

Appendix 1: Cefas European lobster stock assessment methods



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Cefas Document Control

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1. General methodology

The general approach of these stock assessments is to use data from two sources, which are partially, but not fully independent. These are:

- A time series of aggregate reported landings and effort data which provide a perspective on the fishery and exploitation level
- Aggregated length distribution data, used to model length based Virtual Population Analysis (LVPA) and per recruit analysis which provides a perspective on stock and fishery status, including reference points.

There are major uncertainties in the commercially reported (landings and effort) data which vary widely through time in response to changes in the reporting and recording systems. Length sampling has varied in quality over time but provides a perspective on the stock status. However, aggregation of length distributions to annual and fishery management scale relies on commercial landings data in order to raise to the different strata, so the two data sources (landings and lengths distributions) are not truly independent.

The length-based assessment methodology assumes dynamic pool and steady state conditions which are frequently violated but provides a snapshot of stock and fishery status, as well as trends over time. As well as the consideration of the steady state snapshots, time series of simple length-based metrics and outputs from assessments (average F and reference point trends) provide an indication of trends in the length-based characteristics of the fisheries. The Virtual Population Analysis (VPA) model is applied to aggregated length distributions individually by sex and averaged over three years to smooth out inter-annual variability.

High levels of uncertainty in the data and violations of methodological assumptions mean the assessments should be considered as providing evidence that is broadly indicative of status rather than precise.

1.1 Biological parameters

Biological parameters used in the assessments are based on the best available data and are reviewed periodically (Table 1).

Length-weight relationship

Length-weight relationship parameters are applied using the standard relationship

$$w = al^b$$

where w is weight, l is length or in the case of lobsters carapace length (CL) and a and b are the parameters.

Proportion mature

Maturity is modelled using a logistic relationship

$$p = 1 - 1 * (1 + ae^{(b*l)})^{-1}$$

where p is the proportion mature and a and b are the parameters.

Fecundity

Fecundity is modelled as a function of size

$$f=aCL-b$$

where the parameters $a = 217.74$ and $b = 12490.3$ (Hepper & Gough, 1978). Linear and logarithmic functions were considered but these provided negative fecundity when the model was extrapolated beyond the available data and down to sizes where maturity was evident.

Natural mortality

Natural mortality is poorly quantified for European lobster and the parameters used for assessment are therefore highly uncertain. Unfortunately, the length structured VPA and per recruit analysis are highly sensitive to the level of natural mortality used.

Estimates of annual natural mortality of crabs and lobsters reported in the literature range from 5% to 50% of the population. However, natural mortality is difficult to observe directly, and a range of different evidence is required.

A temperature and growth rate empirical formula (Pauly, 1980) gives maturity-based formula generally higher natural mortality estimates than longevity based estimates. It should be remembered that the empirical formulae have generally been derived from fish rather than invertebrates and rarely from crustaceans. Sparre *et al.* (1989) explicitly warn against the use of Pauly's (1980) formula for crustaceans. It should further be noted that natural mortality in lobsters is highly likely to be size structured due to the direct consequence of size in relation to predation rates and because moulting may induce direct mortality. Lobsters are particularly vulnerable when moulting and this process is also size structured. However, at the present time, determining a constant value for natural mortality is difficult without the additional complexity of realistically structuring this according to size.

Natural mortality is estimated as 0.15 for the current assessments. Further work to improve knowledge and quantification of natural mortality for lobsters should be developed. This should explore the use of existing data, as well as developing new directed data collection programmes.

Growth

Growth is probabilistic, based on moult probability and moult increment. Although reference aged data for lobsters are available, these are generally limited to relatively young lobsters, so extrapolation well beyond the range of the data is used to predict the age of older animals. Growth data for the older part of crustacean populations are particularly lacking, because intermoult periods are long and this causes additional problems for both tagging and aquarium experiments. The key problems with data obtained from aquarium studies relate to the artificial environment and whether observed growth reflects what would occur under natural conditions, while differential tag loss during moulting and tag loss and over extended intermoult periods (where variable reporting rates may also occur) are critical difficulties with tagging programmes.

Several authors have presented lipofuscin based age and growth studies for European lobsters and the consensus is that lipofuscin concentration is a relatively accurate age predictor for European lobster. Other authors noted that there was also a good relationship between size and age, with Uglem *et al.*, (2005).

Table 1. Parameters used in current European lobster *Homarus gammarus* assessments

Parameter	Female	Male	Source
Plus group	130mm	130mm	
Terminal exploitation rate	0.941	0.918	Recursively estimated
von Bertalanffy k	0.069-0.211	0.091-0.24	Bannister <i>et al.</i> (1983)
von Bertalanffy L _∞	150-200	150-209.25	Bannister <i>et al.</i> (1983)
Weight length a	0.001086	0.000447	Bannister <i>et al.</i> (1983)
Weight length b	2.896	3.01	Bannister <i>et al.</i> (1983)
Maturity a	-28.20609	-33.114	Best assumption on basis of current knowledge
Maturity b	0.33623	0.4642	Best assumption on basis of current knowledge
Fecundity a	0.0044	NA	Tully <i>et al.</i> , 2001
Fecundity b	3.1554	NA	Tully <i>et al.</i> , 2001
Natural mortality (all sizes)	0.15	0.15	Plausible alternatives

1.2 Length sample processing

Historically biological length samples were collected by the Marine Management Organisation (MMO), augmented by Cefas sampling in some years. In 2010 Cefas took over sample collection from the MMO. Since 2013, some IFCAs (Inshore Fisheries and Conservation Authority) have been able to provide length samples to supplement the data collected for the Cefas biological sampling programme. These samples have been included in the assessments where possible. Quality assurance is carried out on the samples selected for use in the production of length distributions. Samples from the landed component of the catch are validated before the aggregation process. Annual length distributions by sex are created for each fishery unit area using the following raising and combination procedures and the landed weight recorded on the official Integrated Fisheries System Holding (IFISH):

- Raise sample by sex to the vessel landing
- Combine samples and raise by sex to quarter, port and ICES rectangle
- Combine ports and raise by sex, quarter and ICES rectangle
- Combine rectangles to fishery units and raise by sex and quarter
- Combine quarters to annual and raise by fishery units and sex
- raise from pot landings to all gear landings

The Shellfish Association of Great Britain (SAGB) commissioned Cefas to develop a multiple indicator framework for crustacean fishery assessment and management under their Shellfish Industry Development Strategy (SIDS) programme. R scripts to interrogate the database, aggregate length distributions and carry out the length-based stock assessments were developed as part of this Seafish/Defra funded work, resulting in a more automated process for conducting the length-based stock assessments. Changes to the process include modifications to aggregation procedure for lobsters, as detailed above, but also includes checks to exclude the use of small samples. These specify that at each level stratum the length distribution must contain a minimum of 10 individuals and that the raising factor to be applied to it must not exceed 1000, if it is to be included in further raising. These constraints are intended to limit the use of unrepresentative samples that could be raised substantially to give biased aggregate length distributions.

1.3 Length based VPA

Length based cohort analysis (Jones, 1981; 1984) produces estimates of abundance and fishing mortality at length given growth parameters, assumptions regarding natural mortality and a catch length frequency distribution from a population assumed to be at equilibrium. The duration of time spent in each length class is calculated using the growth parameters. Although estimates of the population number entering each length class can be made using Pope's cohort analysis approximation (Sparre *et al.*, 1989), in these assessments the catch equation was solved numerically. The process continues recursively estimating fishing mortality and numbers backwards along the 'pseudo-cohort', or numbers in each length class. The model can be summarised using the catch equations modified to take account of the time spent in each length class,

$$N_{l+1} = N_l e^{-(F+M)\delta t}$$

and

$$C_l = N_l \frac{F}{(F+M)} \left(1 - e^{-(F+M)\delta t}\right)$$

or using Pope's mid-year approximation

$$N_l = \left(N_{l+1} e^{(M/2)\delta t} + C_l\right) e^{(M/2)\delta t}$$

where N is population numbers, F is fishing mortality, M is natural mortality, l is an index indicating length class and δt is the time spent in a length class, given after manipulation of the von Bertalanffy growth equation by

$$\delta t = \frac{1}{K} \ln \left(\frac{L_\infty - L_1}{L_\infty - L_2} \right)$$

where L_1 and L_2 are the upper and lower limits of the length class, L_∞ is the asymptotic length of a fish and K a growth parameter determining how rapidly fish approach the asymptotic length.

Mean annual population numbers are calculated using

$$\overline{N}_{l,l+1} \Delta t = \frac{N_l - N_{l+1}}{Z}$$

This equilibrium method has been criticised as a poor alternative to age-structured VPA (Lai & Gallucci, 1988; Hilborn & Walters, 1992), but does still provide a useful method for estimating a length structured exploitation pattern which can be subsequently used for per recruit analyses (Smith & Addison, 2003).

1.4 Fishing mortality and spawning stock biomass

Time series of fishing mortality and spawning stock biomass estimates and reference levels are derived from the time series of LVPAs.

Average fishing mortalities (Fbars) are estimated by averaging fishing mortality at length over a range of length classes. Two estimates are produced, a wide Fbar taken as the average over most length classes above the MLS and a narrow Fbar taken as the average of F at length over a few length classes just above the MLS. Inclusive ranges are provided below. The wide size range is used in the assessment model.

Fishery management unit	Narrow Fbar size range	Wide Fbar size range
Northumberland and Durham	86mm-96mm	86mm-120mm
Yorkshire Humber	86mm-96mm	86mm-126mm
East Anglia	86mm-96mm	86mm-126mm
Southeast South Coast	86mm-96mm	86mm-126mm
Southwest	86mm-96mm	86mm-126mm

Spawning stock biomass (SSB) is calculated by summing (over length classes) the product average annual population numbers from the LVPA, maturity and weight at length.

Proxy MSY levels are derived from 35% virgin spawner per recruit (SPR) reference points. Hence $F_{35\%VirginSPR}$ is used as the proxy F_{MSY} reference level for fishing mortality, while the proxy for SSB_{MSY} is derived by taking the product of the most recent 35%VirginSPR estimate and multiplying this by mean recruitment (population numbers recruiting to the first (modelled) size class). Both arithmetic and geometric means were considered, with the latter chosen as it provided more stability to outliers that sometimes occurs. Recruitment observations are frequently log normally distributed, hence the geomean might be appropriate to describe the likely outcome of a recruitment, however SSB is a variable made up of many recruitments and this together with long term considerations might be better represented by the arithmetic mean.

1.5 Yield, spawner and egg per recruit

The yield per recruit (YPR) model (Beverton & Holt, 1957) works by assuming an arbitrary number of recruits and projecting them forward based on fishing and natural mortality to estimate numbers in each size class during the lifetime of the cohort. Numbers are subsequently divided by the number of recruits to obtain the 'per recruit' estimates. Weight, proportion mature and fecundity by size are applied to estimate yield, SSB or number of eggs by size class, which are summed over all classes. Per recruit models have been extensively used for crustacean fisheries.

The length-based yield per recruit model may be summarised

$$YPR = \sum_{l=FirstLength}^{LastLength} e^{-\sum_{i=FirstLength}^{l-1} (F_i + M_i) \delta t_i} Wt_l \frac{F_l}{F_l + M_l} (1 - e^{-(F_l + M_l) \delta t_l}) + YPR_{PG}$$

where F is fishing mortality, M is natural mortality, Wt is average weight for a length class, l is an index indicating length class and δt is the time spent in a length class. The yield in the plus group (YPR_{PG}) may be treated simplistically since δt tends to infinity and all fish will die before reaching L infinity. However, if the final length class is far below L infinity this will lead to under estimation of the yield in this length class.

For length-based spawner and egg per recruit (SPR and EPR) the mean number of animals present in the population over a given year (for the time period δt) are estimated in order to adjust for annual periodicity of spawning. Spawner or egg per recruit for a given fishing

mortality pattern and level (e.g. F_{sq}) are often expressed as a percentage of the SPR or EPR that would result if no fishing took place (virgin SPR or virgin EPR).

Plotting the values of YPR, SPR or EPR against a range of F multipliers (on the exploitation pattern) produces a family of curves from which various reference points can be estimated. These include F_{max} , the fishing mortality at which YPR is maximised and $F_{0.1}$, the F at which the slope of the YPR curve is 0.1 of the slope at the origin, and a more conservative reference point. These reference points reflect the influence of growth, natural mortality and fishing mortality pattern and level on equilibrium yield.

The spawner and egg per recruit reference points are often used as conservation limits or targets as they reflect the influence of maturity and fecundity as well as growth, natural mortality, fishing mortality pattern and level on equilibrium spawning biomass or egg production. They do not take account of stock recruitment relationships (SRRs), which are difficult to estimate, but provide an indication of stock resilience. However, meta-analyses for a wide range of fish stocks, where stock recruitment relationships (SRRs) were 'known', have indicated that resilience was positively related to body size, which is a proxy for fecundity, longevity and low M (Mace and Sissenwine, 1993). Such species require a lower proportion of virgin SPR (or EPR) to maintain their populations. $F_{35\%VirgSPR}$ was suggested as a default that achieves at least 75% of MSY over a wide range of SRRs (Clark, 1991), but taking account of empirical estimates (Mace, 1991; Mace and Sissenwine, 1993) and recruitment variability (Clark, 1993), Mace (1994) suggested that $F_{40\%VirgSPR}$ is a more robust proxy for F_{MSY} . $F_{10\%VirgEPR}$ and $F_{25\%VirgEPR}$ have been suggested as potential limit and target reference points, respectively, for the Irish lobster fishery (Tully *et al.*, 2006) and $F_{15\%VirgEPR}$ has been suggested as a recommended limit level.

1.6 Operational assumptions and constraints applied to the assessment methodology.

Averaging length frequencies over years

Prior to the length-based assessment, length frequencies are averaged over the 3 most recent years. The length distribution is delimited by the maximum length classes sampled in any of these years and length classes not present in some years are treated as zero frequencies rather than missing values.

Plus group

Plus groups are defined to take account of the size range of animals generally occurring in the different regions. Automated scripting (in R) is used to truncate the length distribution (lower the plus group) if the frequency in the nominal plus group is zero.

Mean weight in the plus group was taken using the same offset as for other size classes rather than interpolating between the plus group size and L_{∞} . This reflects the fact that most individuals occur in the lower portion of the plus group and will also reduce effects due to accumulation of individuals in the plus group, which can cause problems in per recruit analyses.

Terminal exploitation rate

Terminal exploitation rate is estimated using a single recursive iteration. In the first instance it is set to 0.5 and a length based VPA is run. F at length is averaged over all length classes between 90mm and the 2 length classes below the plus group. This value is used along with M to calculate a new terminal exploitation rate which is fed into the length based VPA. Using the average over this wide range may tend to produce a terminal F that is quite high and

reduce doming in the exploitation pattern. However, LVPA generally converges quickly and is relatively insensitive to this parameter.

Introducing leading zeros for small size classes

Spawning potential per recruit reference points are frequently expressed as percentage of virgin spawning potential. A proportion of the population may mature before recruitment to the fishery, so in order to properly represent percentage of virgin spawning potential this should be taken into account. Size classes with zero catch frequencies are therefore introduced for small sized animals not captured in the fishery down to a size where a very small proportion will be mature. This enables the full extent of the spawning potential to be assessed, taking both the level of fishing and exploitation pattern into account.

2. Stock and fishery identity

Stock boundaries for lobster are poorly understood. Little is known about the larval distribution and consequently the main sources of recruitment. Catches of lobsters are distributed mainly in coastal waters and lobsters are generally considered fairly sedentary, however some inshore/offshore and longshore migration may take place.

Significant lobster fisheries occur in a number of areas, which can be geographically defined and may be separated by areas with lower levels of landings. Eight areas have therefore been defined for the purpose of fishery monitoring and assessment (Table 2).

Table 2. Lobster fishery districts (LFD's) in England and Wales

LFD	Name	Approximate borders
1	Northumberland and Durham	Scottish border to river Tees
2	Yorkshire/Humber	River Tees to river Humber
3	Lincolnshire (60t 2007, not assessed)	River Humber to The Wash
4	East Anglia	The Wash to river Thames
6	Southeast and south coast	River Thames to Lyme Bay
7	Southwest	Lyme Bay to Bristol Channel

Fishery units (FUs) are currently defined on the basis of port of landing for lobsters.

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