Narrative

• Introduction

- problem statement and motivation
- introduce reference point and management decision making
- introduce BH & Derizo

• Methods

- State the Bio Model (Pella v. Schaffer)
- integration details
- Appendix A: SRR exposition and examples (reference to proposal section)
 - * two v. three parameter
 - * Pella v. Schaffer
 - * ?Derizo Model?
 - * Shepherd v. BH
- Reference Point Inversion (Math) data generation
- profile likelihood on q and MLE parameterization
- distributional results (Appendix B) for reference point and biological inference
- State Stats Model

• Results

- bias surface
- table of estimated equilibrium values at examples
- yeild/srr curves at example locations
- ?discussion?
- Proposal (<6 pages)
 - challanges of filling out response space with three parameter SRR (numerical methods)

- embedded simulator space filling (output space-filling)
 - * Shepherd-BH, Derizo-BH?
 - \ast Age Structured Models and Data Weighting
- Age Structured Model and Data Weighting
- ?MSEs?
- timeline (gant chart

• Appedicies

- Appendix A: SRR exposition and examples
- Appendix B: Distributional Results for SRR parameterizations

The data for a typical surplus-production model comes in the form of a time series of observations of an index of abundance for some population of interest. The index is often observed alongside a varienty of other known quantities, but at a minimum, each observed index will be observed in the presence of some known catch for the period. The index of abundance is assumed to be proportional to biomass with the proportionality constant being a nuisance parameter that is often referred to as the catchability parameter.

Plot Index Series and Catches

The observed indicies are assumed to have multiplicative log-normal errors, and thus the following observation model arises naturally,

$$I_t = qB_t e^{\epsilon} \quad \epsilon \sim N(0, \sigma^2). \tag{1}$$

Above q is the catchability parameter and σ^2 models residual variation. Biologically speaking these parameters are often treated as nuisance parameters with the more biological parameters entering the model thru a process model on biomass.

Biomass is assumed to evolve as an ordinary differential equation; in this case I focus on the following form,

$$\frac{dB}{dt} = R(B; \boldsymbol{\theta}) - C. \tag{2}$$

Here biomass is assumed to change in time by two processes, net recruitment into the population and catches removing biomass from the population.

Firstly, the population grows through a stock recruitment relationship (SRR). Recruitment in this setting is defined as the net biomass increase due to all birth, maturation, and migration processes after accounting for all other naturally occurring sources of mortality other than the recorded fishing from humans. The recruitment function is assumed to be parametric function that relates the current biomass of the population to an aggregate production of biomass.

Secondly, the population decreases as biomass is removed due to catch (C). While catches are observable quantities (cite), the model assumes that catch is proportional to biomass with the proportionality constant representing the fishing rate (F), so that C = FB. From a management perspective a major goal of the model is to accuratly infer a quantity known as

maximum sustainable yeild (MSE). One could maximize simple yeild at a particular moment in time (and only for that moment) by fishing all available biomass in that moment. This strategy is penny-wise but pound-foolish (not to mention ecologically devastating) since it doesn't leave biomass in the population to reproduce for future time periods. We seek to fish in a way that allows (or even encourages) future productivity in the population. This is accomplished by maximimzing the equilibrium level of catch (or yeild) over time. Equilibrium yeild is considered by replacing the steady state biomass (\bar{B}) in the assumed form for catch, so that $\bar{C} = F\bar{B}(F)$, where \bar{B} indicates a value at steady state. Naturally the steady state biomass is a function of \bar{B} ; we will see a specific example of this in Section (0.1). MSY is found by optimizaing $\bar{C}(F)$ with respect to \bar{B} , and \bar{B} is the fishing rate at MSY. Going forward let * decorate any value derived under the condition of MSY.

The canonical production model in fisheries is the Schaeffer model. The Schaeffer model is formed by choosing R to be logistic growth parameterized so that $\theta = [r, K]$ and the family takes the following form,

$$R(B; [r, K]) = rB\left(1 - \frac{B}{K}\right). \tag{3}$$

r is parameter controlling the average reproducive rate of the population. K is the so called "carrying capacity" of the population. The carrying capacity can be formally stated as steady state biomass in the absence of fishing $\bar{B}(0)$.

Logistics SRR produces idealized parabolic recruitment with equilibrium quantities taking very simple forms that can be easily understood from the graphical construction seen in Figure (1). Positive recruitment is observed when $B \in (0, K)$. Due to the second order parabolic shape of the logistic SRR it is straightforward to see that MSY will be maximized by fishing at the peak productivity of the stock. By symmetry it is clear that this peak occurs at $B^* = \frac{K}{2}$. The fishing rate required to position the stock at MSY is $F^* = \frac{r}{2}$, which is half of the stock's average reproductive rate at the origin. In the absence of fishing $\frac{dB}{dt}$ would be driven entirly by RWe can also notice that at MSY the $\frac{dB}{dt}$

While this idealized form is instructive, and convienient, these simplistic dynamics are also potentially problematic. The symmetry of the logistic functional form is very rigid in

Relationship between Catch, Logistic SRR, and dB/dt

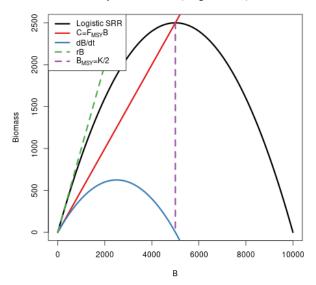


Figure 1:

that it assumes dynamics in the lower (growth limited) regime of the dynamics $(B \in (0, \frac{K}{2}))$ have the same shape as the upper (density limited) regime of the recruitment dynamics $(B \in (\frac{K}{2}, K))$. What in nature ties these phenomena together so that this assumption should be true?

Furthermore, and more practically, the fishery is managed based on

$$\xi = \frac{F^*}{M} \qquad \qquad \zeta = \frac{B^*}{B_0} \tag{4}$$

$$\xi = \frac{r}{2M} \tag{5}$$

$$(\xi,\zeta)\in\left(\mathbb{R}^+,\frac{1}{2}\right)$$

Beverton Holt and Ricker Introduction In practice, at this time, the SRR is typically chosen to depend only on two parameters. Which struggle similarly to model the full space of referece points.

Below I present the three parameter Pella-Tomlinson (PT) family, which has a convinient

form that includes the logistic SRR as a special case to form the Schaeffer model. The Pella-Tomlinson SRR is parameterized so that $\boldsymbol{\theta} = [r, K, \gamma]$ and the family takes the following form,

$$R(B; [r, K, \gamma]) = \frac{rB}{\gamma - 1} \left(1 - \frac{B}{K} \right)^{\gamma - 1}. \tag{6}$$

 γ is a parameter which breaks PT out of the restrictive symmetry of the logistic curve. In Figure (2) PT recruitment is shown for a range of parameter values so as to demonstrate the various recruitment shapes that can be achieved by PT recruitment.

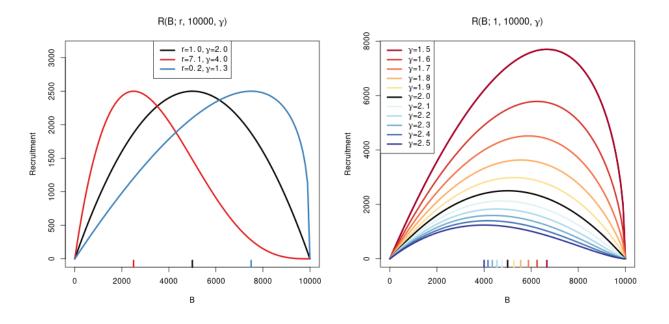


Figure 2:

While the particular form of how γ appears in PT still produces some limitations to the form of the SRR, importantly the introduction of a third parameter allows enough flexibility fully describe the space of reference points used in management $(\xi, \zeta) \in \mathbb{R}_2^+$. To see this, the reference points are analytically derived for the PT model in the following section.

0.1 PT Reference Points

Under PT recuitment the process model is defined by the following ODE,

$$\frac{dB}{dt} = \frac{rB}{\gamma - 1} \left(1 - \frac{B}{K} \right)^{\gamma - 1} - FB. \tag{7}$$

An expression for the equilibrium biomass is attained by setting Eq(7) equal to zero and rearranging the resulting equation to solve for B. Thinking of the result as a function of F gives,

$$\bar{B}(F) = K \left(1 - \left(\frac{F(\gamma - 1)}{r} \right)^{\frac{1}{(\gamma - 1)}} \right). \tag{8}$$

By definition $B_0 = K$. Alternatively, setting F = 0 in Eq(8) makes it convicient to notice that $\bar{B}(0) = K$ to arrive at the same result. The expression for B^* is given by evaluating Eq(8) at F^* .

To get an expression for F^* , the equilibrium yeild is maximized with respect to F,

$$F^* = \operatorname*{argmax}_F F\bar{B}(F). \tag{9}$$

For PT maximization can be done analytically, however many three parameter SRR's do not result in tractable analytical solutions. For PT proceeds by differentiating the equilibrium yield with respect to F as follows,

$$\frac{d\bar{Y}}{dF} = \bar{B}(F) + F\frac{d\bar{B}}{dF} \tag{10}$$

$$\frac{d\bar{B}}{dF} = -\frac{K}{F(\gamma - 1)} \left(\frac{F(\gamma - 1)}{r}\right)^{\frac{1}{\gamma - 1}}.$$
(11)

Setting Eq(10) equal to 0 and solving for F produces the following expression for the fishing rate required to produce MSY, Below any quantity evaluated at MSY shall be decorated with *.

$$F^* = \frac{r}{\gamma - 1} \left(\frac{\gamma - 1}{\gamma}\right)^{\gamma - 1}.$$
 (12)

Plugging the above expression for F^* back into Eq(8) gives the following expression for

biomass at maximum sustainable yeild,

$$B^* = K \left(1 - \left(\frac{(\gamma - 1)}{\gamma} \right) \right). \tag{13}$$

By substituting the expressions given above for B_0 , B^* , and F^* into Eq(4), ξ and ζ can take a specific analytical form in terms of the biological model parameters.

$$\xi = \frac{r}{M(\gamma - 1)} \left(\frac{\gamma - 1}{\gamma}\right)^{\gamma - 1} \qquad \zeta = 1 - \left(\frac{(\gamma - 1)}{\gamma}\right) \tag{14}$$

demonstration of the restricted case with graph over RP space as used.

0.2 Simulation Study

Indices of abundance are simulated from the three parameter PT SRR over an unrestricted grid of ξ and ζ values. After data are generated, γ is then fixed to two so that the PT SRR reduces to the special case of logistic recruitment. The restricted Schaeffer model is then fit to the simulated PT indices. Let $\tilde{}$ decorate any quantity that is derived under the restricted two parameter SRR.

Generating simulated indicies of abundanance from the PT model requires inverting the relationship between (ξ, ζ) , and (r, γ) . It is not generally possible to analytically invert this relationship for very many forms of the SRR (cite derizo paper). Most SRRs lead to RPs that require expensive numerical methods to invert, more over the numerical inversion proceedure is often extremely unstable. That said, for the case of PT this relationship is analytically invertible, and leads to the following relationship

$$r = M\xi \left(\frac{1-\zeta}{\zeta}\right) (1-\zeta)^{\left(\frac{\zeta-1}{\zeta}\right)} \qquad \gamma = \frac{1}{\zeta}. \tag{15}$$

Indicies are generated under the following condistions. A regular grid of biologically important values for ξ and ζ are considered. For each (ξ, ζ) , the associated pair (r, γ) are computed from Eq (15). Since K does not enter the RP calculation its value is fixed at

10000. A relatively large value of K is selected to allow a full range of population dynamics to be defined in this setting. The value of M is fixed at 0.2 to represent species. The value of q is fixed at the typically small value of 0.0005. σ is fixed at the relatively samll value of 0.01 to focus specifically on the behaviour of population parameters. These parameters fully specify the PT model and are used to generate index data for each considered (ξ, ζ) pair.

0.3 Model Fitting

q proceedure

By working with the resulting models parameterized in terms of $\log(\tilde{F}^*)$ it tends to improve optimization convergence. Furthermore, the normality this induces on the log scale, via the Laplace approximation, yields Log-Normality on \tilde{F}^* , as seen in Appendix 0.3.

0.4 Gaussian Process Model

A GP is a stochastic process generalizing the normal distribution to an infinite dimensional analog. GPs are often specified primarily through the choice of a covariance function which defines the relationship between locations in an index set. Typically the index set is spatial for GPs, and in this setting the model is in reference point space (ξ, ζ) . A GP model implies an n dimensional multivariate normal distribution on the observations of the model and the covariance function fills out the covariance matrix for the observations.

Each iteration of the simulation produces a single fitted $\hat{\mu}_i$ at an associate (ξ_i, ζ_i) location with $i \in \{1, ..., n\}$. $\hat{\boldsymbol{\mu}}$ is jointly modeled over the space of reference points as the following GP,

$$\mathbf{x} = (\xi, \zeta)$$

$$\hat{\boldsymbol{\mu}} = \beta_0 + \boldsymbol{\beta}' \mathbf{x} + f(\mathbf{x}) + \boldsymbol{\epsilon}$$

$$f(\mathbf{x}) \sim \text{GP}(0, \tau^2 \mathbf{K}(\mathbf{x}, \mathbf{x}'))$$

$$\epsilon_i \sim \text{N}(0, \hat{\sigma}_i^2). \tag{16}$$

 $\hat{\sigma}_i^2$ is the observed variance for $\hat{\mu}_i$ from inference in the simulation step. This model allows for the full propagation of inferred information from the simulation step to be propagated into the reference point metamodel.

Here \mathbf{K} has been extended to account for the possibility of geometric anisotropy as well as to model the smoothness of the relationship. The previously used squared exponential correlation function has been replaced with the Matern correlation function (?, ?). The updated correlation structure for filling out \mathbf{K} can be summarized as follows,

$$\mathbf{K}(\boldsymbol{x}, \boldsymbol{x'}) = Matern(\|\boldsymbol{x} - \boldsymbol{x'}\|_{\boldsymbol{R}}; \nu)$$
(17)

$$\|\boldsymbol{x} - \boldsymbol{x'}\|_{\boldsymbol{R}} = \sqrt{(\boldsymbol{x} - \boldsymbol{x'})^{\top} \boldsymbol{R}^{-1} (\boldsymbol{x} - \boldsymbol{x'})}$$
(18)

$$\mathbf{R} = \mathbf{P} \mathbf{\Lambda} \mathbf{P}^{\top} \quad \mathbf{P} = \begin{pmatrix} \cos(\theta) & -\sin(\theta) \\ \sin(\theta) & \cos(\theta) \end{pmatrix} \quad \mathbf{\Lambda} = \begin{pmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{pmatrix}. \tag{19}$$

The full GP model has linear predictor parameters $(\beta_0, \boldsymbol{\beta})$, a process variance parameter (τ^2) , kernel length scale parameters (λ_1, λ_2) , a kernel rotation parameter (θ) , and the Matern smoothness parameter (ν) . All of these parameters are estimated by maximization of the posterior (MAP) inference.

When $\gamma = 2$ Eq(6) becomes the Logistic SRR and Eq(2) produces the Schaffer model (cite).

$$R(B; [r, K, 2]) = \tilde{R}(B; [r, K]) = rB\left(1 - \frac{B}{K}\right).$$
 (20)

Plot a Representative PT SRR, next to a Schaffer (logistic) SRR

$$\tilde{F}^* = \frac{r}{2} \qquad \qquad \tilde{B}^* = \frac{K}{2} \tag{21}$$

1 Objectives

Over the reporting period the primary objective has been to further apply and extend our code base for working with production and Gaussian process (GP) models. The focus is to further explore how model misspecification in a variety of commonly used forms of the stock recruitment relationship (SRR) can affect inference on key reference points. In particular, if data are generated under a three parameter true SRR but fit using a two parameter analog how does this affect inference on $\frac{F^*}{M}$ and $\frac{B^*}{B_0}$. What bias is induced by the choice of SRR?

2 Methods

Under both the Beverton-Holt and Schaefer production models, $\frac{F^*}{M}$ and $\frac{B^*}{B_0}$ are known to be fixed when steepness and natural mortality are a'priori fixed constants (?, ?, ?). An additional degree of freedom can be added to these models by adding a third parameter (γ) to the SRR of these models respectively. Several formulations of these expanded three parameter SRR have been studied (?, ?).

The focus here is on three parameter SRRs which have the Beverton-Holt or Schaefer models as a special case (?, ?, ?). Exploration continues across many different choices of three parameter SRRs, although the new results presented here focus on the Shepherd and Pella-Tomlinson SRRs

$$R_1 = \frac{\alpha B}{1 + \beta B^{\frac{1}{\gamma}}} \qquad R_2 = \frac{rB}{\gamma - 1} \left(1 - \frac{B}{K} \right)^{\gamma - 1}.$$
 (22)

 R_1 is equivalent to the Beverton-Holt SRR when $\gamma = 1$, and R_2 is equivalent to the Schaefer model's logistic SRR when $\gamma = 2$. Given an informative series of observed catches, and natural mortality fixed at M = 0.2, these production models are integrated forward based upon,

$$\frac{dB}{dt} = R - (M+F)B. \tag{23}$$

Above R is recruitment, F is fishing mortality, and B represents biomass. The decorator * is added to indicate values at maximum sustainable yield (MSY) and B_0 is virgin biomass. Biomass and mortality reference point inference is monitored by a GP metamodel. The

following variables are defined for ease of use working with these metamodels.

$$\xi = \frac{F^*}{M} \qquad \qquad \zeta = \frac{B^*}{B_0} \tag{24}$$

Let $\tilde{\xi}$ decorate any quantity that is derived under the restricted two parameter case, so that $\tilde{\xi}$ and $\tilde{\zeta}$ represent the above reference points under the assumption of a Beverton-Holt or Schaefer model. The construction of a metamodel around these reference points is based upon the restricted relationship in $(\tilde{\xi}, \tilde{\zeta})$ for the two parameters models. First under the Beverton-Holt, and subsequently under the Schaefer model, these structured relationships can be used to show that the reference points are restricted to the following curves respectively,

$$\tilde{\zeta}_1 = \frac{1}{\tilde{\xi} + 2} \qquad \tilde{\zeta}_2 = \frac{\tilde{\xi}}{2\tilde{\xi} + 1}.$$
(25)

2.1 Simulation

Indices of abundance are simulated from each three parameter SRR over an unrestricted grid of ξ and ζ values. After data are generated, γ is then fixed so that the SRR reduces to the special cases previously described under each model, and the restricted model is subsequently fit to the simulated indices.

By working with the resulting models parameterized in terms of $\log(\tilde{F}^*)$ it tends to improve optimization convergence. Furthermore, the normality this induces on the log scale, via the Laplace approximation, yields Log-Normality on \tilde{F}^* . Let $\hat{\mu}$ be the maximum likelihood estimate (MLE) of $\log(\tilde{F}^*)$. Additionally let $\hat{\sigma}^2$ be the inverted Hessian information of the log likelihood evaluated at $\hat{\mu}$.

2.2 Gaussian Process Model

A GP is a stochastic process generalizing the normal distribution to an infinite dimensional analog. GPs are often specified primarily through the choice of a covariance function which defines the relationship between locations in an index set. Typically the index set is spatial for GPs, and in this setting the model is in reference point space (ξ, ζ) . A GP model implies an n dimensional multivariate normal distribution on the observations of the model and the

covariance function fills out the covariance matrix for the observations.

Each iteration of the simulation produces a single fitted $\hat{\mu}_i$ at an associate (ξ_i, ζ_i) location with $i \in \{1, ..., n\}$. $\hat{\boldsymbol{\mu}}$ is jointly modeled over the space of reference points as the following GP,

$$\mathbf{x} = (\xi, \zeta)$$

$$\hat{\boldsymbol{\mu}} = \beta_0 + \boldsymbol{\beta}' \mathbf{x} + f(\mathbf{x}) + \boldsymbol{\epsilon}$$

$$f(\mathbf{x}) \sim GP(0, \tau^2 \mathbf{K}(\mathbf{x}, \mathbf{x}'))$$

$$\epsilon_i \sim N(0, \hat{\sigma}_i^2). \tag{26}$$

 $\hat{\sigma}_i^2$ is the observed variance for $\hat{\mu}_i$ from inference in the simulation step. This model allows for the full propagation of inferred information from the simulation step to be propagated into the reference point metamodel.

Here \mathbf{K} has been extended to account for the possibility of geometric anisotropy as well as to model the smoothness of the relationship. The previously used squared exponential correlation function has been replaced with the Matern correlation function (?, ?). The updated correlation structure for filling out \mathbf{K} can be summarized as follows,

$$\mathbf{K}(\boldsymbol{x}, \boldsymbol{x'}) = Matern(\|\boldsymbol{x} - \boldsymbol{x'}\|_{\boldsymbol{R}}; \nu)$$
(27)

$$\|\boldsymbol{x} - \boldsymbol{x'}\|_{\boldsymbol{R}} = \sqrt{(\boldsymbol{x} - \boldsymbol{x'})^{\top} \boldsymbol{R}^{-1} (\boldsymbol{x} - \boldsymbol{x'})}$$
(28)

$$\mathbf{R} = \mathbf{P} \mathbf{\Lambda} \mathbf{P}^{\top} \quad \mathbf{P} = \begin{pmatrix} \cos(\theta) & -\sin(\theta) \\ \sin(\theta) & \cos(\theta) \end{pmatrix} \quad \mathbf{\Lambda} = \begin{pmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{pmatrix}. \tag{29}$$

The full GP model has linear predictor parameters $(\beta_0, \boldsymbol{\beta})$, a process variance parameter (τ^2) , kernel length scale parameters (λ_1, λ_2) , a kernel rotation parameter (θ) , and the Matern smoothness parameter (ν) . All of these parameters are estimated by maximization of the posterior (MAP) inference.

3 Results

Let $\check{}$ decorate values which are predictions from the GP metamodel as opposed to predictions from the base-level model. In the posterior, the GP metamodel produces a predictive surface for the estimated $\check{\mu}$ values across the reference point domain. This $\check{\mu}$ surface is used to back out a predictive surface for \check{F}^* under each reduced model. The bias in estimating F^* across the reference point domain is the predicted \check{F}^* minus the true F^* at a given spatial location. Similarly the bias in estimating ξ is given by $\frac{\check{F}^*}{M} - \xi$; using Eq. (21) the bias in estimating ξ is given by $\check{\zeta}(\check{F}^*) - \zeta$. Individually these bias measures indicate a magnitude of bias in each of the reference point directions; together they form a vector field of biases.

The above figures show the bias surfaces for the Beverton-Holt and Schaefer models respectively. Red colors indicate over estimation of the reference points and blue colors indicate underestimation of the reference points respectively. The black curves plotted above show the restricted reference point space as defined by Eq. (21) in each case.

3.1 Future Results

The results presented above are generated with limited simulation runs due to issues introduced by the mapping of reference point values to SRR parameters. We are currently developing novel adaptive sampling space-filling methods which are capable of avoiding these issues and will allow for a broader and more stable result to be presented across a wide variety of SRRs as well as age structured models.

Appendix A: Distributional results for $\tilde{\xi}$ and $\tilde{\zeta}$

Given the Log-Normality of \tilde{F}^* as seen in Eq. (??), for fixed M, $\tilde{\xi}$ is clearly just a scaled Log-Normal distribution (Log-Normal parameters are given in terms of the mean and variance on the log scale).

$$\tilde{\xi} = \frac{\tilde{F}^*}{M}$$

$$\tilde{\xi} \sim \operatorname{LN}\left(\frac{1}{M}e^{\mu + \frac{\sigma^2}{2}}, \frac{1}{M^2}(e^{\sigma^2} - 1)e^{2\mu + \sigma^2}\right)$$

Now working with $\tilde{\zeta}$ in terms given by Eq. (??) and considering the quantity $\log(2\tilde{\zeta})$ provides a simplification in terms of $\log(\tilde{F}^*)$.

$$\begin{split} \tilde{\zeta} &= \frac{1}{\tilde{\xi} + 2} \\ \operatorname{logit}(2\tilde{\zeta}) &= \log \left(\frac{\frac{2}{\tilde{\xi} + 2}}{1 - \frac{2}{\tilde{\xi} + 2}} \right) \\ &= \log \left(2/\tilde{\xi} \right) = \log(2) - \log \left(\tilde{\xi} \right) = \log(2M) - \log \left(\tilde{F}^* \right) \end{split}$$

The given simplification of $\log \operatorname{it}(2\tilde{\zeta})$ reveals the distribution of ζ as a scaled and shifted Logit-Normal distribution.

$$\begin{split} & \operatorname{logit}(2\tilde{\zeta}) \ \sim \ \operatorname{N}\left(\operatorname{log}(2M) - \mu, \sigma^2\right) \\ & 2\tilde{\zeta} \ \sim \ \operatorname{logit-N}\left(\operatorname{log}(2M) - \mu, \sigma^2\right) \end{split}$$

Notice that due to Eq. $(\ref{eq:condition})$ these distribution results hold for any fixed M Beverton Holt model with Log-Normality in \tilde{F}^* . These results are not specific to the Laplace approximation setting here. For example under Beverton Holt and fixed M, a Log-Normal prior on \tilde{F}^*

necessarily implies a scaled Log-Normal prior on $\tilde{\xi}$ and a scaled Logit-Normal prior on $\tilde{\zeta}$. Furthermore if M is not fixed, but instead it also follows a Log-Normal distribution, this also implies Log-Normality for $\tilde{\xi}$ and Logit-Normality on $\tilde{\zeta}$, albeit with slightly different parameters.