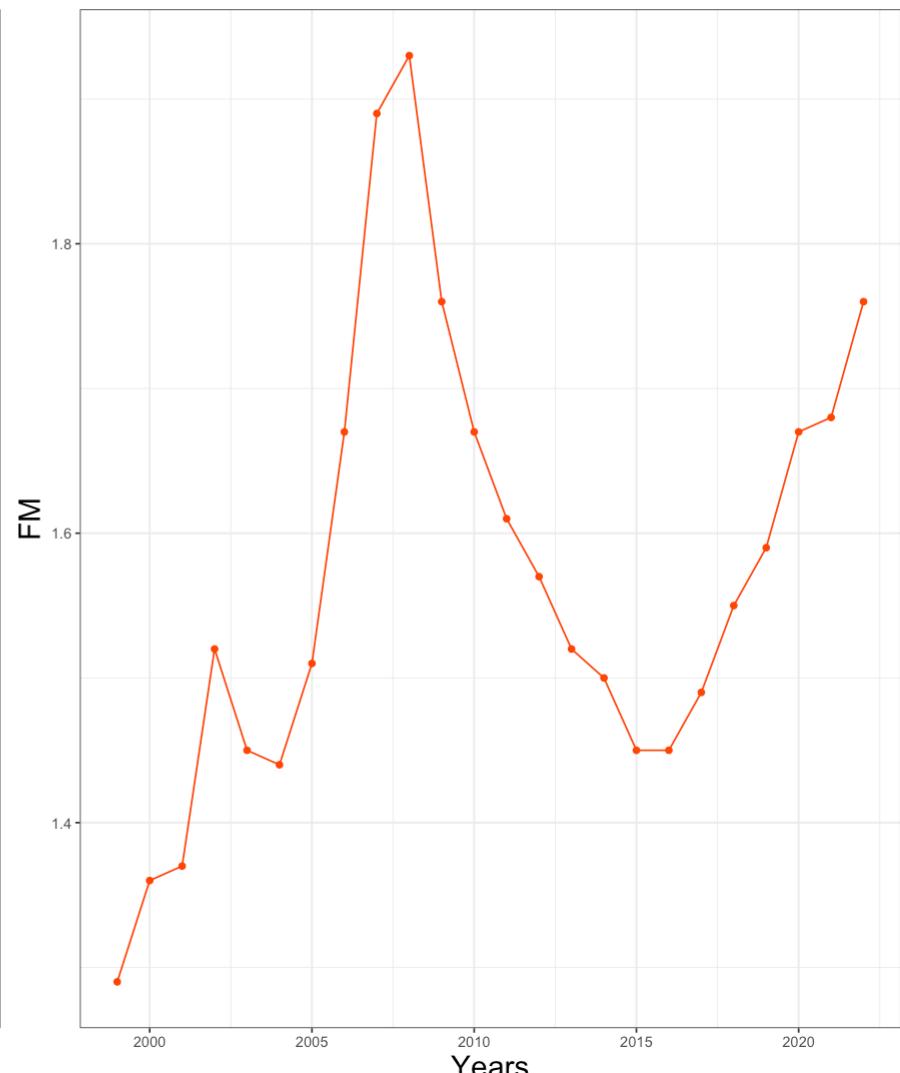
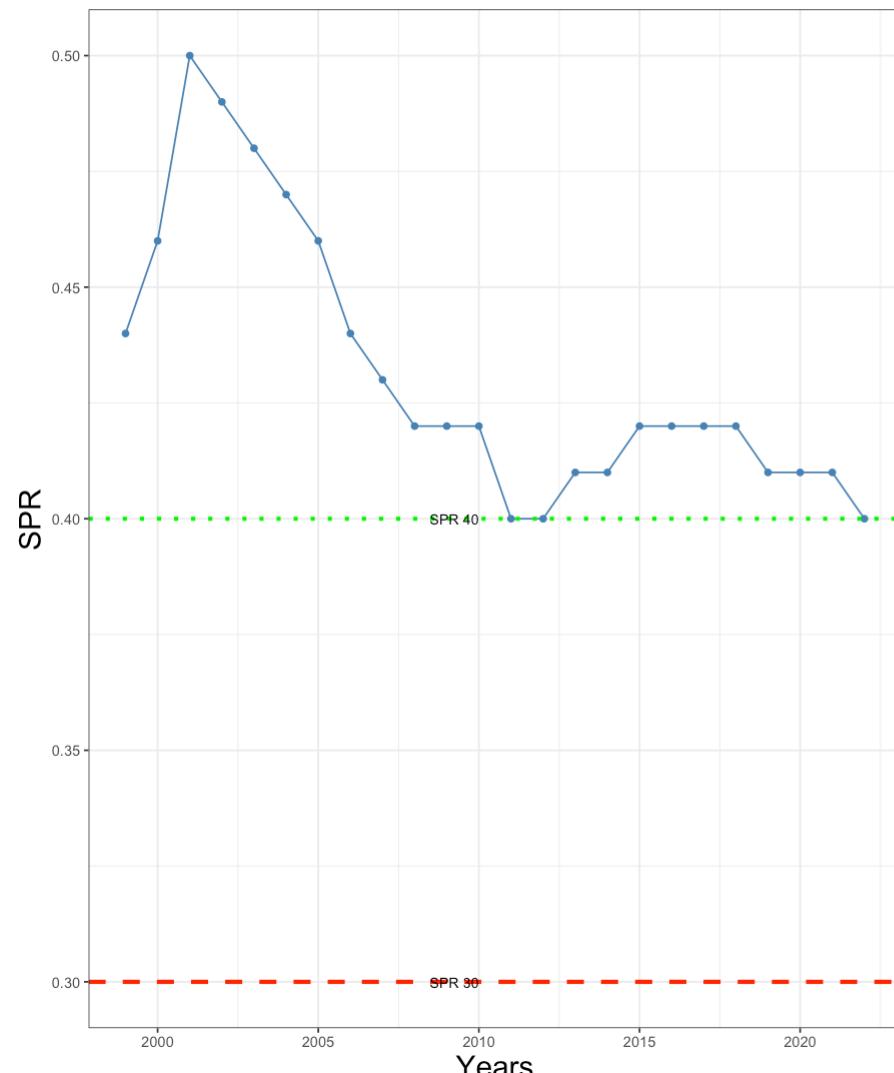
SL50	SL95	FM	SPR	years
<dbl>	<dbl>	<dbl>	<dbl>	<int>
28.45	34.47	1.67	0.41	2020
28.42	34.31	1.68	0.41	2021
28.49	34.30	1.76	0.40	2022

- **Along the columns** are laid the **outputs** that the algorithm has estimated
- **Each cell** for each row provides the value for a **single output per year**.

10.3 LBSPR plotting

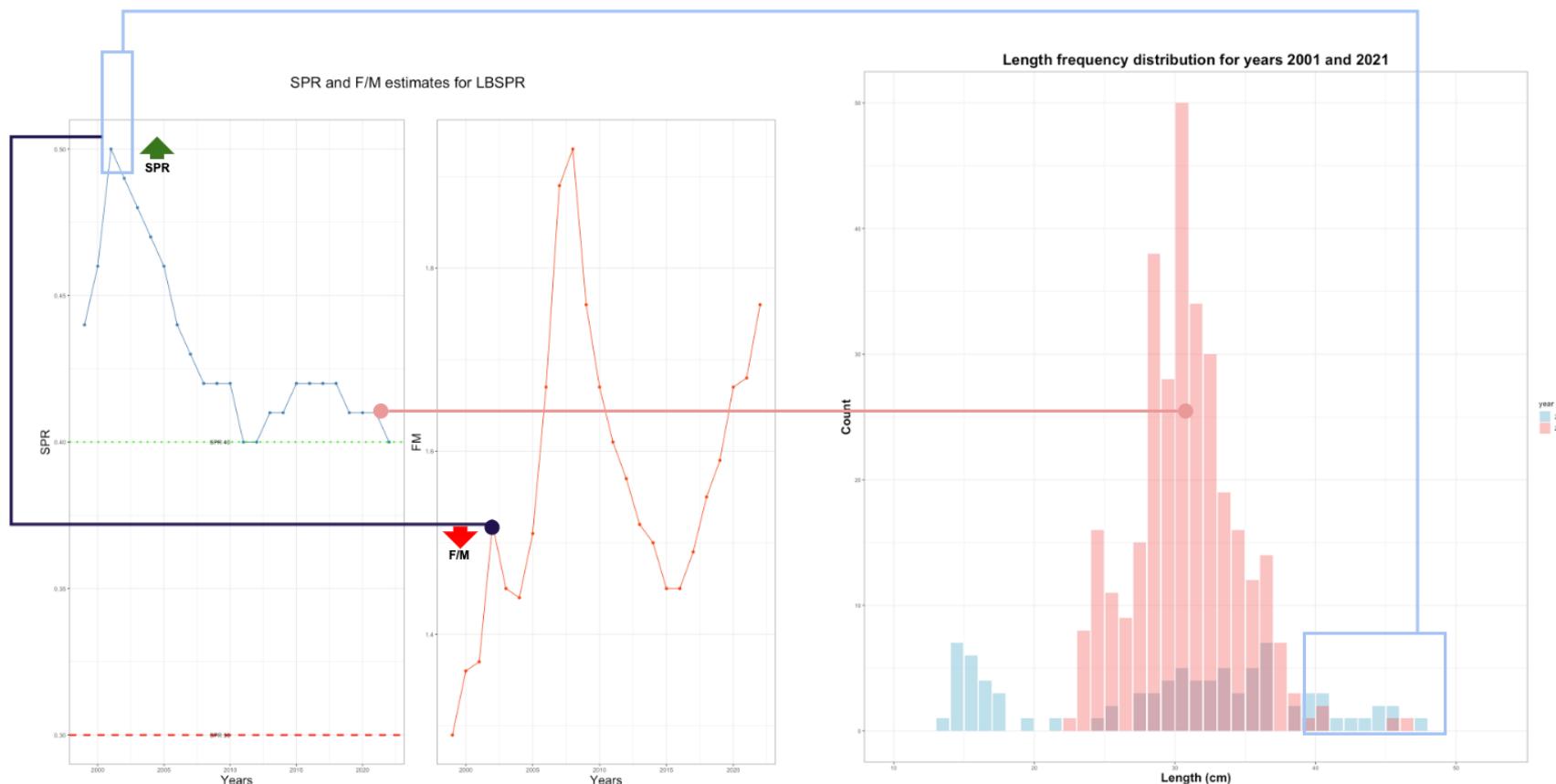
```
In [16]: options(repr.plot.width = 15, repr.plot.height = 10)
lbspr_plotter <- LbsprOutputPlotter$new(data)
grid <- lbspr_plotter$generate_outputs(title_size=22, title = "SPR and F/M estimates for LBSPR")
grid
```

SPR and F/M estimates for LBSPR



- On the left, the estimated **SPR** seems to be **above 0.4** line
- Again 2001 the **highest SPR**
- On the right, the **F/M** estimates follow a **see-saw** pattern with regards to the SPR.

10.3 An explanation of the outputs by looking at the length frequency distribution

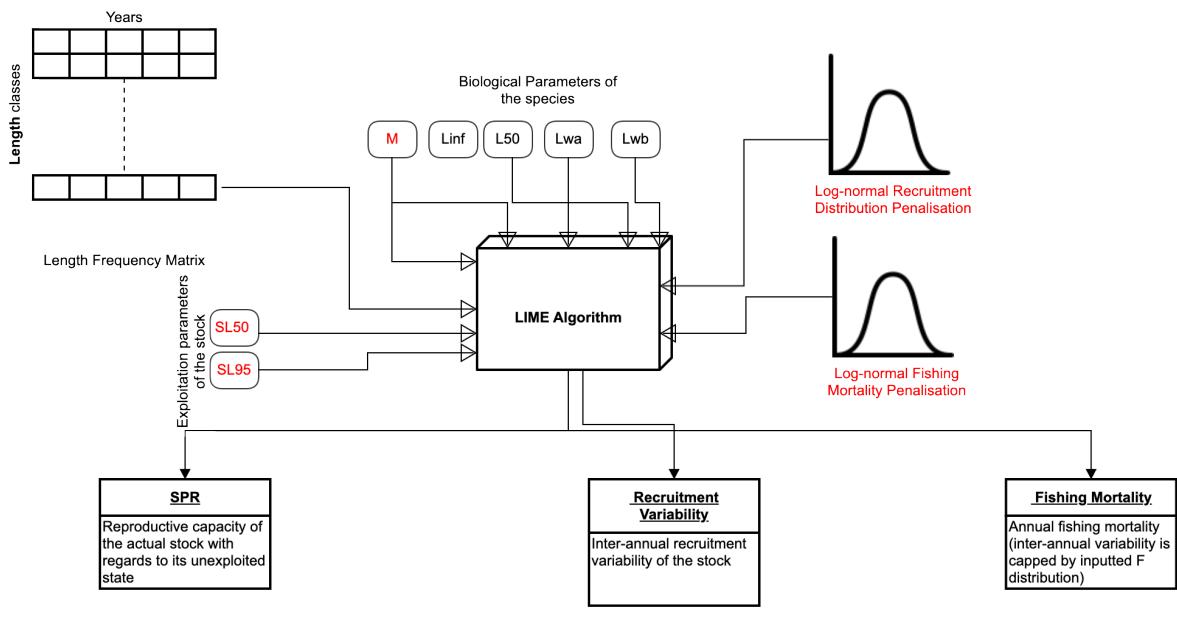


- Likewise for the LBI, the year 2001 has the highest estimated SPR, while **2021 one of the lowest**.

- Again looking at the frequency distributions below, it seems that the **right thick tale for 2001** may have something to say about why the SPR value is the highest in the whole timeseries. There seems to be a substantial set of **large individuals that are rising the average length above the L50**, therefore most likely a higher contribution to the spawning biomass.
- On the other hand, given that the SPR is estimated based on the F/M, **low estimates of F/M** would yield **high estimates of SPR**.

11. LIME algorithm

11.1 Lime Overview



Minimum threshold: > 0.3 Equilibrium condition $= 1$ $\uparrow F \rightarrow \downarrow SPR$

Desired threshold: > 0.4 Maximum value $= 2$

Lime is a fully **age-structure** length-based mixed effects model that **does not assume equilibrium**. To do so introduce the effect of the **recruitment variability as a random effect**. It also has extra parameterisation requirements:

- **M**: Natural mortality
- **SL50 and SL95**: exploitation parameters concerning the length at 50% and 95% selectivity. The mean of the **outputs of LBSPR** for selectivity are **inputted into LIME**.
- **Recruitment variability** (log-normal): to account for recruitment as a **random effect** in the outputs and **delimit** the estimated recruitment variability.
- **Fishing mortality** (log-normal): to cap the estimated inter-annual fishing mortality **avoiding** so to derail to and produce **unexpected values**.

Lime outputs are:

- **SPR**
- Actual inter-annual **fishing mortality** as opposed to a relative score like in LBSPR.
- **Recruitment variability**: equilibrium = 1. The maximum value allowed is twice the equilibrium ($<=2$).
- SPR is calculated as a function of **F**, hence the lower F the higher the **SPR** is.

Important:

- The **recruitment variability** prior was obtained from a meta-analysis study involving **154 species**. The mean and standard deviation in this example is the one available at **order level** instead of species-level or even better, stock-level.
- The standard deviation of fishing mortality has been set to the default one: **0.2** (log-normal)

11.2 Run LIME

```
In [ ]: exp_params$s50 <- mean(lbspr_results$estimates$SL50)
exp_params$s95 <- mean(lbspr_results$estimates$SL95)
exp_params$sigmaF <- 0.2
lime_algo <- Lime$new(bio_params, exp_params, catch_weight_data)
lime_results <- lime_algo$run()
```

```
In [24]: data <- lime_results$estimates
data$years <- lime_results$years
data
```

A data.frame: 24 × 9

SL50	SL95	SPR	F	Recruitment	max_gradient	hessian	convergence	years
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<lgl>	<lgl>	<int>
33.07792	40.79524	0.4682300	0.7549956	0.3763214	2.134293e-12	TRUE	TRUE	1999
33.07792	40.79524	0.5070027	0.6050539	0.6953288	2.134293e-12	TRUE	TRUE	2000
33.07792	40.79524	0.5112497	0.5909107	1.0264104	2.134293e-12	TRUE	TRUE	2001
33.07792	40.79524	0.4801454	0.7045254	1.0700896	2.134293e-12	TRUE	TRUE	2002
33.07792	40.79524	0.4735839	0.7317840	0.9502202	2.134293e-12	TRUE	TRUE	2003
33.07792	40.79524	0.4572295	0.8056324	0.6732046	2.134293e-12	TRUE	TRUE	2004
33.07792	40.79524	0.4452236	0.8658611	0.7099721	2.134293e-12	TRUE	TRUE	2005
33.07792	40.79524	0.4336046	0.9296885	0.8067454	2.134293e-12	TRUE	TRUE	2006
33.07792	40.79524	0.4197551	1.0138647	1.6088450	2.134293e-12	TRUE	TRUE	2007
33.07792	40.79524	0.4097004	1.0812257	1.2440893	2.134293e-12	TRUE	TRUE	2008
33.07792	40.79524	0.4044273	1.1188853	1.0227436	2.134293e-12	TRUE	TRUE	2009
33.07792	40.79524	0.3850498	1.2729559	1.1359815	2.134293e-12	TRUE	TRUE	2010
33.07792	40.79524	0.3878819	1.2487693	1.2143307	2.134293e-12	TRUE	TRUE	2011
33.07792	40.79524	0.3938324	1.1998861	1.3385019	2.134293e-12	TRUE	TRUE	2012
33.07792	40.79524	0.4000078	1.1517757	0.8901760	2.134293e-12	TRUE	TRUE	2013
33.07792	40.79524	0.4049413	1.1151398	1.3582575	2.134293e-12	TRUE	TRUE	2014
33.07792	40.79524	0.4025809	1.1324753	0.6611948	2.134293e-12	TRUE	TRUE	2015
33.07792	40.79524	0.4035527	1.1252959	1.3222478	2.134293e-12	TRUE	TRUE	2016
33.07792	40.79524	0.4014552	1.1408666	0.9945268	2.134293e-12	TRUE	TRUE	2017
33.07792	40.79524	0.3924713	1.2108432	0.5787236	2.134293e-12	TRUE	TRUE	2018
33.07792	40.79524	0.3797198	1.3201755	0.3312320	2.134293e-12	TRUE	TRUE	2019

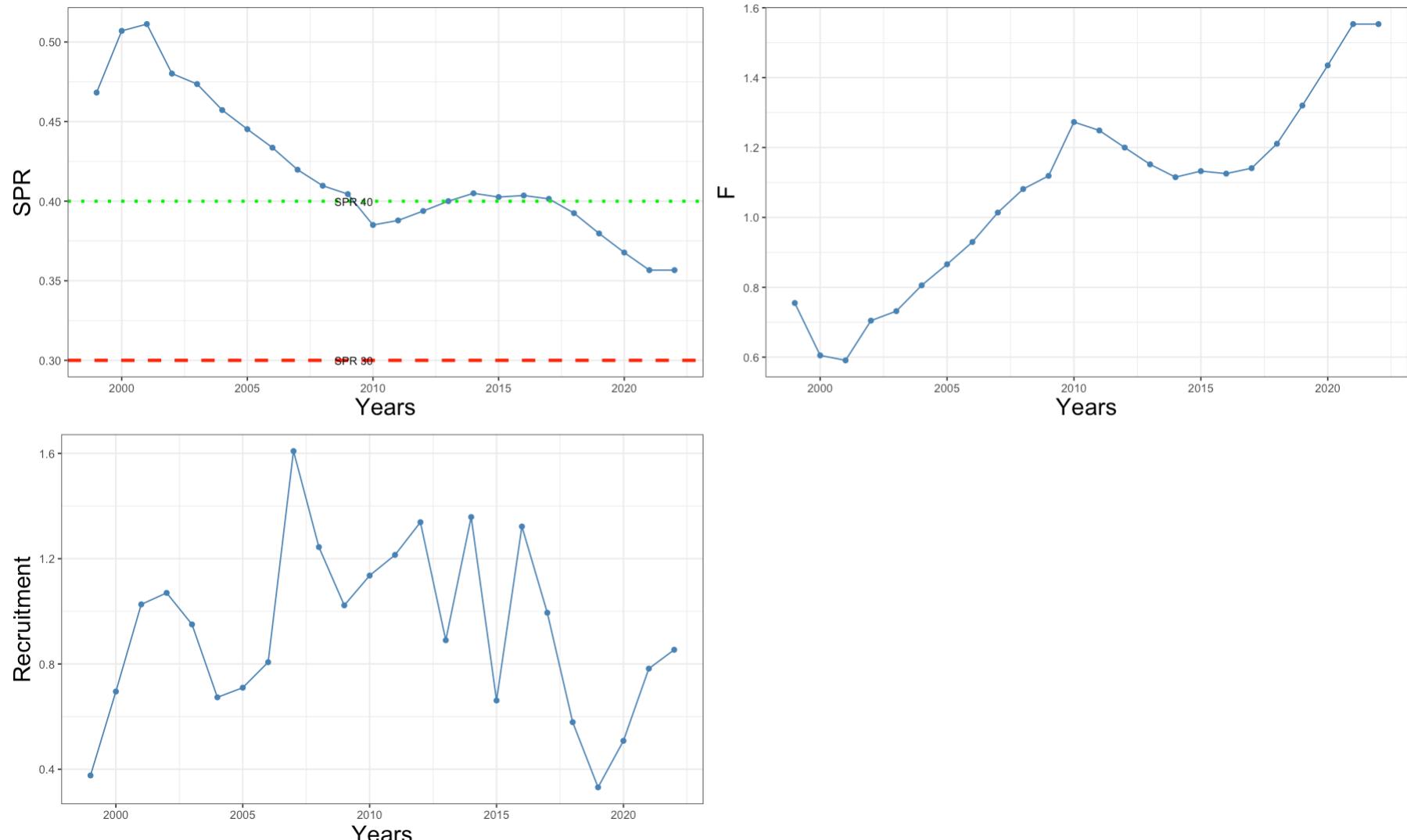
SL50	SL95	SPR	F	Recruitment	max_gradient	hessian	convergence	years
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<lgl>	<lgl>	<int>
33.07792	40.79524	0.3677394	1.4350852	0.5080519	2.134293e-12	TRUE	TRUE	2020
33.07792	40.79524	0.3566783	1.5532487	0.7822646	2.134293e-12	TRUE	TRUE	2021
33.07792	40.79524	0.3566783	1.5532487	0.8539276	2.134293e-12	TRUE	TRUE	2022

- **Along the columns** are laid the **outputs** that the algorithm has estimated
- **Each cell** for each row provides the value for a **single output per year**.

11.3 LIME plotting

```
In [25]: options(repr.plot.width = 15, repr.plot.height = 10)
lime_plotter <- LimeOutputPlotter$new(data)
grid <- lime_plotter$generate_outputs(title_size=22, title = "SPR, F and Recruitment estimates for LIME")
grid
```

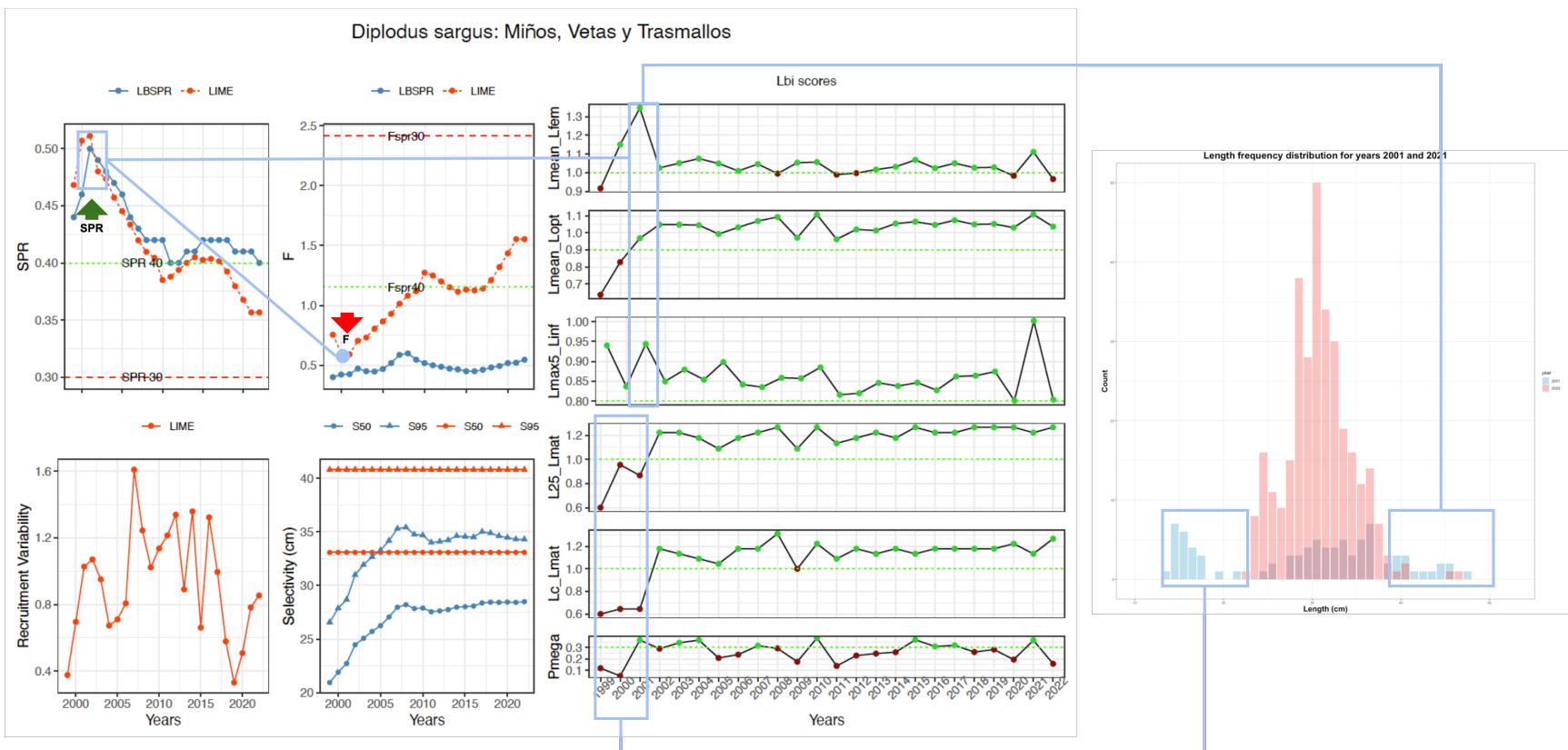
SPR, F and Recruitment estimates for LIME



- On the top left, the estimated **SPR** is **no longer above 0.4** line all the time. LIME seems to be a little bit more pesimist.
- Again 2001 the **highest SPR**
- On the top right, the **F** estimates follow a **see-saw** pattern with regards to the SPR.

- Hard to interpret the recruitment variability without knowing more about the biology of the species. For example, what's the lag that a recruitment for the fisheries could become a recruitment for spawning biomass.

12. LBI, LBSPR and LIME outputs combined



- It seems that LBI, LBSPR AND LIME agree that when **SPR** is the highest, roughly so occurs for the **adult conservation**.
- However LBI nonetheless, issues a **warning** about the **juvenile conservation** in the first years of the timeseries even

though with high SPR scores.

- **Selectivity** for LIME is estimated as **constant** while for LBSPR is **interannual**.
- **F/M** has been multiplied by M so that LBSPR's output can be converted to the **domain** of fishing mortality (**F**).