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The lobster stock dynamics (LSD) model

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EXECUTIVE SUMMARY

Webber, D.N.¹; Rudd, M.B.²; Starr, P.J.³; Roberts, J.⁴; Pons, M.³ (2023). The lobster stock dynamics (LSD) model.

New Zealand Fisheries Assessment Report 2023/11. 28 p.

This document describes the lobster stock dynamics (LSD) model: a size-structured model specifically designed for developing stock assessments of red rock lobsters (*Jasus edwardsii*) in New Zealand. The LSD model tracks the numbers of individuals in discrete size classes for three different sex / maturity categories (i.e., males, immature females, and mature females). The model can be used to develop single-area or multi-area stock assessment models. The LSD model was coded in Stan, setting it apart from most other stock assessment models. The Stan language was developed specifically for Bayesian inference and uses the Hamiltonian Monte Carlo algorithm – a Markov chain Monte Carlo method that uses the derivatives of the density function being sampled to help generate efficient transitions. This document serves as a reference for the model and provides potential users with an understanding of the model by presenting the equations related to the model code.

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1. INTRODUCTION

This document describes the lobster stock dynamics (LSD) model: a size-structured model specifically designed for developing stock assessments of red rock lobsters (*Jasus edwardsii*), and for use as an operating model in management procedure evaluation (MPE). Although this software was specifically designed for modelling New Zealand red rock lobster stocks, it could potentially be used for length based modelling of other species with similar life histories and fishing fleet dynamics (e.g., packhorse rock lobster, *Sagmariasus verreauxi*) if enough data are available. This document serves as a reference for the model and provides potential users with an understanding of the model by presenting the equations implemented in the model code. A summary of model options available at the time of publication is provided in Appendix A.

The LSD model is a size-structured model that tracks the numbers of individuals in discrete size classes for three different sex / maturity categories (hereafter referred to as sex categories). These categories include males, immature females, and mature females. For instance, during any given fishing year⁵ (or season within a year), the model stores an estimate of the number of individuals within each sex category that are at least 30 mm tail width (TW) but less than 32 mm TW. This is referred to as the 30 to 32 mm size class and is represented mathematically as $[30, 32)$ ⁶.

The model can be used to develop single-area or multi-area size-structured stock assessment models (model areas are frequently referred to as ‘regions’). In New Zealand, for example, a single-area red rock lobster stock assessment model can be developed for any defined Quota Management Area (QMA) or stock (e.g., the CRA 2 stock assessment by Rudd et al. in prep.); or a multi-area assessment for more than one QMA or stock (e.g., the CRA 7 and CRA 8 stock assessment by Webber et al. 2022). Alternatively, a multi-area assessment can be developed for a single stock, by specifying multiple model areas within the stock, such as defined by statistical areas or some combination of statistical areas (e.g., the CRA 3 and CRA 5 stock assessments by Webber et al. 2020 and Webber et al. 2021). Spatial models can be constructed with or without movement between model areas (using estimated or fixed parameters) and many parameters can be shared among model areas or can be specific to each area.

The LSD model can be informed by several different data types including:

- tag-recapture data for estimating growth;
- abundance indices such as catch per unit effort (CPUE);
- size compositions of the catch for each sex category (i.e., length frequency or LF);
- sex ratios of the catch; and
- recruitment strength indices (e.g., puerulus indices or other indices of temporal recruitment variability, such as annual SST).

Catch is also an important input to the LSD model but is treated differently to data because the catch is assumed to be without error (i.e., catch is treated as a covariate). The full list of covariates that can be used to inform the LSD model include:

- the size limited (SL) and non-size limited (NSL) catch;
- the handling mortality rate;
- the minimum legal size (MLS);
- the proportion of mature females in berry;
- the proportion of individuals retained by fishers when considering other forms of retention (e.g., high grading, return of soft-shelled lobsters);
- the size at first measurement of tagged individuals and the time spent at liberty prior to recapture;

⁵ A fishing year is defined as 1 April to 31 March of the following year.

⁶ The notation $z \in [x, y]$ means that a random variable z can take any value between x and y inclusive; $[x, y)$ means that a random variable is at least x but less than y ; $(x, y]$ means that a random variable is greater than x and can be at most y ; and (x, y) means that a random variable can take any value between x and y , but not x or y .

- the standard deviations of any abundance indices, recruitment indices, the length frequencies, and the sex ratios; and
- the proportion of individuals moving between model areas.

The covariates and data that inform New Zealand red rock lobster stock assessments implemented using LSD are documented elsewhere (Table 1). A general reference for New Zealand red rock lobster covariates and data can be found in the annual Fisheries New Zealand stock assessment Plenary report (Fisheries New Zealand 2021). The input data and methods used in their preparation are fully documented for all recently completed red rock lobster stock assessments (e.g., Starr et al. 2022).

Table 1: Summary of data and covariates used by LSD stock assessments of red rock lobsters, the source of these inputs, and some relevant references.

Input	Source	Reference
Commercial catch	Introductory red rock lobster chapter of Fisheries New Zealand (2022)	Bentley et al. (2005)
Non-commercial catch (i.e., recreational, illegal, and customary)	Rock lobster chapters of Fisheries New Zealand (2022)	Fisheries New Zealand (2022)
Historical daily catch rate (CR)	1963–1973 catch/effort data	Annala & King (1983)
Standardised CPUE indices	pre-1989 Fisheries Statistics Unit (FSU) data Fisheries New Zealand statutory catch and effort data	Bentley et al. (2005) Starr (2022)
Size and sex compositions of the catch	Voluntary logbook programme data	Webber & Starr (2022)
	Observer catch sampling data	<i>rlcs – schema a</i> ⁷
	Voluntary logbook programme data	<i>rlcs – schema b</i> ⁸
Tag recapture observations	Commercial and recreational tag recovery data	<i>tag.pdf</i> ⁹
Recruitment indices	Puerulus settlement and environmental data	Fisheries New Zealand (2022)

The LSD model was coded in Stan (Stan Development Team 2016, 2017), setting it apart from most other stock assessment models. The Stan language was developed specifically for Bayesian inference and uses the Hamiltonian Monte Carlo (HMC) algorithm (Duane et al. 1987). HMC is a Markov chain Monte Carlo (MCMC) method that uses the derivatives of the density function being sampled to help generate efficient transitions. This enables efficient MCMC mixing, which is advantageous when dealing with highly correlated model parameters, as will typically be the case for stock assessment models. In contrast, most other stock assessment models use less efficient MCMC algorithms, such as Metropolis-Hastings (Metropolis et al. 1953, Hastings 1970).

The LSD model was described briefly by Webber et al. (2018a). It was used alongside the 2016 CRA 4 stock assessment that used the multi-stock length-based model (MSLM) (Breen et al. 2017), during which time extensive testing and model validation were done between the LSD model and the MSLM (Haist et al. 2009). At the same time, an exploratory multi-area CRA 4 assessment was developed (Webber et al. 2018a). The LSD model was the primary software used for the 2017 CRA 2 stock assessment, with MSLM serving as a comparison (Webber et al. 2018b). The LSD model has been used exclusively for all New Zealand red rock lobster stock assessments since 2017.

⁷ <https://marlin.niwa.co.nz/files/dataHoldings/scientificResearchDbs/rlcs.pdf>

⁸ https://marlin.niwa.co.nz/files/dataHoldings/scientificResearchDbs/rlcs_b.pdf

⁹ <https://marlin.niwa.co.nz/files/dataHoldings/scientificResearchDbs/tag.pdf>

2. MODEL EQUATIONS

All model dimensions, or subscripts used in equations, are provided in Table 2. Parameters that can be estimated are indicated in red throughout the document (Table 3). Any of these parameters can be fixed. Parameters that are always fixed and covariates are indicated in blue throughout the document (Table 4 and Table 5). Observations, or data, are indicated in orange throughout the document (Table 6). Other variables and derived quantities referred to in this document are defined in Table 7.

Table 2: Model dimensions or subscripts used in equations.

Symbol	Definition	Description
i	Individual	An individual animal where $i = 1, \dots, n$
j	Abundance index	An abundance index series (e.g., CR, FSU, CELR, and/or logbook CPUE)
y	Fishing year	1 April to 31 March the following year where $y = 1, \dots, Y$
t	Season	There are one or two seasons each year. The number of seasons each year is specified using τ_y . The seasons are referred to as spring/summer (SS) and autumn/winter (AW) when two seasons are specified
r	Region	Could refer to a QMA (e.g., CRA 1, CRA 2, ...), a statistical area (e.g., 901, 902, ..., 942, 943), or a combination of statistical areas
s	Sex	male, immature female, or mature female
l	Size class	$\{[30, 32), [32, 34), \dots, [90, \infty)\}$

Table 3: Parameters that can be estimated or fixed within the model.

Symbol	Support	Units	Description
R_0	> 0	–	Average number of recruits
δ_y^R	$\in (-\infty, \infty)$	–	Recruitment deviations (in log space)
M	> 0	yr ⁻¹	Natural mortality
U_0	≥ 0	–	Initial exploitation rate
G_s^α	> 0	mm	Growth at α
G_s^d	> 0	mm	$G_s^d = G_s^\beta / G_s^\alpha$ where G_s^β is the growth at β
G_s^γ	> 0	–	Shape of the growth model
c_s	> 0	–	Process error (coefficient of variation) for growth increments
σ_o	> 0	mm	Observation error (standard deviation) for growth increments
μ^m	> 0	mm	Size at 50% female maturation
κ^m	> 0	mm	Steepness of the female maturation curve
$\mu_{y,s}^s$	> 0	mm	Size at 50% selectivity
$\gamma_{y,s}^s$	> 0	mm	Steepness of the left-hand limb of the selectivity curve
$\sigma_{y,s}^s$	> 0	mm	Steepness of the right-hand limb of the selectivity curve
$v_{y,t,s}$	$\in (0, 1)$	–	Relative vulnerability (i.e., analogous to the height of a selectivity curve)
q_j^{CPUE}	> 0	tonnes ⁻¹	Catchability for each abundance index
q^R	> 0	–	Catchability for the recruitment index
$\varphi_{r,y}$	≥ 0	–	Proportion moving by region and year

Table 4: Fixed parameters and data set weights.

Symbol	Default value	Units	Description
a_s	varies by stock – see Fisheries New Zealand (2022) ¹⁰	mm	Length-weight scalar
b_s	varies by stock – see Fisheries New Zealand (2022) ¹⁰	kg	Length-weight exponent
α	30 to 50	mm	Size for which G_s^α is calculated
β	80	mm	Size for which G_s^β is calculated
σ_{\min}	0.0001	mm	Minimum standard deviation of growth increment at each size class
μ_ϕ^R	32	mm	Mean recruitment size
σ_ϕ^R	2.0	mm	Standard deviation of recruitment size
σ_R	0.4	–	Recruitment standard deviation
q^{drift}	0.01	–	Rate of change of catchability for the abundance index
λ^{tag}	1.0	–	Tag-recapture data set weight
λ_j^{CPUE}	found iteratively	–	Abundance index data set weight
λ^R	found iteratively	–	Recruitment index data set weight
λ_s^{LF}	found iteratively	–	Proportions in the catch at size data set weight
λ^{sex}	found iteratively	–	Sex ratio data set weight

Table 5: Covariates.

Symbol	Support	Units	Description
$C_{y,t}^{\text{SL}}$	≥ 0	tonnes	Size limited (SL) catch by year and season
$C_{y,t}^{\text{NSL}}$	≥ 0	tonnes	Non-size limited (NSL) catch by year and season
h_y	$[0, 1]$	–	Handling mortality rate each year
$\vartheta_{y,t,s,l}$	$[0, 1]$	–	Legal status (i.e., MLS) by year, season, sex, and size class
$\varsigma_{y,t}$	$[0, 1]$	–	Proportion of mature females that are in berry by year and season
$\varrho_{y,l}$	$[0, 1]$	–	Proportion of lobsters retained resulting from non-retention by year and size class (e.g., high-grading, return of soft-shelled lobsters)
L_i^1	≥ 0	mm	Size at first measurement (i.e., size when first tagged for individual)
δ_i	≥ 0	years	Time at liberty for each tagged individual
$\sigma_{j,y,t}^{\text{CPUE}}$	≥ 0	tonnes	Standard deviation of the abundance index by year and season for each series
σ_y^R	≥ 0	–	Standard deviation of the recruitment index by year
$\sigma_{y,t,s}^{\text{LF}}$	≥ 0	–	Standard deviation of the proportion of the catch from each size class by year, season, and sex
$\sigma_{y,t}^{\text{sex}}$	≥ 0	–	Standard deviation of the sex ratio in the catch each year and season
$\psi_{s,l}$	$[0, 1]$	–	Proportion moving by sex and size class

Table 6: Observations.

Symbol	Support	Units	Description
L_i^2	≥ 0	mm	Size at second measurement (i.e., size when recaptured)
$I_{j,y,t}^{\text{CPUE}}$	≥ 0	tonnes per potlift	Abundance index (e.g., CPUE) by year and season for each series
I_y^R	≥ 0	–	Recruitment index (e.g., puerulus index or SST index) by year
$(P_l)_{y,t,s}$	$[0, 1]$	–	Proportion at length by year, season, and sex category
$(X_s)_{y,t}$	$[0, 1]$	–	Proportion in each sex category by year and season

¹⁰ Specifically, see table 11, Introduction – Red Rock Lobster (CRA) of Fisheries New Zealand (2022).

Table 7: Other model specifications and derived quantities.

Symbol	Support	Units	Description
τ_y	{1, 2}	–	Number of time steps within each year
ℓ_l	≥ 0	mm	Mid-point of each size class
$w_{s,l}$	≥ 0	tonnes	Weight of each size class
m_l	[0, 1]	–	Maturation curve (i.e., logistic)
$s_{y,t,s,l}$	[0, 1]	–	Selectivity curve (e.g., logistic or double normal)
$\eta_{y,t,s,l}$	[0, 1]	–	The combination of selectivity ($s_{y,t,s,l}$) and vulnerability ($v_{y,t,s}$)
$y_{y,t,s,l}$	[0, 1]	–	Legal status
$\bar{F}_{y,t}^{SL}$	≥ 0	–	Fishing mortality for the SL fishery by year and season
$\bar{F}_{y,t}^{NSL}$	≥ 0	–	Fishing mortality for the NSL fishery by year and season
$\bar{U}_{y,t}^{SL}$	≥ 0	–	Exploitation rate for the SL fishery by year and season
$\bar{U}_{y,t}^{NSL}$	≥ 0	–	Exploitation rate for the NSL fishery by year and season
R_l	[0, 1]	–	Proportion recruiting to each size class
R_y	≥ 0	–	Number of recruits each year
$R_{y,l}$	≥ 0	–	Number of recruits to each size class (l) each year (y)
ρ_R	≥ 0	–	Recruitment autocorrelation
$SSB_{y,t}$	≥ 0	tonnes	Spawning stock biomass (SSB) each year and season
SSB_0	≥ 0	tonnes	Unfished SSB in the autumn/winter season
B_0	≥ 0	tonnes	Unfished vulnerable biomass in the autumn/winter season
$B_{y,t}$	≥ 0	tonnes	Vulnerable biomass each year and season
$B_{y,t}^a$	≥ 0	tonnes	Adjusted vulnerable biomass each year and season
$T_{y,t}$	≥ 0	tonnes	Total biomass each year and season
H_y	≥ 0	tonnes	Handling mortality each year (i.e., the sum of AW and SS handling mortality)

2.1 Size classes

An l is used to subscript a size class and ℓ_l to define the midpoint (mm) of size class l . Generally, the model includes 31 size classes with midpoints ranging from 31 to 90 mm in 2 mm bin widths, thus $l = \{[30, 32), [32, 34), \dots, [90, \infty)\}$, where the size class $[30, 32)$ includes individuals (i) that are $30 \leq i < 32$ mm, and the size class $[90, \infty)$ includes individuals that are $90 \leq i < \infty$ mm. The final size class is often referred to as the ‘plus group’ and is an aggregate of all individuals within the final size class and larger. The plus group can be increased (or decreased) to accommodate stocks with larger individuals. This was done for CRA 6 (Starr et al. 2019) where the plus group was set to 120 mm and CRA 7&8 (Starr et al. 2022) with a 100 mm plus group. The LSD model tracks numbers of individuals by fishing year (y), season (t), region (r), sex (s), and size class (l). We denote the number of individuals in each category mathematically as

$$N_{y,t,r,s,l} \text{ where } N_{y,t,r,s,l} \in (0, \infty)$$

Generally, each model year contains only one season before 1979 because data limitations preclude accurate temporal placement of the data. From 1979 onwards, each model year is split in two seasons: autumn/winter (AW) and spring/summer (SS). There are three sex categories in the model including: males, immature females, mature females. Throughout most of this document the region (r) subscript has been omitted for clarity.

2.2 Weight

The sex-specific average weight (in tonnes) of all individuals in a size class is denoted $w_{s,l}$ and is calculated using the sex-specific parameters of the length-weight relationship (a_s and b_s , with units in kilograms) and the midpoint of each size class (ℓ_l)

Equation 1:
$$w_{s,l} = \frac{a_s \ell_l^{b_s}}{1000} \quad \text{where } w_{s,l} \in (0, \infty)$$

2.3 Maturation

A logistic maturation curve specifies the proportion of the immature female individuals by size class that become mature within a time step

Equation 2:
$$m_l = 1/1 + \exp\left(-\frac{\log(19)}{\kappa^m(\ell_l - \mu^m)}\right) \quad \text{where } m_l \in [0, 1]$$

The parameters μ^m and κ^m define the curves midpoint and steepness, respectively. Key references for the maturation of New Zealand red rock lobsters include MacDiarmid (1989), Annala et al. (1980), and Booth (1984).

2.4 Selectivity, vulnerability, legal status, and retention

The probability of catching an animal of size l , or selectivity, is year (y), season (t), sex (s), and size class (l) specific and is denoted as $s_{y,t,s,l}$ where $s_{y,t,s,l} \in [0, 1]$. Selectivity can be logistic or double-normal (see APPENDIX B).

Vulnerability refers to the relative scaling of the selectivity curves (i.e., the height of the selectivity curve) by year (y), season (t), and sex (s) and is denoted $v_{y,t,s}$. The vulnerability for one of the sexes within a season is fixed to a value of one¹¹ and the remaining vulnerability parameters are estimated to be between zero and one, thus $v_{y,t,s} \in [0, 1]$. The combination of selectivity ($s_{y,s,l}$) and vulnerability ($v_{y,t,s}$) is year, season, sex, and size class specific and is denoted $\eta_{y,t,s,l}$

Equation 3:
$$\eta_{y,t,s,l} = \begin{cases} s_{y,t,s,l} \sum_t v_{y,t,s} / 2 & \text{if 1 season} \\ s_{y,t,s,l} v_{y,t,s} & \text{if 2 seasons} \end{cases} \quad \text{where } \eta_{y,t,s,l} \in [0, 1]$$

The death of an individual due to fishing comes in two forms: an individual is captured and retained; or an individual is captured then discarded and dies due to handling effects. An individual may be discarded for several reasons. For example, many invertebrate fisheries impose minimum legal size (MLS) limits that stipulate individuals that are below this MLS must be returned to the water. For red rock lobster individuals are discarded due to:

- sex-specific MLS restrictions;
- egg bearing (berried) females must be returned to the water;
- soft-shelled lobsters must be returned to the water;
- commercial high-grading¹².

¹¹ This should be the sex/season category with the greatest vulnerability.

¹² High-grading is the practice of retaining high value individuals and returning lower value individuals to the water. For example, generally higher prices are paid per kg for smaller red rock lobster than larger individuals.

To account for retention and discarding, we define retention ($\zeta_{y,t,s,l}$) as the probability of retaining an individual by year (y), season (t), sex (s), and size class (l). Retention includes any legal status rules such as MLS by year, season, sex, and size class ($\vartheta_{y,t,s,l}$), the proportion of mature females that are in berry by year and season ($\varsigma_{y,t}$), and any information on other forms of retention (e.g., high-grading or return of soft-shelled lobsters) by year, sex, and size class ($Q_{y,s,l}$)

Equation 4:
$$\zeta_{y,t,s,l} = \vartheta_{y,t,s} \varsigma_{y,t} Q_{y,s,l}$$

The voluntary logbook programme collects information about high-grading in lobsters and is considered in all stock assessments. The observer catch sampling programme collects information about moult status (i.e., hard shell or soft shell) but the return of soft-shelled lobsters has not been considered in past assessments.

2.5 Recruitment

All current New Zealand red rock lobster stock assessments assume there is no stock-recruit relationship. Stock-recruit relationships for all species are difficult to quantify without evaluating the stock at a wide range of depletion levels. This relationship is particularly uncertain for spiny lobsters (Palinuridae) due to their long larval stage with dispersal over large areas, and the probable sensitivity to environmental conditions of larval dispersal, rates of puerulus settlement, and mortality processes affecting lobsters prior to recruitment to the fishery. Thus, the LSD model assumes recruitment occurs in each year (y) and season (t) and is spread normally across several size classes (l) according to R_l

Equation 5:
$$r_l = \exp\left(-\frac{(\ell_l - \mu_\phi^R)^2}{\sigma_\phi^R}\right)$$

$$R_l = \frac{r_l}{\sum_l r_l} \text{ where } \sum_l R_l = 1$$

where μ_ϕ^R and σ_ϕ^R are the mean and standard deviation of recruitment size (in mm). Recruitment each year is defined as

Equation 6:
$$R_y = R_0 \exp\left(\delta_y^R - \frac{\sigma_R^2}{2}\right) \text{ where } R_y \in (0, \infty)$$

where R_0 is the mean number of recruits over all modelled years, δ_y^R represents the logarithm of the deviation from this mean each year (defined in Equation 33 in Section 3.1), and σ_R is the standard deviation of recruitment deviations. The recruitment to each size class each year, season, and size class is

Equation 7:
$$R_{y,t,l} = R_y R_l \frac{1}{\tau_y} \text{ where } R_{y,t,l} \in (0, \infty)$$

2.6 Natural mortality, fishing mortality, and handling mortality

Natural mortality (M) is assumed to be constant across all size classes and sexes in the current LSD model parameterisation. Sex-specific natural mortality and functional forms to account for variability in M across size classes could be added in the future. Uncertainty in natural mortality has been explored in recent LSD red rock lobster assessments, but is confounded with other parameters such that more detailed parameterisations of M may not be parsimonious.

There are two different types of rock lobster fisheries operating: the size limited (SL) fishery which is subject to input controls (MLS and no taking of berried females) and the non-size limited (NSL) fishery

that ignores these regulations. The SL fishery includes the commercial and recreational catch. The NSL fishery includes the illegal and customary catch. The catch (tonnes) taken during year and season in each of these fisheries is denoted $C_{y,t}^{SL}$ and $C_{y,t}^{NSL}$, respectively. A handling mortality rate (h_y) is applied to those fish that are discarded (i.e., caught and returned to the water, see Equation 11 and Equation 16). These catches and handling mortalities are removed from the model in one of two ways: instantaneous fishing mortalities (Section 2.6.1) or exploitation rates (Section 2.6.2).

2.6.1 Instantaneous fishing mortality

Fishing mortalities associated with catch by the SL and NSL fisheries are denoted $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$, respectively. The combination of selectivity and vulnerability ($\eta_{y,t,s,l}$), retention ($\zeta_{y,t,s,l}$), and handling mortality (h_y) is used to translate $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ into $F_{y,t,s,l}^{SL}$, $F_{y,t,s,l}^{NSL}$, $F_{y,t,s,l}^{Handling}$, and $F_{y,t,s,l}^{LF}$

Equation 8:

$$\begin{aligned} F_{y,t,s,l}^{SL} &= \bar{F}_{y,t}^{SL} \eta_{y,t,s,l} \zeta_{y,t,s,l} \\ F_{y,t,s,l}^{NSL} &= \bar{F}_{y,t}^{NSL} \eta_{y,t,s,l} \\ F_{y,t,s,l}^{Handling} &= \bar{F}_{y,t}^{SL} \eta_{y,t,s,l} (1 - \zeta_{y,t,s,l}) h_y \\ F_{y,t,s,l}^{LF} &= \bar{F}_{y,t}^{SL} \eta_{y,t,s,l} \end{aligned}$$

The total mortality is

Equation 9:

$$Z_{y,t,s,l} = F_{y,t,s,l}^{SL} + F_{y,t,s,l}^{NSL} + F_{y,t,s,l}^{Handling} + M \tau_y$$

where M is natural mortality and τ_y is one divided by the number of time steps (i.e., number of seasons) in each year. Total mortality is then removed from the model using

Equation 10:

$$N_{y,t+1,s,l} = N_{y,t,s,l} e^{-Z_{y,t,s,l}}$$

The catch associated with the SL and NSL fisheries, the mortality that is associated with the SL fishery due to handling, and the catch that is associated with the size frequencies are

Equation 11:

$$\begin{aligned} C_{y,t}^{SL} &= \sum_{s,l} \left[\frac{F_{y,t,s,l}^{SL}}{Z_{y,t,s,l}} (1 - e^{-Z_{y,t,s,l}}) N_{y,t,s,l} W_{s,l} \right] \\ C_{y,t}^{NSL} &= \sum_{s,l} \left[\frac{F_{y,t,s,l}^{NSL}}{Z_{y,t,s,l}} (1 - e^{-Z_{y,t,s,l}}) N_{y,t,s,l} W_{s,l} \right] \\ C_{y,t}^{Handling} &= \sum_{s,l} \left[\frac{F_{y,t,s,l}^{Handling}}{Z_{y,t,s,l}} (1 - e^{-Z_{y,t,s,l}}) N_{y,t,s,l} W_{s,l} \right] \\ C_{y,t,s,l}^{LF} &= \frac{F_{y,t,s,l}^{SL}}{Z_{y,t,s,l}} (1 - e^{-Z_{y,t,s,l}}) N_{y,t,s,l} \end{aligned}$$

There is no closed-form equation for the Baranov catch equation to solve for $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ given the other parameters, so this equation must either be solved numerically (Pope's approximation, Pope 1972, or the Newton-Raphson algorithm, Press 2007) or by treating $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ as estimated parameters and the catches as observations with small standard deviations (so that the estimated catches are close to the observed catches). The LSD model uses the Newton-Raphson method for finding the values of $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ and this algorithm is provided in Appendix C. Treating $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ as estimated parameters was tested in the past but resulted in poor MCMC performance.

2.6.2 Exploitation rate

Exploitation rates associated with catch by the SL and NSL fisheries are denoted $\bar{U}_{y,t}^{SL}$ and $\bar{U}_{y,t}^{NSL}$, respectively. These exploitation rates are defined as

Equation 12:

$$\bar{U}_{y,t}^{SL} = C_{y,t}^{SL} / \sum_{s,l} N_{y,t,s,l} \eta_{y,t,s,l} \zeta_{y,t,s,l} W_{s,l}$$

$$\bar{U}_{y,t}^{NSL} = C_{y,t}^{NSL} / \sum_{s,l} N_{y,t,s,l} \eta_{y,t,s,l} W_{s,l}$$

The following constraint is imposed for $\bar{U}_{y,t}^{SL}$ and $\bar{U}_{y,t}^{NSL}$

$$\bar{U}_{y,t}^{SL} + \bar{U}_{y,t}^{NSL} \leq U^{\max}$$

where $U^{\max} = 0.99$. The combination of selectivity and vulnerability ($\eta_{y,t,s,l}$), retention ($\zeta_{y,t,s,l}$) (i.e., MLS, proportion of berried females, high-grading), and handling mortality (h_y) is used to translate $\bar{U}_{y,t}^{SL}$ and $\bar{U}_{y,t}^{NSL}$ into $U_{y,t,s,l}^{SL}$, $U_{y,t,s,l}^{NSL}$, $U_{y,t,s,l}^{\text{Handling}}$, and $U_{y,t,s,l}^{LF}$

Equation 13:

$$U_{y,t,s,l}^{SL} = \bar{U}_{y,t}^{SL} \eta_{y,t,s,l} \zeta_{y,t,s,l}$$

$$U_{y,t,s,l}^{NSL} = \bar{U}_{y,t}^{NSL} \eta_{y,t,s,l}$$

$$U_{y,t,s,l}^{\text{Handling}} = \bar{U}_{y,t}^{SL} \eta_{y,t,s,l} (1 - \zeta_{y,t,s,l}) h_y$$

$$U_{y,t,s,l}^{LF} = U_{y,t}^{SL} \eta_{y,t,s,l}$$

The total exploitation rate is

Equation 14:

$$U_{y,t,s,l} = U_{y,t,s,l}^{SL} + U_{y,t,s,l}^{NSL} + U_{y,t,s,l}^{\text{Handling}}$$

Total mortality is then removed from the model using

Equation 15:

$$N_{y,t+1,s,l} = N_{y,t,s,l} (1 - U_{y,t,s,l}) e^{-M\tau_y}$$

The mortality that is associated with the SL fishery due to handling and the catch that is associated with the size frequencies are

Equation 16:

$$C_{y,t}^{\text{Handling}} = \sum_{s,l} U_{y,t,s,l}^{\text{Handling}} N_{y,t,s,l} W_{s,l}$$

$$C_{y,t,s,l}^{LF} = U_{y,t,s,l}^{LF} N_{y,t,s,l}$$

2.7 Growth

2.7.1 Growth increment model

The growth increment of individual i between the time of tagging and recapture is represented as g_i . The growth increment depends on the initial size of the individual (L_i^1) and the time at liberty (δ_i) and can be calculated as the size at second measure (L_i^2) minus the size at first measure (L_i^1)

$$g_i = L_i^2 - L_i^1$$

In reality, L_i^1 and L_i^2 cannot be directly observed. Instead, $L_i^1 + \varepsilon_i^1$ and $L_i^2 + \varepsilon_i^2$ are observed, where ε_i^1 and ε_i^2 represent the respective observation errors, thus

$$g_i = (L_i^2 + \varepsilon_i^2) - (L_i^1 + \varepsilon_i^1)$$

Considering both observation and process error

$$g_i = (L_i^2 + \varepsilon_i^p + \varepsilon_i^2) - (L_i^1 + \varepsilon_i^1)$$

We can only observe $L_i^1 + \varepsilon_i^1$ and $L_i^2 + \varepsilon_i^p + \varepsilon_i^2$, therefore L_i^1 and L_i^2 are unobservable and should be estimated. However, inference becomes intractable if trying to estimate L_i^1 and L_i^2 for every individual as well as all of the other estimated model parameters (especially within a stock assessment). Instead, the error is combined into a single term

$$g_i = L_i^2 - L_i^1 + \varepsilon_i^p + \varepsilon_i^2 - \varepsilon_i^1 = L_i^2 - L_i^1 + \varepsilon_i$$

but in doing so, our ability to estimate the variance components (observation and process error) accurately is compromised.

The size at second measure (L_i^2) can be modelled conditional on L_i^1 , the time at liberty δ_i , and some estimated model parameters (Θ) thus

$$g_i = f(L_i^2 | L_i^1, \delta_i, \Theta) - L_i^1$$

In the LSD model, the growth increment is modelled using the Schnute-Francis growth model (Francis 1995, a modification of Schnute 1981)

$$g_i = \left((L_i^1)^{G_s^Y} e^{-k\delta_i} + \frac{\beta^{G_s^Y} - \alpha^{G_s^Y} \left((\beta + G_s^\beta)^{G_s^Y} - \beta^{G_s^Y} \right) / \left((\alpha + G_s^\alpha)^{G_s^Y} - \alpha^{G_s^Y} \right)}{1 - \left((\beta + G_s^\beta)^{G_s^Y} - \beta^{G_s^Y} \right) / \left((\alpha + G_s^\alpha)^{G_s^Y} - \alpha^{G_s^Y} \right)} (1 - e^{-k\delta_i}) \right)^{\frac{1}{G_s^Y}} - L_i^1 + \varepsilon_i$$

Equation 17: where

$$k = \log \left(1 - \frac{\left((\alpha + G_s^\alpha)^{G_s^Y} - \alpha^{G_s^Y} \right) - \left((\beta + G_s^\beta)^{G_s^Y} - \beta^{G_s^Y} \right)}{\beta^{G_s^Y} - \alpha^{G_s^Y}} \right)$$

where the error term (ε_i) includes both observation and process error. Observation error is represented as a standard deviation σ_o and process error as a coefficient of variation c_s and the two errors are combined as

$$\text{Equation 18:} \quad \sigma_i = \sqrt{\frac{\min(c_s g_i, \sigma_{\min}^2)}{\delta_i} + \sigma_o^2}$$

2.7.2 Size transition matrix

Moving fish between size classes due to growth is done using an $n \times n$ growth matrix \mathbf{G}

$$\text{Equation 19:} \quad \mathbf{G} = G_{l,l'} = \begin{pmatrix} G_{1,1} & G_{1,2} & \cdots & G_{1,n} \\ G_{2,1} & G_{2,2} & \cdots & G_{2,n} \\ \vdots & \vdots & \ddots & \vdots \\ G_{n,1} & G_{n,1} & \cdots & G_{n,n} \end{pmatrix} \quad \text{where} \quad \sum_{l'}^n G_{l,l'} = 1 \quad \forall l$$

$G_{l,l'}$ represents the proportion of fish growing from the size class l to size class l' and has the property $G_{l,l'} \geq 0$. A year (y), season (t), and sex (s) specific size transition matrix ($\mathbf{G}_{y,t,s}$) defines the probability that an individual of length l will grow to size l' within a time step

$$\Pr(l \rightarrow l') = \mathbf{G}_{y,t,s} = G_{y,t,s,l,l'}$$

This is derived by first defining the expected length $\mathbb{E}[x_l]$ of an animal of midpoint ℓ_l one time step later as

Equation 20:
$$\mathbb{E}[x_l] = \mu_l = \ell_l + \bar{\Delta}_l$$

where $\bar{\Delta}_l$ is the predicted growth increment for an individual of length ℓ_l given the time step. Stochasticity is incorporated for an individual of midpoint ℓ_l by assuming that its size (x_l) one time step later can be modelled as a normal distribution

Equation 21:
$$N(x_l | \mu_l, \sigma_l) = \frac{1}{\sqrt{2\sigma_l^2\pi}} \exp\left(-\frac{(x_l - \mu_l)^2}{2\sigma_l^2}\right) \quad \text{where} \quad \sigma_l = \mu_l c_s$$

with expected size $\mathbb{E}[x_l] = \mu_l$ and variance $\mathbb{V}[x_l] = \sigma_l$. If a and b are the two ends of the size class l' , the growth transition probabilities (from size class l to size class l') can be computed and placed in the growth transition matrix

Equation 22:
$$\mathbf{G}_{y,t,s} = P_{l',l} = \int_a^b N(x_l | \mu_l, \sigma_l) dx_l$$

2.8 Movement

Movement, or migration, has been documented for red rock lobsters around New Zealand (Annala 1981, McKoy 1983, Street 1995, Kelly & MacDiarmid 2003). In LSD, movement is modelled by specifying the direction of movements and the size classes by sex that move ($\psi_{s,l}$). The proportion of individuals that move each year for each region is estimated ($\phi_{r,y}$). The number of individuals moving from region r to region r' is calculated and applied as

Equation 23:
$$\begin{aligned} N_{y,t,s,l} &= N_{y,t,s,l} - N_{y,t,s,l} \psi_{s,l} \phi_{r,y} \\ N_{y,t,r',s,l} &= N_{y,t,r',s,l} - N_{y,t,s,l} \psi_{s,l} \phi_{r,y} \end{aligned}$$

2.9 Initial conditions

The initial (or equilibrium) number in each size class for each sex depends on average unfished recruitment (R_0), natural mortality (M), the initial exploitation rate (U_0), the recruitment size (R_l), the maturation ogive (m_l), and the size transition matrix ($\mathbf{G}_{y,t,s}$) and is represented as $N_{s,l}^0$. The initial numbers are calculated by first defining

Equation 24:
$$\begin{aligned} N_{s,l}^0 &= 0 \quad \forall s, l \\ N_{s,l}^t &= 0 \quad \forall s, l \\ R_l^0 &= R_0 R_l \tau_y \quad \text{where } y = 1 \\ \mathbf{Z}_{t,s} &= \left(1 - U_0 \zeta_{y,t,s,l} \eta_{y,t,s,l}\right) e^{-M\tau_y} \mathbf{G}_{y,t,s} \quad \text{where } y = 1 \end{aligned}$$

then looping over each season to calculate

$$\begin{aligned}
& N_{s,l}^t = N_{s,l}^t \mathbf{Z}_{t,s} \\
\text{Equation 25: } & m_l^0 = N_{s,l}^t m_l \tau_y \quad \text{where } s = 2 \\
& N_{s,l}^t = N_{s,l}^t - m_l^0 \quad \text{where } s = 2 \\
& N_{s,l}^t = N_{s,l}^t + m_l^0 \quad \text{where } s = 3 \\
& N_{s,l}^t = R_l^0 \quad \text{where } y = 1, s = 1, s = 2
\end{aligned}$$

Finally for many iterations (usually 50 is sufficient) loop over each season and calculate

$$\begin{aligned}
& N_{s,l}^0 = N_{s,l}^0 + N_{s,l}^t \\
& N_{s,l}^t = N_{s,l}^t \mathbf{Z}_{t,s} \\
\text{Equation 26: } & m_l^0 = N_{s,l}^t m_l \tau_y \quad \text{where } s = 2 \\
& N_{s,l}^t = N_{s,l}^t - m_l^0 \quad \text{where } s = 2 \\
& N_{s,l}^t = N_{s,l}^t + m_l^0 \quad \text{where } s = 3
\end{aligned}$$

The initial numbers are then used in the model by specifying

$$N_{y,t,s,l} = N_{s,l}^0 \quad \text{where } y = 1, t = 1$$

2.10 Population dynamics

First, the initial conditions are calculated (see Section 2.9). The LSD model then does the following calculations for each year and season:

1. removes animals due to natural mortality and fishing (see Section 2.6);
2. applies growth (see Section 2.7);
3. applies maturation (see Section 2.3);
4. applies movement, if specified (see Section 2.8); and
5. adds new recruits (see Section 2.5).

Once the population dynamics are done, the model calculates the biomass (see Section 2.11 below) and then evaluates the priors and likelihoods (see Section 3 below).

2.11 Biomass

Several measures of biomass are calculated by the model including the spawning stock biomass (*SSB*), vulnerable biomass, adjusted vulnerable biomass, and total biomass. All of these are measured in tonnes. The *SSB* each year and season ($SSB_{y,t}$) and the unfished *SSB* (SSB_0) are

calculated as

$$\begin{aligned}
& SSB_{y,t} = \sum_l N_{y,t,s,l} w_{s,l} \quad \text{where } s = 3 \\
\text{Equation 27: } & SSB_0 = \sum_l N_{s,l}^0 w_{s,l} \quad \text{where } s = 3
\end{aligned}$$

Vulnerable biomass each year and season ($B_{y,t}$) is calculated as

$$\text{Equation 28: } B_{y,t} = \sum_{s,l} N_{y,t,s,l} w_{s,l} \eta_{y,t,s,l} \gamma_{y,t,s,l} e^{-0.5Z_{y,t,s,l}}$$

while adjusted vulnerable biomass each year and season ($B_{y,t}^a$) are calculated as

Equation 29:

$$B_{y,t}^a = \sum_{s,l} N_{y,t,s,l} W_{s,l} \eta_{y=Y,t,s,l} \gamma_{y=Y,t,s,l} e^{-0.5Z_{y,t,s,l}}$$

where $\eta_{y=Y,t,s,l} \gamma_{y=Y,t,s,l}$ represents the combination of selectivity, vulnerability, and legal status in the final model year (Y). Finally, the total biomass each year and season ($T_{y,t}$) is calculated as

Equation 30:

$$T_{y,t} = \sum_{s,l} N_{y,t,s,l} W_{s,l}$$

3. INFERENCE

We are interested in the probabilistic relationship between the following:

- The **data**: the size of tagged individuals at recapture (L_i^2), the abundance indices ($I_{y,t}^{\text{CPUE}}$), the proportion of the catch at size for each sex ($(P_l)_{y,t,s}$), the sex ratios of the catch ($(X_s)_{y,t}$), and the recruitment indices (I_y^R). Let

$$Y = \{L_i^2, I_{y,t}^{\text{CPUE}}, I_y^R, (P_l)_{y,t,s}, (X_s)_{y,t}\}$$

- The **covariates**: the catch ($C_{y,t}^{\text{SL}}$ and $C_{y,t}^{\text{NSL}}$), the handling mortality associated with the SL catch (h_y), the size at initial capture and the time at liberty of tagged individuals (L_i^1 and δ_i), and the standard deviations of the abundance index observations, length frequency observations, sex ratio observations, and puerulus index observations ($\sigma_{y,t}^{\text{CPUE}}$, σ_y^{LF} , and $\sigma_{y,t}^{\text{sex}}$, and σ_y^R). Let

$$\Phi = \{C_{y,t}^{\text{SL}}, C_{y,t}^{\text{NSL}}, h_y, L_i^1, \delta_i, \sigma_{y,t}^{\text{CPUE}}, \sigma_y^{\text{LF}}, \sigma_{y,t}^{\text{sex}}, \sigma_y^R\}$$

- The **estimated parameters**: the average recruitment (R_0), the recruitment deviations (δ_y^R), the natural mortality (M), the initial exploitation rate (U_0), the growth parameters (G_s^α , G_s^d , G_s^γ , c_s , and σ_o), the maturation parameters (μ^m and κ^m), the selectivity parameters ($\gamma_{y,s}^s$ and $\mu_{y,s}^s$), the vulnerability parameters ($v_{y,t,s}$), the abundance index catchability coefficient (q^{CPUE}), and the settlement index (e.g., puerulus or SST) proportionality coefficient (q^R). Let

$$\Theta = \{R_0, \delta_y^R, M, U_0, G_s^\alpha, G_s^d, G_s^\gamma, c_s, \sigma_o, \mu^m, \kappa^m, \gamma_{y,s}^s, \mu_{y,s}^s, v_{y,t,s}, q^{\text{CPUE}}, q^R\}$$

- The **fixed parameters**: the parameters of the length-weight relationship (a_s and b_s), the growth parameters (α and β), the recruitment size parameters (μ_ϕ^R and σ_ϕ^R), the standard deviation of recruitment deviations (σ_R), the parameter describing the change in the catchability coefficient through time (q^{drift}), and the data set weights (λ^{tag} , λ^{CPUE} , λ^R , λ_s^{LF} , and λ^{sex}). Let

$$\Omega = \{a_s, b_s, \alpha, \beta, \mu_\phi^R, \sigma_\phi^R, \sigma_R, q^{\text{drift}}, \lambda^{\text{tag}}, \lambda^{\text{CPUE}}, \lambda^R, \lambda_s^{\text{LF}}, \lambda^{\text{sex}}\}$$

Using Bayes' theorem, the posterior distribution of the model parameters (Θ), given the data (Y), fixed parameters (Ω), and covariates (Φ), is

$$\pi(\Theta|Y, \Omega, \Phi) \propto \pi(\Theta|\Omega)\pi(Y|\Theta, \Omega, \Phi)$$

where $\pi(\Theta|\Omega)$ is the prior and $\pi(Y|\Theta, \Omega, \Phi)$ is the likelihood.

3.1 Prior

The prior is

$$\begin{aligned} \pi(\Theta|\Omega) &= \pi(R_0, \delta_y^R, M, U_0, v_{y,t,s}, \mu^m, \kappa^m, G_s^\alpha, G_s^d, G_s^y, c_s, \sigma_o, \gamma_{y,s}^s, \mu_{y,s}^s, q^{\text{CPUE}}, q^R|\Omega) \\ \text{Equation 31:} \quad &= \pi(R_0)\pi(\delta_y^R|\sigma_R)\pi(M)\pi(U_0)\pi(v_{s,t})\pi(\mu^m)\pi(\kappa^m)\pi(G_s^\alpha)\pi(G_s^d)\pi(G_s^y) \\ &\quad \times \pi(c_s)\pi(\sigma_o)\pi(\gamma_{y,s}^s)\pi(\mu_{y,s}^s)\pi(q^{\text{CPUE}})\pi(q^R) \end{aligned}$$

Generally, for New Zealand red rock lobster stock assessments, priors are not applied to R_0 , q^{CPUE} , and q^R (i.e., a uniform prior between the parameter bounds is assumed), so the prior can be simplified to

$$\begin{aligned} \text{Equation 32:} \quad \pi(\Theta|\Omega) &= \pi(\delta_y^R|\sigma_R)\pi(M)\pi(U_0)\pi(v_{y,t,s})\pi(\mu^m)\pi(\kappa^m) \\ &\quad \times \pi(G_s^\alpha)\pi(G_s^d)\pi(G_s^y)\pi(c_s)\pi(\sigma_o)\pi(\gamma_{y,s}^s)\pi(\mu_{y,s}^s) \end{aligned}$$

The prior for the recruitment deviations (δ_y^R) is always

$$\text{Equation 33:} \quad \delta_y^R \sim N(0, \sigma_R^2)$$

For all parameters that are bounded to be between 0 and 1, a flat Beta prior is advised

$$\begin{aligned} U_0 &\sim \text{Beta}(1, 1) \\ v_{y,t,s} &\sim \text{Beta}(1, 1) \\ G_s^d &\sim \text{Beta}(1, 1) \end{aligned}$$

Uninformative normal priors with large standard deviations are specified for the maturation and selectivity parameters. The maturation priors are

$$\begin{aligned} \mu^m &\sim N(50, 15) \\ \kappa^m &\sim N(10, 10) \end{aligned}$$

The selectivity priors are different depending on the type of selectivity curve assumed (i.e., logistic or double-normal) and these priors are described in Appendix B. The remaining priors for the other model parameters differ from assessment to assessment, but common priors are outlined below.

A mixture of uninformative and informative priors are specified for the growth parameters. These priors are based on a growth meta-analysis (Webber unpublished) and are generally set to

$$\begin{aligned} G_s^\alpha &\sim N(2, 30) \\ G_s^y &\sim N(4.81, 1) \\ G_s^y &\sim N(4.51, 1) \\ c_s &\sim N(0.59, 1) \\ c_s &\sim N(0.82, 1) \\ \sigma_o &\sim N(1.48, 0.074) \end{aligned}$$

Finally, an informative prior is specified for natural mortality

$$M \sim \log N(0.12, 0.4)$$

3.2 Data set weighting

Data set weights include the tag-recapture weight λ^{tag} , the abundance index weight λ_j^{CPUE} for each series, the puerulus index weight λ^R , the size composition weight λ^{LF} , and the sex ratio weight λ^{sex} . Their purpose is to specify the relative likelihood weight among the various data sets in the model. Their

use in the model is described in Section 3.3. These are all fixed parameters that can be updated iteratively by inspecting the standard deviation of normalised residual (SDNR, which should be close to 1) or median absolute residual (MAR, which should be close to 0.67), or using the Francis iterative weighting method (Francis 2011).

3.3 Likelihood

The full likelihood is the product of the likelihood components for the tags, abundance indices, recruitment indices, size compositions, and sex ratios. The full likelihood is defined as

$$\begin{aligned} \pi(\mathbf{Y}|\Theta, \Omega, \Phi) &= \prod_i \pi(L_i^2|\Theta, \Omega, \Phi) \prod_{j,y,t} \pi(I_{j,y,t}^{\text{CPUE}}|\Theta, \Omega, \Phi) \prod_y \pi(I_y^{\text{R}}|\Theta, \Omega, \Phi) \\ \text{Equation 34:} \quad &\times \prod_{y,t,s} \pi((Pl)_{y,t,s}|\Theta, \Omega, \Phi) \prod_{y,t} \pi((X_s)_{y,t}|\Theta, \Omega, \Phi) \end{aligned}$$

Each of these components is expanded below.

3.3.1 Tags

The likelihood for the tags can be expanded to

$$\begin{aligned} \prod_i \pi(L_i^2|\Theta, \Omega, \Phi) &= \prod_i \pi(L_i^2|L_i^1, \delta_i, G_s^\alpha, G_s^d, G_s^\gamma, c_s, \sigma_o, \lambda^{\text{tag}}) \\ \text{Equation 35:} \quad \bar{\sigma}_i^{\text{tag}} &= \sigma_i \times \frac{1}{\lambda^{\text{tag}}} \\ \varepsilon_i &\sim \text{N}\left(0, (\bar{\sigma}_i^{\text{tag}})^2\right) \end{aligned}$$

where the growth model is described in Equation 17 and the standard deviation (σ_i) is derived in Equation 18. The error term (see Equation 17) could, for example, be assumed normally distributed with mean zero and standard deviation σ_i as shown above. In the LSD model a robust normal distribution is assumed. The tag likelihood is self-weighting and therefore λ^{tag} is always set to 1. The standardised residuals for the robust normal are defined as

$$\text{Equation 36:} \quad \frac{L_i^2 - \bar{L}_i^2}{\bar{\sigma}_i^{\text{tag}}}$$

3.3.2 Abundance indices

Expected abundance indices, such as CPUE ($I_{j,y,t}^{\text{CPUE}}$), are assumed to be proportional to either the vulnerable biomass ($B_{y,t}$) or the number of lobsters above the MLS ($N_{y,t,r,s,l} \vartheta_{y,t,s,l}$). Thus

$$\begin{aligned} \text{Equation 37:} \quad q_{j,y}^{\text{CPUE}} &= \begin{cases} q_j^{\text{CPUE}} & \text{if } y \notin S \\ q_{j,y-1}^{\text{CPUE}}(1 + q^{\text{drift}}) & \text{if } y \in S \end{cases} \\ \bar{I}_{j,y,t}^{\text{CPUE}} &= \begin{cases} q_{j,y}^{\text{CPUE}} B_{y,t} & \text{if CELR CPUE} \\ q_{j,y}^{\text{CPUE}} \sum_{s,l} N_{y,t,s,l} \vartheta_{y,t,s,l} & \text{if logbook CPUE} \end{cases} \end{aligned}$$

where q_j^{CPUE} is the catchability coefficient, q^{drift} is the rate of change of catchability for the abundance index, and S is the set of years over which q^{drift} is assumed to occur. The likelihood for the abundance indices assuming a lognormal distribution can be expanded to

$$\prod_{j,y,t} \pi(I_{j,y,t}^{\text{CPUE}} | \Theta, \Omega, \Phi) = \prod_{j,y,t} \pi(I_{j,y,t}^{\text{CPUE}} | V_{y,t}, q_j^{\text{CPUE}}, q^{\text{drift}}, \sigma_{j,y,t}^{\text{CPUE}}, \lambda_j^{\text{CPUE}})$$

Equation 38:

$$\bar{\sigma}_{y,t}^{\text{CPUE}} = \sigma_{j,y,t}^{\text{CPUE}} \times \frac{1}{\lambda_j^{\text{CPUE}}}$$

$$I_{j,y,t}^{\text{CPUE}} \sim \text{logN}(\bar{I}_{j,y,t}^{\text{CPUE}}, (\bar{\sigma}_{j,y,t}^{\text{CPUE}})^2)$$

where λ_j^{CPUE} is the data set weight. The standardised residuals for the lognormal are defined as

Equation 39:

$$\frac{\log(I_{j,y,t}^{\text{CPUE}} / \bar{I}_{j,y,t}^{\text{CPUE}})}{\bar{\sigma}_{j,y,t}^{\text{CPUE}}} + 0.5 \bar{\sigma}_{j,y,t}^{\text{CPUE}}$$

3.3.3 Recruitment indices

Booth & McKenzie (2009) identified a potential positive relationship between the annual rate of puerulus settlement, based on counts from crevice collectors and the subsequent catch rate of New Zealand red rock lobsters, when assuming suitable time lags to recruitment. Also, Breen & Starr (2010) obtained tentative evidence for positive correlations between annual sea surface temperature (SST) indices and estimated recruitment to the fished populations of some QMAs. These and other candidate indices can be included in LSD models where they are related to estimated recruitment deviates. Expected recruitment indices are assumed to be proportional to recruitment

Equation 40:

$$I_y^{\text{R}} = q^{\text{R}} R_y$$

where q^{R} is the proportionality constant. The likelihood for the recruitment indices can be expanded to

$$\prod_y \pi(I_y^{\text{R}} | \Theta, \Omega, \Phi) = \prod_y \pi(I_y^{\text{R}} | R_y, q^{\text{R}}, \sigma_y^{\text{R}}, \lambda^{\text{R}})$$

Equation 41:

$$\bar{\sigma}_y^{\text{R}} = \sigma_y^{\text{R}} \times \frac{1}{\lambda^{\text{R}}}$$

$$I_y^{\text{R}} \sim \text{logN}(\bar{I}_y^{\text{R}}, (\bar{\sigma}_y^{\text{R}})^2)$$

where λ^{R} is the data set weight. The standardised residuals for the lognormal are defined as

Equation 42:

$$\frac{\log(I_y^{\text{R}} / \bar{I}_y^{\text{R}})}{\bar{\sigma}_y^{\text{R}}} + 0.5 \bar{\sigma}_y^{\text{R}}$$

3.3.4 Proportions in the catch at size

Observed proportions in the catch at size by year (y), season (t), and sex (s) are represented as $(P_l)_{y,t,s}$. Expected proportions in the catch at size, or length frequency (LF) distributions, by year, season, and sex are represented as $(\bar{P}_l)_{y,t,s}$ and defined as

Equation 43:

$$(\bar{P}_l)_{y,t,s} = \frac{C_{y,t,s,l}^{\text{LF}}}{\sum_l C_{y,t,s,l}^{\text{LF}}} \quad \text{where} \quad \sum_l (\bar{P}_l)_{y,t,s} = 1 \quad \forall y, t, s$$

where $C_{y,t,s,l}^{\text{LF}}$ is defined in Equation 11 or $U_{y,t,s,l}^{\text{LF}}$ in Equation 16. Tail compression for size classes $l = 1, \dots, n$ results in size classes $l = a, \dots, b$ and produces in a new proportion in the catch at size variable $P'_{l=\{a,\dots,b\}}$

Equation 44:

$$\begin{aligned} P'_{l=a} &= \sum_{l=1, \dots, a} P_l \\ P'_{l=a+1, \dots, b-1} &= P_{a+1, \dots, b-1} \\ P'_{l=b} &= \sum_{l=b, \dots, n} P_l \end{aligned}$$

The likelihood component for the proportions in the catch at size is assumed to be multinomial and is written

Equation 45:

$$\begin{aligned} \prod_{y,t,s} \pi((P_l)_{y,t,s} | \Theta, \Omega, \Phi) &= \prod_{y,t,s} \pi((P_l)_{y,t,s} | (\bar{P}_l)_{y,t,s}, \sigma_{y,t,s}^{\text{LF}}, \lambda_s^{\text{LF}}) \\ &= \sum_{y,t,s} \bar{\sigma}_{y,t,s}^{\text{LF}} (P_l)_{y,t,s} \log((\bar{P}_l)_{y,t,s}) \\ \bar{\sigma}_{y,t,s}^{\text{LF}} &= \frac{1}{\sigma_{y,t,s}^{\text{LF}} \lambda_s^{\text{LF}}} \\ (P_l)_{y,t,s} &\sim \text{Multinomial}(\bar{\sigma}_{y,t,s}^{\text{LF}}, (\bar{P}_l)_{y,t,s}) \end{aligned}$$

The standardised residuals for the multinomial are defined as

Equation 46:

$$\frac{(P_l)_{y,t,s} - (\bar{P}_l)_{y,t,s}}{\sqrt{(\bar{P}_l)_{y,t,s} (1 - (\bar{P}_l)_{y,t,s}) / \bar{\sigma}_{y,t,s}^{\text{LF}}}}$$

3.3.5 Sex ratio

Observed proportions of the catch by sex, or the sex ratio, is year (y), and season (t) specific, represented by $(X_s)_{y,t}$. Expected proportions of the sex ratio are represented as $(\bar{X}_s)_{y,t}$, and defined as

Equation 47:

$$(\bar{X}_s)_{y,t} = \frac{C_{y,t,s,l}^{\text{LF}}}{\sum_l C_{y,t,s,l}^{\text{LF}}} \quad \text{where} \quad \sum_s (\bar{X}_s)_{y,t} = 1 \quad \forall y, t$$

where $C_{y,t,s,l}^{\text{LF}}$ is defined in Equation 11 or $U_{y,t,s,l}^{\text{LF}}$ in Equation 16. The likelihood component for the sex ratio observations is assumed to be multinomial and is written

Equation 48:

$$\begin{aligned} \prod_{y,t} \pi((X_s)_{y,t} | \Theta, \Omega, \Phi) &= \prod_{y,t} \pi((X_s)_{y,t} | (\bar{X}_s)_{y,t}, \sigma_{y,t}^{\text{sex}}, \lambda_s^{\text{sex}}) \\ &= \sum_{y,t} \bar{\sigma}_{y,t}^{\text{sex}} (X_s)_{y,t} \log((\bar{X}_s)_{y,t}) \\ \bar{\sigma}_{y,t}^{\text{sex}} &= \frac{1}{\sigma_{y,t}^{\text{sex}} \lambda_s^{\text{sex}}} \\ (X_s)_{y,t} &\sim \text{Multinomial}(\bar{\sigma}_{y,t}^{\text{sex}}, (\bar{X}_s)_{y,t}) \end{aligned}$$

The standardised residuals for the multinomial are defined as

Equation 49:

$$\frac{(X_s)_{y,t} - (\bar{X}_s)_{y,t}}{\sqrt{(\bar{X}_s)_{y,t} (1 - (\bar{X}_s)_{y,t}) / \bar{\sigma}_{y,t}^{\text{sex}}}}$$

3.4 Stan

LSD was coded using the Stan language. Stan is a probabilistic programming language for statistical inference written in C++ (Stan Development Team 2016, 2017). The Stan language is used to specify a Bayesian statistical model with an imperative program calculating the log probability density function. Stan can be accessed through several interfaces including the command-line and the statistical programming language R.

Stan implements gradient-based MCMC algorithms for Bayesian inference, stochastic, gradient-based variational Bayesian methods for approximate Bayesian inference, and gradient-based optimisation for penalised maximum likelihood estimation. Stan uses reverse-mode automatic differentiation to calculate gradients of the model, which is required by HMC, specifically the No-U-Turn sampler (NUTS), a variant of HMC and Stan's default MCMC engine. Stan provides an elegant solution to parameter transformations and will automatically add the Jacobian adjustments to the objective function when doing MCMC (the Jacobian adjustments are not added to the objective function when doing maximum *a posteriori*, MAP).

Stan has had limited use in fisheries, but, as demonstrated in the update from MSLM to LSD, has great potential for stock assessments (also see Monnahan et al. 2017).

3.4.1 Maximum *a posteriori* (MAP)

Because Bayesian inference requires much greater computing time than frequentist inference, we use maximum *a posteriori* (MAP) estimates to explore potential model options. MAP estimates serve as a starting point to develop a base model and other sensitivities before choosing models to bring through to MCMC.

MAP can be used to search for a base case. This can involve, for example, deciding which year to start the model, determining the LF bins for fitting, adjusting dataset weights iteratively, checking the season and sex used to set the vulnerability to 1, and deciding if the model should be a multi area model or not. Each stock assessment usually involves a range of tests and tuning before deciding on the base model. Such model development using MCMC would likely be an inefficient use of time, precluding a thorough search across a range of potential model assumptions.

MAP is also used to explore important sensitivities. Again, using the CRA 2 assessment as an example, sensitivity trials were developed using ideas from within the science team and from Rock Lobster Working Group (RLWG) feedback. After presenting results using frequentist inference, we could then choose the most important sensitivity trials to bring through to MCMC.

3.4.2 Markov chain Monte Carlo (MCMC)

Bayesian inference is used to estimate parameter uncertainty in stock assessments. LSD uses Stan to run MCMC simulations using the HMC algorithm. Generally, a total of 1000 samples from the posterior distribution are obtained by combining samples across four chains, with each chain consisting of a burn-in period of 500 discarded samples and then extracting 250 samples from the remaining 500 samples by discarding every second sample.

4. GENERATED QUANTITIES

4.1 Projections

Projections are used to examine potential effects of future catch scenarios, either in the short term (e.g., five years) or over a longer period (e.g., 30 years). Projections require assumptions to be made about the future catch levels, the future MLS, and recruitment while maintaining assumptions about model structure. LSD models use all samples from the posterior distribution for each estimated parameter to

propagate parameter uncertainty in model projection years. For each sample from the posterior, the same equations for population dynamics are applied, as described in Section 2.10. Differences between projection population dynamics and the stock reconstruction population dynamics include:

1. For each iteration, projected recruitment deviates are drawn from a lognormal distribution based on attributes of the estimated recruitment deviates over a user-specified sampling period S ; and
2. Even if q^{drift} is assumed or estimated to be greater than zero in the model, it is not applied in the projections as this may artificially inflate q_j^{CPUE} .

4.1.1 Recruitment

Recruitment deviates during the projection period (δ_y^R) are sampled from a normal distribution with fixed standard deviation (σ_R), and autocorrelation (ρ_R)

Equation 50:

$$\delta_y^R \sim N(\rho_R \delta_{y-1}^R + \bar{\delta}_S^R \sqrt{1 - \rho_R^2} \sigma_R)$$

where $\bar{\delta}_S^R$ is the mean of estimated recruitment deviates over the user-specified period S (as opposed to the mean recruitment over the full time-period (R_0) as is shown in Equation 6), and ρ_R is autocorrelation calculated from estimated recruitment deviates during the ‘data period’, the first year with length frequency data to the last year of estimated recruitment deviates (typically two years prior to the last model year). The mean recruitment period (S) is typically the last ten years of estimated recruitment deviates for short term (i.e., five-year) projections. Longer-term projections have considered recruitment deviates over the data period (the same years as are used for calculating autocorrelation). Projected recruitment is then calculated using Equation 6 and Equation 7.

4.1.2 Catch

Projected catch needs to be specified for each sector (i.e., commercial, recreational, customary, and illegal) by region, year, and season.

In the first projection year, commercial catch is known and input as a static value. After the first projection year, commercial catch follows either a static input or a management procedure (MP) which dynamically varies the commercial catch based on a pre-defined input (e.g., CPUE or vulnerable biomass). Projected commercial catch may be specified in terms of output control rules (e.g., catch in tonnes) or input control rules (e.g., effort as a discrete exploitation rate or instantaneous fishing mortality rate). When projecting effort, the LSD model calculates the predicted catch internally based on the projected vulnerable biomass. Fixed catch and fixed exploitation rate rules are used for 30-year projections to calculate reference levels (Rudd et al. 2021). Assuming that the current TACC will be fully caught over the next five years is the most common projection done. Alternatively, specific TACC scenarios as requested by managers can be done.

Non-commercial catches are currently programmed to require static inputs only (no dynamic rules relating non-commercial catch to a separate input). Non-commercial catches must be specified in tonnes (i.e., no dynamic MP rules are currently programmed for non-commercial catches, and non-commercial projections cannot currently be specified in terms of effort).

4.1.3 Management procedures

Management procedures (MPs) are another approach for projecting commercial catches that relate CPUE or vulnerable biomass to the total allowable commercial catch (TACC). Before electronic reporting discontinued the use of the CELR CPUE series, the ‘input’ used for MPs was offset-year CPUE, rather than vulnerable biomass. However, with the discontinuation of a CPUE series starting in

2019 and the development of rapid updates, model-predicted vulnerable biomass has replaced offset-year CPUE as the driver of MP rules.

4.2 Management quantities

The Harvest Strategy Standard (HSS, Ministry of Fisheries 2008) provides guidance in applying New Zealand's fisheries laws in practice. The HSS consists of three main elements:

1. a specified target around which a stock should fluctuate,
2. a soft limit that triggers a formal, time-constrained rebuilding plan, and
3. a hard limit below which fisheries should be considered for closure.

The default soft and hard limits are defined by the HSS as 20% and 10% of unfished equilibrium SSB , respectively. SSB is used for the soft and hard limits to safeguard stock sustainability.

The target is defined as a maximum sustainable yield (MSY)-based reference point or better (Ministry of Fisheries 2008). Rock lobster MSY -related reference points are defined in terms of the start-of-year (AW) adjusted vulnerable biomass ($B_{y,t}^a$). The AW adjusted vulnerable biomass is more appropriate than SSB to base the target for rock lobsters because most New Zealand red rock lobster stocks have considerable numbers of mature females below the MLS. While SSB will satisfy the sustainability requirements of the HSS through the soft and hard limits, managing to a target SSB would often result in populations with unacceptably low incidence of harvestable lobsters (Rudd et al. 2021).

Reference levels by QMA (B_R) are defined as the average AW adjusted vulnerable biomass between fixed catch and fixed exploitation rate rules that maximise catch while meeting risk constraints based on SSB (Rudd et al. 2021). The procedure to calculate B_R is detailed by Rudd et al. (2021). Because the maximum constrained fixed catch and fixed exploitation rate rules must meet risk constraints defined by the SSB -related soft limit, the reference level may be set equal to the target under the target definition in the HSS. However, the decision on where to set the target above the reference level is left to managers and stakeholders on a QMA-specific basis.

The probability that the vulnerable biomass is less than B_R represents the probability of the stock being overfished. Overfishing is defined as the probability the exploitation rate (U) being above U_R , where U_R is the annual exploitation rate (weighted by the seasonal vulnerable biomass) expected to produce B_R on average at equilibrium (the latter 20 years of a 30-year projection).

Management quantities are reported in terms of the current year (defined as one year past the last model year because the commercial catch in the last model year is generally known) and last projected year. The last projected year is typically five years beyond the last model year for short-term projections presented in stock assessment reports.

Key reference points include those representing unfished levels:

- B_0 : AW adjusted vulnerable biomass (tonnes) before fishing
- SSB_0 : AW SSB (tonnes) before fishing
- T_0 : AW total biomass (tonnes) before fishing
- B_0^{now} : AW vulnerable biomass using the mean of the last 10 years of estimated recruitment deviates
- SSB_0^{now} : AW SSB using the mean of the last 10 years of estimated recruitment deviates
- T_0^{now} : AW total biomass using the mean of the last 10 years of estimated recruitment deviates

Other key reference points are used to represent states within the time series and projections:

- B_{\min} : the lowest beginning adjusted vulnerable biomass in the series
- B_{curr} : AW adjusted vulnerable biomass one year after the last model year
- SSB_{curr} : AW SSB one year after the last model year
- T_{curr} : AW total biomass one year after the last model year
- $CPUE_{\text{curr}}$: predicted AW CPUE at the beginning of the last model year + 1 (kg/potlift)
- H_{curr} : total handling mortality (tonnes) for the last model year
- U_{curr} : exploitation rate one year after the last model year (approximated from seasonal exploitation rate weighted by seasonal vulnerable biomass)
- B_{proj} : AW adjusted vulnerable biomass in the last projection year
- SSB_{proj} : AW SSB one year after the last projection year
- T_{proj} : AW total biomass one year after the last projection year
- $CPUE_{\text{proj}}$: predicted AW CPUE at the beginning of the last projection year
- H_{proj} : total handling mortality (tonnes) for the last projection year
- U_{proj} : exploitation rate in the last projection year (approximated from seasonal exploitation rate weighted by seasonal vulnerable biomass)

Performance indicators relate various states and reference levels:

- $B_{\text{proj}}/B_{\text{curr}}, SSB_{\text{proj}}/SSB_{\text{curr}}, T_{\text{proj}}/T_{\text{curr}}$: ratio of projected to current adjusted vulnerable biomass, SSB , and total biomass
- $B_{\text{curr}}/B_0, SSB_{\text{curr}}/SSB_0, T_{\text{curr}}/T_0$: ratio of current to unfished adjusted vulnerable biomass, SSB , and total biomass
- $B_{\text{proj}}/B_0, SSB_{\text{proj}}/SSB_0, T_{\text{proj}}/T_0$: ratio of projected to unfished adjusted vulnerable biomass, SSB , and total biomass
- B_{curr}/B_R : ratio of current adjusted vulnerable biomass to the reference level
- B_{proj}/B_R : ratio of projected adjusted vulnerable biomass to the reference level
- $U_{\text{proj}}/U_{\text{curr}}$: ratio of projected to current exploitation rate (weighted by seasonal vulnerable biomass)
- U_{curr}/U_R : ratio of current exploitation rate (weighted by seasonal vulnerable biomass) to the exploitation rate associated with the reference level at equilibrium
- U_{proj}/U_R : ratio of projected exploitation rate (weighted by seasonal vulnerable biomass) to the exploitation rate associated with the reference level at equilibrium

The LSD model also outputs probabilities to account for uncertainty in key management quantities. Probabilities are calculated based on the proportion of posterior samples where a certain management state is occurring. Key probabilities include:

- $P(B_{\text{proj}} > B_{\text{curr}})$: probability that projected adjusted vulnerable biomass is above current adjusted vulnerable biomass
- $P(B_{\text{curr}} > B_R)$: probability that current adjusted vulnerable biomass is above the reference level
- $P(B_{\text{proj}} > B_R)$: probability that projected adjusted vulnerable biomass is above the reference level
- $P(SSB_{\text{proj}} > SSB_{\text{curr}})$: probability that projected SSB is above current SSB
- $P(SSB_{\text{curr}} < 20\% SSB_0)$: probability that current SSB is below the soft limit
- $P(SSB_{\text{curr}} < 10\% SSB_0)$: probability that current SSB is below the hard limit
- $P(SSB_{\text{proj}} < 20\% SSB_0)$: probability that projected SSB is below the soft limit
- $P(SSB_{\text{proj}} < 10\% SSB_0)$: probability that projected SSB is below the hard limit

5. DISCUSSION

The LSD model has been used to develop New Zealand red rock lobster stock assessments for all stocks assessed since 2017.

LSD was coded using the Stan language. The Stan language was developed specifically for Bayesian inference and uses the Hamiltonian Monte Carlo algorithm – a Markov chain Monte Carlo method that uses the derivatives of the density function being sampled to help generate efficient transitions. This means that MCMCs for most LSD model runs can be done within just a few hours.

LSD is less general when compared with other stock assessment software (e.g., CASAL) as it was written specifically for New Zealand red rock lobster stock assessments. However, the lack of generalisation makes the code more approachable to users with some programming knowledge, and hence code changes are easy to implement.

Although LSD has only been applied New Zealand red rock lobster stock assessments, it is likely to be applicable to red rock lobster stocks in other countries (e.g., Australia) or other rock lobster species (e.g., New Zealand packhorse rock lobster). With some modification, the model could be used for other species requiring length-based assessment methods (e.g., scampi, oysters). A similar length-based stock assessment model that also uses Stan was coded for New Zealand pāua stock assessments (Neubauer & Tremblay-Boyer 2019, Neubauer 2020).

5.1 Future research

Some ideas for the LSD model include:

- Add the ability to treat some model parameters as group level effects (i.e., random effects), for example, time varying selectivity parameters
- Add alternative multivariate distributions for LFs (e.g., the logistic normal and Dirichlet distributions)
- Add the Dirichlet distribution as sex ratio option
- Investigate moult status (i.e., soft or hard shell) in the observer catch sampling data and determine if this process can/should be included in future assessments.

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APPENDIX A MODEL OPTIONS

Model options include:

- Initial conditions by region, sex, and length calculated at equilibrium given average recruitment (R_0), natural mortality (M), movement, recruitment size, maturation, growth, legal status, selectivity, vulnerability, and a constant initial exploitation rate (U_0)
 - Unfished ($U_0 = 0$)
 - Fished with constant initial exploitation rate (U_0) estimated
- Natural mortality (M) by region
- Growth by region, sex, and/or year
 - Schnute-Francis growth model
 - Specify the number of G_s^α parameters
 - Specify the number of G_s^d parameters
 - Specify the number of G_s^y parameters
 - Specify the number of c_s parameters
 - Specify the number of σ_o parameters
 - The user specifies the number of growth morphs. The growth model parameters are mapped to each of these growth morphs and the growth morphs are mapped to growth for each region, sex, and year
- Maturation by region and/or year
 - Logistic
- Selectivity by region, sex, season, and/or year
 - Logistic
 - Double-normal
- Vulnerability by region, sex, season, and/or year
 - User specifies the vulnerabilities that are set to 1
- Catch by region, year, and season
 - Fishing mortality
 - Number of Newton-Rhapson iterations
 - Exploitation rates
- Abundance indices by year, season, and/or region
 - Units as numbers or biomass
 - With or without a rate of change of catchability parameter for the abundance index catchability coefficient (i.e., q^{drift})
- Recruitment indices by year and/or region
 - User specifies the lag (i.e., number of years between index and recruitment to the model)
- Priors
 - Uniform
 - Normal
 - Lognormal
 - Beta
- Likelihoods
 - Tag-recaptures
 - Robust normal
 - Abundance indices
 - Lognormal
 - Puerulus indices
 - Lognormal
 - Size compositions
 - Multinomial
 - Sex ratios
 - Multinomial

APPENDIX B SELECTIVITY OPTIONS

Currently, the LSD model has two different options for selectivity curves: the logistic and the double-normal. Each of these options are defined below.

Logistic

Logistic selectivity is defined as

$$s_{y,t,s,l} = 1/1 + \exp\left(-\frac{\log(19)}{\sigma_{y,s}^s(\ell_l - \mu_{y,s}^s)}\right)$$

where $\sigma_{y,t,s}^s$ defines the steepness of the curve and $\mu_{y,t,s}^s$ is the value of the sigmoid midpoint (mm). The priors for a logistic selectivity curve are generally assumed to be

$$\begin{aligned}\sigma_{y,s}^s &\sim N(10, 30) \\ \mu_{y,s}^s &\sim N(50, 30)\end{aligned}$$

Double-normal

Double-normal selectivity is defined as

$$\begin{aligned}j_{y,t,s,l} &= 1/\left(1 + \exp\left(-5(\ell_l - \mu_{y,t,s}^s)\right)\right) \\ s_{y,t,s,l} &= j_{y,t,s,l} \exp\left(\frac{\ell_l - \mu_{y,t,s}^s}{\gamma_{y,t,s}^s}\right)^2 + (1 - j_{y,t,s,l}) \exp\left(\log(0.5) \left(\frac{\ell_l - \mu_{y,t,s}^s}{\sigma_{y,t,s}^s}\right)^2\right)\end{aligned}$$

where $\sigma_{y,t,s}^s$ defines the curvature of the left-hand limb, $\gamma_{y,t,s}^s$ defines the curvature of the right-hand limb, and $\mu_{y,t,s}^s$ is the midpoint. The priors for a double-normal selectivity curve are generally assumed to be

$$\begin{aligned}\sigma_{y,s}^s &\sim N(10, 30) \\ \mu_{y,s}^s &\sim N(50, 30) \\ \gamma_{y,s}^s &\sim N(30, 500)\end{aligned}$$

APPENDIX C FISHING MORTALITY

There is no closed-form equation for the Baranov catch equation to solve for $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ given the other parameters, so this equation must either be solved numerically (Popes approximation, Pope (1972), or the Newton-Raphson method, Press 2007) or by treating $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ as estimated parameters and the catches as observations with small standard deviations (so that the estimated catches are close to the observed catches). The LSD model uses the Newton-Raphson method for finding the values of $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$. To begin with an initial guess at $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ is made

$$\bar{F}_{y,t}^{SL} = \frac{C_{y,t}^{SL}}{0.995B_{y,t}^{SL}} \quad \text{where} \quad B_{y,t}^{SL} = \sum_{s,l} N_{y,t,s,l} W_{s,l} \zeta_{y,t,s,l}$$

$$\bar{F}_{y,t}^{NSL} = \frac{C_{y,t}^{NSL}}{0.995B_{y,t}^{NSL}} \quad \text{where} \quad B_{y,t}^{NSL} = \sum_{s,l} N_{y,t,s,l} W_{s,l}$$

Then the following is looped over for a fixed number of iterations (usually between 3 and 5 is sufficient)

$$F_{y,t,s,l}^{SL} = \bar{F}_{y,t}^{SL} \eta_{y,t,s,l} \zeta_{y,t,s,l}$$

$$F_{y,t,s,l}^{NSL} = \bar{F}_{y,t}^{NSL} \eta_{y,t,s,l}$$

$$F_{y,t,s,l}^{Handling} = \bar{F}_{y,t}^{SL} \eta_{y,t,s,l} (1 - \zeta_{y,t,s,l}) h_y$$

$$Z_{y,t,s,l} = F_{y,t,s,l}^{SL} + F_{y,t,s,l}^{NSL} + F_{y,t,s,l}^{Handling}$$

$$C_{y,t}^{SL} = \sum_{s,l} \left[\frac{F_{y,t,s,l}^{SL}}{Z_{y,t,s,l}} (1 - e^{-Z_{y,t,s,l}}) N_{y,t,s,l} W_{s,l} \right]$$

$$C_{y,t}^{NSL} = \sum_{s,l} \left[\frac{F_{y,t,s,l}^{NSL}}{Z_{y,t,s,l}} (1 - e^{-Z_{y,t,s,l}}) N_{y,t,s,l} W_{s,l} \right]$$

$$D_{y,t}^{SL} = \sum_{s,l} \left[\frac{\eta_{y,t,s,l} N_{y,t,s,l} W_{s,l}}{Z_{y,t,s,l}} \left((1 - e^{-Z_{y,t,s,l}}) + F_{y,t,s,l}^{SL} e^{-Z_{y,t,s,l}} - \frac{F_{y,t,s,l}^{SL} (1 - e^{-Z_{y,t,s,l}})}{Z_{y,t,s,l}} \right) \right]$$

$$D_{y,t}^{NSL} = \sum_{s,l} \left[\frac{\eta_{y,t,s,l} N_{y,t,s,l} W_{s,l}}{Z_{y,t,s,l}} \left((1 - e^{-Z_{y,t,s,l}}) + F_{y,t,s,l}^{NSL} e^{-Z_{y,t,s,l}} - \frac{F_{y,t,s,l}^{NSL} (1 - e^{-Z_{y,t,s,l}})}{Z_{y,t,s,l}} \right) \right]$$

$$D_{y,t}^{Handling} = \sum_{s,l} \left[\frac{\eta_{y,t,s,l} (1 - y_{y,t,s,l}) \epsilon_y N_{y,t,s,l} W_{s,l}}{Z_{y,t,s,l}} \left((1 - e^{-Z_{y,t,s,l}}) + F_{y,t,s,l}^{SL} e^{-Z_{y,t,s,l}} - \frac{F_{y,t,s,l}^{SL} (1 - e^{-Z_{y,t,s,l}})}{Z_{y,t,s,l}} \right) \right]$$

$$\bar{F}_{y,t}^{SL} = \bar{F}_{y,t}^{SL} - \frac{C_{y,t}^{SL} - C_{y,t}^{SL}}{D_{y,t}^{SL} + D_{y,t}^{Handling}}$$

$$\bar{F}_{y,t}^{NSL} = \bar{F}_{y,t}^{NSL} - \frac{C_{y,t}^{NSL} - C_{y,t}^{NSL}}{D_{y,t}^{NSL}}$$

This iteratively updates $\bar{F}_{y,t}^{SL}$ and $\bar{F}_{y,t}^{NSL}$ until $C_{y,t}^{SL} \approx C_{y,t}^{SL}$ and $C_{y,t}^{NSL} \approx C_{y,t}^{NSL}$.