# Question 1

Many stock assessments worldwide do not have the necessary resources to conduct annual surveys to obtain an index of abundance for the population, nor are there sufficient resources to conduct large-scale ageing efforts, to support the use of data-rich integrated age-structured assessments, that are common across the United States. Furthermore, even within the United States, certain stocks do not have sufficient data to support the use of traditional data-rich methods (i.e., age-or stage-structured models), either due to difficulties in conducting surveys (i.e., tropical billfish species) or reduced commercial interest, relative to other species. As such, many species worldwide remain unassessed, or rely strictly on data-limited methods, utilizing catch time-series or length data.

Several methods utilizing only catch time-series are available to estimate management reference points, most of which are generalizations of each other. In particular***, most catch-only methods are generalizations of stock reduction analysis*** (SRA; Kimura and Tagart 1982), which utilizes a single catch-time series with pre-specified values for changes in abundance (i.e., depletion) during the initial year and the last year, as well as natural mortality to back-calculate a time series of fishing mortality and estimate abundance. Thus, these SRA based methods couple traditional catch equations with biomass dynamics (can be formulation in a variety of ways; Schaeffer-Gordon, delay-difference models, etc) to estimate abundance and derive reference points using equilibrium assumptions. ***Advances to traditional SRA include Depletion-Based SRA (DB-SRA)***, where biomass dynamics are formulated in a delay-difference model, wherein recruitment only incorporates the mature component of the stock (through a pre-specified value for age-at-maturity), relies on priors for M, Fmsy/M, depletion, and Bmsy/B0, and assumes that fishery selectivity is identical to the age-at-maturity ogive (Pons et al. 2020).

Other variations of SRA include the development of surplus production models that estimate abundance using information from a catch time-series and priors for productivity parameters. These variations will be denoted as ***CMSY*** (Froese et al. 2017). Here, CMSY utilizes resilience factors (provided in FishBase) to formulate uniform prior ranges for the maximum intrinsic productivity (*r* parameter in a logistic growth function), as well as information from catch to formulate uniform prior ranges for the carry capacity parameter (*k*). These ranges are then explored for viable pairs, which are defined as corresponding r,k pairs that result in biomass trajectories and catch time-series that are positive. The most plausible r,k pairs are then formulated by the tip of a triangular distribution (*k ~ r*) using the 75th percentile, which is based off the definition that the *r* parameter represents the maximum intrinsic rate of increase, and that a large population can sustain various values for *r,k*, but only certain values of *r,k* will allow you to produce similar biomass trajectories at small population sizes. Thus, the tip of that triangular represents the most plausible pairs of parameters. Additionally, the CMSY method accounts for depensatory recruitment by allowing for a linear decline in recruitment when biomass values are less than ¼ *k*. Lastly, given the use of the logistic growth function to drive biomass dynamics in the CMSY method (i.e., Schaeffer model), reference points can then be derived using the assumptions of MSY = K/2. Similar to previous SRA methods, it relies on priors for depletion, initial biomass, and optionally the depletion towards the middle of the time series.

***Another variation of SRA methods utilizes age-structured dynamics, which is known as Simple Stock Synthesis (SSS)*** (Cope et al. 2015; Pons et al. 2020). Here, biomass dynamics are both structured by ages and time, instead of just time, which is generally more realistic than traditional biomass dynamics models, and similarly requires priors on depletion. Furthermore, given that such model formulations are not necessarily supported by the use of catch time-series, priors are also placed upon natural mortality, steepness, and most demographic factors are treated as fixed inputs (i.e., weight-at-age and maturity), while fishery selectivity is assumed to be equal to the age-at-maturity ogive.

Many of the methods described above strongly rely on priors for depletion, particularly in the terminal year, and misspecification of these depletion priors can strongly impact model results and associated management reference points. Often, priors assume a depletion value of 0.4, although this is often not realistic, and need not be the case. Several other methods can be used to develop priors for depletion. In particular, Cope et al, 2015 derived stock-specific priors for depletion using vulnerability scores derived from a productivity-susceptibility analysis (Patrick et al. 2009). Here, qualitative measures based on species life-history (i.e, maximum age, mortality, maturity, recruitment, geographic concentration of the stock) and fishery characteristics (i.e., catchability, vulnerability to overfishing) are ranked and combined through a calculation of Euclidean distances to formulate vulnerability scores. Vulnerability scores can then be regressed against data-rich assessments with estimates of stock status to derive a predictive relationship for stock status and vulnerability scores. These scores can then be derived for more data-limited stocks to predict a value for stock-status, which are then used as priors for SRA methods.

Many of the methods described above rely solely on catch-data and priors on depletion. ***While the following method described below utilizes a single-year of catch age-composition and catch data, I feel it would be remiss to not mention Catch Curve-SRA*** (CC-SRA), which combines the methods of catch-curves using a single year of age-composition data and SRA using a catch time-series (Thorson and Cope 2015). Here, a prior for depletion is not necessary, considering that the catch-curve provides an estimate for terminal total mortality through the use of a synthetic cohort (thus assumes equilibrium recruitment and mortality up to a given age), which can be used to derive fishing mortality in the terminal year, provided that an analyst has a prior or pre-specified value for natural mortality. This approach appears to be quite promising, particularly for stocks that are planning on collecting age-composition data. Furthermore, similar developments have been made by combining catch and length-data, while utilizing a stock reduction analysis (Length-SRA), and is structured similarly to CC-SRA, except that it utilizes length-data to estimate catch curves (Wor et al. 2018).

Reference points calculations for the catch-only methods described above are fairly straightforward. For SRA-based methods, these can generally be derived by assuming equilibrium conditions using the logistic-growth function to derive our well-known relationship of MSY = ½ k. Assumptions regarding selectivity (i.e., assuming fishery selectivity is equal to the maturity curve) and prior information from natural mortality, weight-at-age, and maturity can also be used to derive SPR-based reference points. However, across the world, some stocks do not utilize model-based methods, and do not necessarily have information regarding demographics and life-history, either due to lack of resources or expertise. As such, other methods for setting catch-limits and quotas are required. In the United States, catch-limits for stocks that do not have a formal model-based assessments are often set using the ***Restrepo approach***, where a reference period of catch is defined (a period in which catch is stable) and some scalar/statistic is applied to the average catch of this reference period to define catch limits (Berkson and Thorson 2015). ***Another similar approach is the Only Reliable Catch Stocks (ORCS) method***, which allows for the incorporation of risk levels and defines scalars using qualitative information about stock status, fishery characteristics species life-history and susceptibility (i.e., includes more ecological information qualitatively) (Berkson et al, 2011). Another similar method that is uses catch-data to define catch-limits is ***Depletion-Corrected Average Catch.*** Here, an average catch period is also defined, although it attempts to correct for depletion in the reference period, and back-calculates what a “pristine unfished sustainable catch” should have been. Thus, it requires some information of catch, as well as natural mortality, Fmsy/M, and some information on how much the stock could have been depleted during the period in which catch is summarized. However, note that many of the methods to set reference points (i.e., using some measure of average catch) can be problematic because setting MSY and catch limits requires knowledge on 1) the production function, 2) growth, 3) compensatory recruitment, 4) natural mortality, and 5) fishery selectivity, which none of the methods described above consider (Berkson and Thorson 2015).

Moving beyond methods that solely rely on catch-data, I will touch on those that rely on catch and length-data, as well as those that rely solely on length-data***. Firstly, integrated size-structured models can be utilized*** (Zheng et al. 1996) to estimate abundance and derive management reference points. Here, catch data can be combined with length data through integrated analysis, where catch-data and length-data are simultaneously fit together to fit abundance. Thus, a time-series of catches and at least one year of length data are required for this method to be used. Changes in biomass are primarily governed by a size-transition matrix, which can be first derived using prior information on growth increments and parameters governing the transition matrix itself can then be estimated from within the model. Although Zheng et al, 1996 also utilized effort data to estimate parameters for fishing mortality, this does not necessarily need to be incorporated. In general, Zheng et al. 1996 showed that relative stock status is generally well estimated when compared to an absolute index of abundance, but the scale of the population is quite sensitive to the assumed values of natural mortality. ***Another method that also simultaneously uses catch and length data and estimates parameter through an integrated analysis framework is Length-based Integrated Mixed Effects*** (***LIME***; ***Rudd and Thorson 2018***). Here, the model structure is analgous to an age-structured model, although only catch and length-data are fit. Note that at least one year of length-data are required, as well as a time-series of catches for LIME. Length-data in LIME is converted from ages to lengths via an age-length transition matrix and is fit assuming a Dirichlet-Multinomial likelihood. Additionally, a catch time-series is utilized to provide information on the scale of the population, as well as removals from the population, and removals from the population are assumed to result from logistic selectivity (selectivity parameters are estimated). Furthermore, unlike many length-based methods that assume equilibrium conditions, LIME can estimate recruitment variability using only length-data by estimating recruitment deviations as random effects from a Beverton-Holt relationship via a state-space approach. I would generally consider LIME a mix between data-limited and data-moderate approach as it requires substantial information on life-history information (e.g., priors on steepness, natural mortality) and demographic information (e.g., weight-at-age, maturity-at-age, length-at-age relationship). Estimation of reference points in methods that combine catch and length-data can be relatively straightforward by assuming some x% of an SPR rate, or by combining the stock recruitment relationship with an SPR analysis to estimate Fmsy in LIME, although care should likely be taken when interpreting these values given that priors for steepness on the stock-recruitment relationship are required (Sissenwine and Shepherd 1987).

While the approaches discussed above constitute more data-moderate methods, more data-limited methods that rely strictly on length-data are available to assess stock status. ***One of the more well-known methods includes Length-Based Spawning Potential Ratio (LB-SPR)***, where one year of length-data is required, an estimate of Linf, maturity data, CV of length-at-age, and an estimate of the ratio of *M/k (Hordyk et al. 2015b, 2015a)*. This method assumes equilibrium conditions (constant recruitment) and can only be applied independently to a given year, unlike methods like LIME that utilize an entire time-series to inform model estimates. Furthermore, this method estimates parameters for selectivity and F/M to derive estimates of SPR (stocks status). A multinomial likelihood is utilized to fit to observed length data, which is compared to the length-structure given a specific level of F under equilibrium conditions. In general, the underlying theory of this method assumes that all dynamics are relative, which are standardized by Linf and the observed maximum age. The standardized von Bertlanffy relationship can be derived by the ratio of *M/k* and a value for the CV of the length-at-age relationship is used to construct a standardized age-length transition matrix, which is utilized to fit to length-data. Total mortality can then be calculated by estimating the ratio of *F/M* and logistic selectivity parameters (which are standardized to Linf). The equilibrium length-structure is derived by assuming an exponential mortality model for relative numbers-at-age (relative to observed maximum age), which is then converted to lengths. Lastly, the estimates of selectivity, F/M, and priors for natural mortality can be input into standard egg production methods to estimate SPR rates (fecundity is derived by a standardized maturity ogive multiplied by length-at-age assuming an isometric relationship).

***Another data-limited method that only utilizes length-data was initially derived by Beverton and Holt, which was later extended by Erhardt and Ault, 1992***. Similar to LB-SPR, these methods assume equilibrium conditions to estimate total mortality and can only be applied independently to a given year. The Beverton-Holt total mortality estimator (BHZ) requires knowledge of the mean length of captured fish that are fully recruited, von Bertalanffy growth parameters, and the length-at-first capture. Thus, in addition to equilibrium assumptions, it also assumes knife-edged selectivity, and that mortality is constant beyond a certain length, as well as a lack of variability in growth. However, Erhardt and Ault (1992) argued that the BHZ method is restrictive in that fish species that have a finite exploitable life span (i.e., high growth rates and mortality), resulting in non-constant mortality. Thus, they developed an extension to the BHZ method (termed EAZ) that allows for specifications of lower and upper truncation of lengths to accommodate the potential for non-constant mortality at larger lengths. Comparing the BHZ and EAZ, it appears that BHZ consistently overestimates total mortality and is more conservative (by about 40%), while EAZ exhibits variable performance, and can demonstrate unintuitive biases, despite both lower and upper length truncations being defined correctly (Then et al. 2015).

In addition to model-based methods for assessing stock-status, some authors have proposed the use of length-based indicators for assessing stocks status and the potential for overfishing. In general, these methods encapsulate the following themes: 1) prevent growth overfishing by selecting only individuals that harvesting individuals at the optimal size (i.e., where cohort biomass is maximized), 2) prevent recruitment overfishing by allowing individual to spawn at least once (i.e., selecting only individuals that are fully mature), and 3) protecting large spawners that may disproportionately contribute to recruitment dynamics (i.e., ensuring that 30-40% of harvested individuals are large fish, or ensuring that 0% of harvest individuals are large fish) (Froese 2004). These indicators are based on the premise that overfishing alters the length-structure of the population. While conceptually appealing, these indicators can potentially be problematic because they are not particularly sensitive to differences in steepness or fishing mortality rates, as well as stocks status (Cope and Punt 2009). For example, sustainable fishing can still occur even if individuals are removed at lengths that are not full mature, through reduced fishing mortality rates. Additionally, a high fishing mortality rate coupled with knife-edged selectivity for lengths where cohort biomass is maximized can quickly overfish a stock, despite harvesting individuals at the optimal length. Lastly, a 0% harvest of large individuals can be maintained if the stock is severely depleted such that no individuals are retained in the population. An alternative to the 3 independent metrics described above would be to develop an indicator that combines them together (Cope and Punt 2009). Combining the three metrics together allows for a better understanding of the selectivity attributes in the population, and when guided by the decision tree developed in Cope and Punt 2009, can be utilized as trigger reference points within harvest control rules.

Lastly, there are methods that are commonly used as proxies to set management reference points that are independent on catch data and length data, and primarily utilizes life-history information (Zhou et al. 2012; Berkson and Thorson 2015; Froese et al. 2016). In particular, the use of natural mortality is commonly used as a proxy for Fmsy, although studies have argued that these values should only be used as limit reference points, and not target reference points.

# Question 2

For stocks where ageing data are not available (i.e., many crustacean species), traditional age-structured stock assessments are not appropriate, given that ages are not clearly defined. As such, the assessment of hard-to-age species are typically conducted using stage-structured assessments, with different length-bins representing different population stages (hereafter, size-structured assessments). While both age-structured and stage-structured assessments can be structurally similar, there are some key distinctions between these methods with respect to model structure.

Similar to many age-structured stock assessments, size-structured assessments that utilized the integrated analysis framework can be fit to a variety of data sources. The data sources that are commonly fit for both methods include catch data as well as indices of abundance. However, a key difference between these models is that age-structured stock assessments are fit to age-data, while size-structured assessments do not have any age-information, and instead, estimate recruitment and growth processes using size-composition data (generally likelihoods for composition are assumed to be multinomially distributed). Another key distinction with respect to data sources that are commonly fit to are the use of mark-recapture data. In size-structured models, mark-recapture data are necessary for estimating size-transition matrices (discussed further below) to project the population dynamics forward (i.e., growth), which is not necessary in age-structured models.

The fundamental difference between size-structured and age-structured assessments is that ages and transitions across stages are not clearly defined by size-structured assessments. The abundance of individuals in an age-structured stock assessment has to transition to the next age-bin/stage by definition of ages and annual time steps, and growth follows discrete ages through changes in weight-at-age and length-at-age. By contrast, size-structured stock assessments are governed by a size-transition matrix to project abundance forward, where the size-transition matrix describes the probability of transitioning/growing from one size-class to the next (or the probability of transitioning from one stage to the next). These size-transition matrices can be estimated in various ways, utilizing different likelihood functions (e.g., multinomial) and functional forms (e.g., gamma, normal), although they all tend to rely on mark-recapture data to estimate the probability of transitioning to different size-classes. Some general examples of different estimation methods of size-transition matrices include: 1) estimating transitions across sizes, 2) estimating a molt probability governed by some functional form, coupled with the growth of an individual after having molted, 3) estimating individual variability in growth parameters (e.g., von Bertalanffy) to derive the size-transition matrix, and 4) assuming different variance formulations for the growth increment (Punt et al. 2009; Siddeek et al. 2016; Cronin-Fine and Punt 2020).

Pertaining to the issue in which ages are not explicitly defined, estimating and defining recruitment remains a key challenge in many size-structured assessments. In stocks where age-information are available, it is straightforward to define which year’s reproductive potential contributes to a particular year’s recruitment, given that ages are explicitly defined. As such, a stock recruitment relationship can be easily derived using age-structured methods, assuming that the relationship is well defined. However, in size-structured assessments, formulating a stock-recruitment relationship is quite difficult and requires various assumptions (i.e., assuming a particular length corresponds to a particular age; see Zheng et al. 1994). As such, even when the steepness of a stock recruitment relationship may be known, it is extremely difficult to define which year’s reproductive potential contributes to a particular year’s recruitment (further complicated by the fact that recruitment to a particular size class can be from multiple cohorts), and thus, size-structured assessments tend to assume mean recruitment.

In age-structured populations, the age-at-recruitment is well defined, and it is straightforward to accurately assign individuals to a given recruitment-age, assuming that ageing error for young ages is small. However, in size-structured assessments, recruitment is size-based given the lack of age data, and thus, an individual could recruit into the population as different sizes. As such, recruitment in size-structured assessments tend to follow some functional form (i.e., gamma) where recruitment deviations can be estimated annually, but are then partitioned out to different length classes by following some probability function.

In addition to recruitment related processes, size-structured assessments are often structured in different partitions (i.e., mature and immature, and new shell and old shell), which are generally not defined in most age-structured stock assessments, although note that spatial age-structured stock assessments will sometimes define mature and immature partitions (Goethel et al. 2023a). Defining partitions for maturity is necessary in size-structured assessments given that individuals can incorrectly “unmature” if the probability of maturation for a given stage/size-class does not equate to 1, despite those individuals having matured in the previous year. Furthermore, defining maturity partitions is also important for recruitment processes because it could be possible that recruitment of a size-class has some probability of being maturity, despite that being biologically unrealistic. As such, maturity partitions can constrain recently recruited individuals to be strictly immature. Additionally, some crustacean size-structured assessments (i.e., crabs) will also define partitions for old and new-shells, given that these different partitions could be defined by different molt probabilities or vital rates (Zheng et al. 1994).

Given the reliance on size-composition data in size-structured models, catches are defined by a selectivity function that is length-based. While there is some debate in age-based models as to whether selectivity should be length-based or age-based, it is not an uncommon assumption for age-structured models to assume age-based selectivity, to account for differences in availability due to ontogenetic movements. However, the estimation of age-based selectivity in size-structured models are not possible, given that there are no age-data to inform this process. As I am not as familiar with crustacean stocks, it is unclear to me whether selectivity processes could be age-based (i.e., through age-based movements), although such assumptions are constrained by the available data, and this issue is likely not consequential.

Lastly, in many size-structured assessment models, the timing of the occurrence particular events is fairly important in driving population dynamics, and mis-specifying the order in which these events occur can lead to differences in the size-structure of the population, and thus, model results. This is largely in part due to the modelling of a size-transition matrix. In particular, the specification of natural mortality after growth (via size-transition matrix) and the specification of natural mortality prior to growth can result in different size-structures. Similarly, if surveys or catches were to take place following the definition of natural mortality or growth processes, it would result in differences in the expected catch-at-length, which could lead to misfits to catch and composition data. A similar problem arises with respect to defining when maturity occurs or when recruitment occurs. In particular, the definition of recruitment processes occurring prior to growth will result in recruited individuals growing within a given year (i.e., growth can occur for recruited individuals, which can potentially result in recruited individuals maturing within a given year), whereas defining recruitment to occur at the end of the year will only allow individuals to grow in the following year (i.e., no growth in the terminal year).

# Question 3

Although many data-rich stock assessments have a variety of data-sources that help inform the estimation of the scale of the population, changes in abundance, and fishery processes, simplifying assumptions are often necessitated, which can be due to institutional inertia, legacy practices, or concerns with respect to overparameterization.

Many data-rich stock assessments in Alaska (which I will define as Tier 3 or above) continue to assume mean recruitment, where annual deviations are estimated about a mean level of recruitment. While there is often an argument as to whether recruitment is driven by changes in reproductive potential (i.e., spawning stock biomass) or changes due to environmental conditions, from a first principles perspective, if reproductive potential is reduced to a level beyond which the stock can support itself (i.e., recruitment overfishing), it is likely that recruitment will be impaired, and hence the presence of a stock recruitment relationship. While from a modelling perspective, this assumption might not be as critical (i.e., abundance and recruitment can still be adequately estimated), assuming mean recruitment for population projections and stock rebuilding plans can be problematic. As an example, when a rebuilding plan is considered and mean recruitment is assumed, there is no benefit to rebuilding the stock to a particular biomass level with respect to its ability to produce a higher level of recruitment, from a modelling perspective (i.e., because recruitment is independent of stock size), and harvest of the stock should be allowed, even when the stock remains at low levels (i.e., there is no recruitment overfishing). However, the perception of a particular stock rebuilding plan can differ from those assuming mean recruitment, if either compensatory or depensatory dynamics are present. Thus, while the assumption of mean recruitment likely adequately estimates annual deviations (likely depends on the value of the variance for recruitment variability), it can lead to misleading rebuilding plans. From the perspective of both estimation and population projections, the use of steepness priors derived from life-history meta-analysis can be a potential solution to these issues, as well as sensitivity test for alternative steepness values.

Another common assumption with many data-rich stock assessments is that vital rates are homogenous within a defined stock boundary, no movement occurs, and that all individuals are well-mixed in the population. However, this assumption is seldom true. For example, differential fishing mortality across harvest areas within a given spatial domain can result in heterogenous demography (i.e., age-structure differs between areas due to disproportionate fishing in areas closer to ports), which can result in bias in stock assessment results (Cope and Punt 2011; McGilliard et al. 2015) if such dynamics are not adequately accounted for. Furthermore, movement likely occurs heterogeneously within areas (i.e., more movement towards favorable feeding areas, or ontogenetic movements, both of which will result in a heterogeneous population distribution), which can similarly lead to biases in population trajectories and localized depletion, if such processes are not accounted for (Goethel et al. 2021; Bosley et al. 2022) There is generally adequate information for these more data-rich assessments (i.e., mark-recapture data and age-composition data) to begin the integration of spatially-explicit stock assessments, although this is seldom done, likely attributed to institutional inertia, concerns with over-parameterization, and a lack of defined criteria for reviewing spatial stock assessments (Berger et al. 2017). While I recognize that single-area stock assessments also driven by political and management boundaries, I believe that continued development of research-oriented spatially explicit models (particularly using real-world data) is the solution for moving away from the assumption of a single stock, which will allow us to explicitly account for population heterogeneity. Additionally, even within single-area assessments, it is now feasible to account for potential movement dynamics (i.e., movement into or outside the modelled area) by allowing for process variation in the exponential mortality model, although this approach has yet to be thoroughly evaluated, and more consideration of this approach is warranted (Stock and Miller 2021).

Another common assumption that is made within stock assessments is that natural mortality is independent of age and time. Furthermore, natural mortality is often fixed *a priori*, which essentially pre-defines the values of resultant reference points (Punt et al. 2021). Fixing natural mortality at the wrong value can result in differences in population scale, given that the population needs to either be larger or smaller to produce the same relative decline in population trends, given a particular level of catch. As such, I believe that most of these assessments should be estimating natural mortality within the assessment model, using a prior based on natural mortality estimators (e.g., maximum observed age) as opposed to fixing this value (some assessments continue to fix this; e.g., GOA walleye pollock). This approach also allows for the propagation of uncertainty with respect to natural mortality as well. As discussed, natural mortality is also often assumed to be age-invariant, although it is well understood that it likely varies across ages. In particular, younger ages likely experience higher mortality rates due to predation and density-dependence, while older ages can potentially experience higher mortality rates due to senesce. Approaches are available to estimate size or age-specific natural mortality, although these are seldom used, and should be further considered and estimated using priors within the assessment model (Lorenzen 2022). Lastly, time-invariant natural mortality is a very common assumption in many data-rich stock assessments. This is not surprising given the difficulty in estimating time-invariant and age-invariant natural mortality. However, with recent advances in multi-species modelling (e.g., CEATTLE; Adams et al. 2022) and prolonged time series of predator data (Dorn and Barnes 2022), wherein estimates of natural mortality are derived using predator-diet data, time-varying natural mortality approaches should be attempted and explored within the context of single-species assessments, utilizing estimates of mortality from multi-species models as priors.

Additionally, many life-history processes within stock assessments are assumed to be time-invariant, despite there being evidence that such processes likely vary over time. These can include changes in maturity-at-age, weight-at-age, and length-at-age. While some assessments allow for time-varying weight-at-age (i.e., EBS pollock), many assessments still continue to treat this process as time-invariant or varies among time blocks, where it generally remains constant for long periods. The assumption of time-invariant maturity, weight, and growth can have large impacts on associated reference points and harvest control rules, given that these processes are used as inputs to calculate spawning biomass, spawner potential ratios, and virgin biomass. If these processes were to vary in a unidirectional manner, it is likely that the resultant management advice would be biased. Thus, more consideration and modelling of these time-varying processes are required. In particular, the amount of weight-at-age data for most stocks are generally adequate for modelling time-varying dynamics. For processes such as weight, growth, and maturity, this can be done by allowing parameters describing functional forms to vary over time, or the functional form itself varying over time. Approaches for time-varying weight could also include the use of empirical weight-at-age weight (Ianelli et al. 2016; Kuriyama et al. 2016; Lee et al. 2024). Furthermore, many of the processes described above are often assumed known and are fixed during the estimation process for many data-rich assessments in Alaska. However, these processes are unlikely to be known, and treating them as fixed will result in underestimating uncertainty in associated stock status and management reference points. Further consideration of their estimation within the integrated analysis framework (i.e., estimating these processes inside the model) is warranted. For example, the integration of conditional age-at-length data within the assessment framework can allow for internal estimation of growth processes, propagating uncertainty associated with growth, while accounting for the effects of selectivity on growth data, which are not accounted for when growth is estimated outside the assessment model (Schueller et al. 2014; Lee et al. 2019).

Fishery selectivity is a fundamental process within many age-structured stock assessments where many assumptions are often made, given that fishery selectivity which is a combination of availability and contact selectivity is an unobservable process. Assumptions typically include different functional forms, as well as how this process varies over time. An important assumption that is commonly made, although can be incorrect, is that at least one fleet exhibits logistic selectivity (Privitera-Johnson et al. 2022). However, it is well known that when there is spatial variation in fishing, selectivity dynamics on the population level can be dome-shaped. In particular, high fishing pressure in one area can result in a lack of older individuals, whereas lower fishing pressure in another area can result in a more protracted age structure. The combination of these two areas then results in the potential for older individuals to be more abundant than younger individuals, manifesting as dome-shaped selectivity (i.e., F = ln(N\_2 / N\_1) – M; Sampson and Scott 2011). However, there is often inertia against modelling dome-shaped selectivity, because it creates cryptic unobservable biomass (and less conservative advice) and is confounded by the fact that less individuals remain available at older ages. Nonetheless, I believe that more assessments in Alaska should be considering the use of dome-shaped population selectivity, which can arise due to seasonal migrations (i.e., Pacific cod) or differences in fishing mortality across areas, while considering the plausibility of such dynamics (i.e., does *a priori* knowledge of survey or fishery characteristics agree with model estimates) (O’Boyle et al. 2016). The plausibility for dome-shaped selectivity can also be investigated through the use of more flexible selectivity functions that are able to mimic logistic selectivity (i.e., double logistic or double normal) and associated model diagnostics (e.g., residuals).

In addition to the functional form of selectivity, assumptions are often made with respect to how time-variation occurs in fishery selectivity (although also true for the processes described above – e.g., growth). It is common to assume that time-variation in fishery selectivity occurs in time-blocks, where blocks are defined by substantial changes in fishery dynamics (i.e., new regulations, technological advances). However, the definition of a time-block can be quite subjective and incorrectly assuming the period in which a block occurs can result in biases in population trajectories (e.g., my third chapter). Furthermore, it is unclear when a new period/block needs to be defined. The objective definition of a new block can potentially be done by embedding a Hidden Markov Model within the assessment model, although this approach has seldom been investigated, and could potentially be interesting to explore (not necessarily a solution given that it is fairly untested). A common argument for the use of time-blocks is that it is generally more parsimonious – however, I argue against such a notion. In particular, assuming logistic selectivity with 2 parameters, and defining 10 time-blocks, that results in 20 additional parameters. By contrast, if we were to assume that selectivity varies continuously over time using formulations of time-series models (i.e., random-walk, autoregressive 1), only a maximum of 4 fixed-effect parameters needs to be estimated (i.e., a50%, slope, and variance parameters for both of these parameters) when estimating deviations as random effects via state-space approaches. Even when these deviations are estimated using a penalized maximum likelihood approach, deviations are penalized and thus do not necessarily equate to one parameter (i.e., effective degrees of freedom do not equate to the number of deviations). As such, I believe that time-variation, particularly in fishery selectivity, should either be allowed to vary continuously over time, or be defined in such a way that it remains relatively invariant over time (i.e., disaggregation of fleets).

Another key assumption that is often made is with respect to compositional likelihoods, and relatedly, how different data sources should be weighted, relative to each other. In particular, the multinomial likelihood is often assumed to fit to compositional data, despite compositional data being rarely distributed as multinomial. Furthermore, sample sizes defining the multinomial likelihood are fixed inputs, and thus, weights for compositional data sources were traditionally defined as the total number of samples aged or lengthed. However, the number of age or length samples collected can be large, and thus, these compositional data can be highly influential when fitting an integrated stock assessment, and prioritizes the fit to compositional data, despite not providing information on the scale and trend of the population (Francis 2011). Furthermore, the total number of samples collected are often not reflective of the true effective sample size (i.e., the number of samples the data reflect had sampling been uncorrelated and random) given correlations within hauls and between adjacent locations. Thus, *ad-hoc* tuning methods are often used in many data-rich assessments to adjust and “estimate” the effective sample size of a multinomial likelihood. However, these approaches do not propagate the uncertainty for the “estimated” weighting parameters and are often not re-weighted when conducting sensitivity or retrospective analyses, which could lead to mis-leading retrospective analyses and sensitivity tests (Thorson et al. 2017). Correlations in compositional data are also often larger than the levels allowed for when assuming a multinomial likelihood. As such, the use of *ad-hoc* tuning methods (e.g., Francis re-weighting) coupled with a multinomial likelihood will tend to underestimate the underlying uncertainty in model results. A potential solution to this is to utilize multivariate likelihoods that allow for additional correlation structure, as well as those that are able to estimate weighting parameters within the model (e.g., Logistic-normal, Logistic-multinomial, Dirichlet-multinomial, or Multivariate Tweedie; Francis 2017; Thorson et al. 2017, 2022).

Lastly, when time-varying processes (this can be from recruitment, selectivity, weight-at-age, maturity-at-age, natural mortality) are present within stock assessment models, it is unclear which period should be used to define how calculations of reference points and how population projections should be conducted. Some common assumptions that are used in our data-rich stocks include: 1) utilizing the most recent period (e.g., the most recent time block), 2) utilizing some moving average of a continuous process, and 3) using estimates from a continuous process by forecasting one-year forward. Using estimates projected one-year forward as well as the terminal period can result in increased variability in reference points and subsequent catches, while assuming a moving average will likely result in bias if changes in the process are unidirectional. Furthermore, some recent studies have shown that re-defining reference points due to non-stationarity can potentially result in unintended consequences (i.e., allow for a higher fishing mortality rate, despite being at a lower population biomass;(Szuwalski et al. 2023). While I do not necessarily have a solution for this particular problem, I believe the solution is to conduct management strategy evaluations on a stock-by-stock basis. It is unlikely that a universally optimal assumption regarding which period to use for a reference point exists, given that each fishery will have its own tolerance to variability and alternative life-histories may respond differently to the various definitions of reference periods.

# Question 4

While Dr. Quinn posits that the golden age of fisheries population dynamics ended in 2000, I respectfully disagree with this assertion. The Golden Age of fisheries stock assessment is still ongoing, particularly with the many advances in computational methods (i.e., use of Laplace Approximation and Hamiltonian Monte Carlo; Kristensen et al. 2016; Monnahan and Kristensen 2018) that just recently been adopted. The use of state-space methods are increasingly popular, which were not necessarily computationally feasible during the presupposed “Golden Age”, and often made many assumptions such as linearity (i.e., Kalman Filter; Quinn 2008). Such advances have resulted in the need for continued advances and research with respect to: 1) whether the modelling of multiple time-varying processes is feasible, 2) the consequences of mis-specification of processes variation, and 3) decisions regarding what process should process variation be imposed on (i.e., use of model diagnostics to detect mis-specification with respect to whether process variation is attributed to the correct process) (Szuwalski et al. 2018; Fisch et al. 2023).

Additionally, many advances have been made with respect to spatially explicit stock assessments and spatiotemporal modelling, and many more advances are required with increasing recognition of the importance of spatial dynamics in marine resources. In particular, only recently has the application of spatially stratified stock assessments been increasing, and there are still numerous issues that remain to be addressed in this particular field. For example, there are no studies to my knowledge that have incorporated process error via random effects in the context of spatially stratified assessment models, which may help with estimation tractability with respect to parameterizing flexible movement dynamics and is a promising avenue for further advancements. Additionally, there remains a need to develop methods for addressing spatially varying growth within spatially stratified stock assessments that are age-structured (i.e., how to ensure individuals do not shrink when moving to an area with differing growth dynamics). Returning back to the roots of Beverton and Holt, 1957, they asserted that when modelling spatial dynamics, areas should be defined in the finest resolution possible, corresponding to the areas in which information are collected. However, many spatial stock assessment models currently are spatially-straitifed, and assume that vital rates are homogenous within a large defined area. Only recently has there been advancements that concur with Beverton and Holt’s initial recommendation that areas should be defined to be as fine-resolution as possible. In particular, advancements in spatial modelling with respect to Gaussian Markov Random Fields has made the representation of fine-scale spatial population dynamics more tractable (Cao et al. 2020; Thorson et al. 2021; Olmos et al. 2023), where population dynamics are modelled following Langragian-like dynamics. However, note that these models are extremely data-rich and require the collection of fine-scale (i.e., geospatial coordinates). Coupling these models with spatially stratified frameworks that allow for the fitting of spatially-stratified data is an advancement that has yet to be made.

In addition to the recent computational advances that have been made, there have been several advances in terms of novel data sources, where good practices have yet to be developed, given the lack of implementation/difficulty in implementation within integrated stock assessment models. This is particullary true for genetic-based tagging (i.e., close-kin mark recapture; Bravington et al. 2016b, 2016a; Trenkel et al. 2022), where their potential use in integrated stock assessments has yet to be fully realized, likely due to: 1) the need to develop a genetics program (i.e., financial overhead) and 2) the need to continue understanding how robust these methods are to violating tagging assumptions (although some recent work has looked at this; Conn et al. 2020). Nevertheless, genetic-based tagging methods are a promising avenue of research that is just beginning, given that the use of these data can allow the estimation of absolute abundance, natural mortality, detection/defintion of population structure, while circumventing the estimation of “nuisance” parameters that are commonly required in most applications of the Brownie tag-attrition submodel (i.e., tag mortality, tag mixing, reporting rates). Additionaly, recent advancements in tagging technology have resulted in an abundance of electronic tags being deployed, although these data are seldom used within integrated stock assessment models. Further integration of these novel tagging data sources within integrated stock assessments and population dynamics models are needed to fully understand how they influence estimates of movement, assumptions that need to be made (e.g., tag mixing, representativeness), and how these novel data sources should best be integrated within the traditional framework of stock assessments (Taylor et al. 2011; Lowerre-Barbieri et al. 2019).

Additionally, there is still much need for advancements with respect to stock assessment model diagnostics. Only recently has it been recognized that the use of Pearson residuals are invalid for composition data, as they assume independence and do not account for correlated residuals, which are inherent in multivariate likelihoods (Trijoulet et al. 2023). Furthermore, only recently has there been methods developed to assess whether a retrospective pattern is significant (Breivik et al. 2023). Consequently, there will likely be more advances and a need for more robust model diagnostics in the coming years. In particular, it still remains unclear how to detect whether a particular process should have process variation imposed upon it (as discussed above). Model diagnostics for spatial models are particularly lacking, especially for assessing violating assumptions of using tag data (i.e., identifying appropriate tag mixing periods; Goethel et al. 2024) and the use of novel tag data types (i.e., model diagnostics for using satellite tag data). In general, most contemporary model diagnostics (e.g., likelihood profiles, residuals) do not necessarily inform the analyst the particular process that is mis-specified, and simply inform analysts that “something is wrong”. More targeted model diagnostics coupled with model diagnostic workflows that correctly identify a mis-specified modelled processes will likely be a future avenue of research (Carvalho et al. 2017, 2021).

Interestingly, Quinn, 2008 contends that multi-species models remain beyond human attainment. However, several advancements in modelling methods (e.g., automatic differentiation, Laplace Approximation) and prolonged time-series of predator diet-data streams that have made the development of integrated state-space multi-species stock assessment models feasible (Holsman et al. 2016; Trijoulet et al. 2020; Adams et al. 2022). Given the increasing recognition of the importance of EBFM, and the ability for multi-species models to produce more informed estimates of natural mortality (Trijoulet et al. 2020; Karp et al. 2023), there will likely be continuing developments in these methods, which will likely include the estimation of system-wide reference points (i.e., similar to a BSAI ecosystem cap in harvest).

Mandates by many fisheries legislations worldwide have necessitated the provision of management advice, event for stocks that do not have the necessary data to support the use of traditional stock assessment methods. Consequently, there has been several advances in conducting stock assessments for data-limited stocks to providing quantitative fisheries management advice. Developments in data-limited methods are likely to continue (i.e., methods that relax the common equilibrium assumption). Importantly, there is still much work to be done in terms of developing and utilizing life-history information (e.g., meta-analyses) to inform data-limited stocks, and for estimating reference points (Zhou et al. 2012; Goethel et al. 2023b; Thorson 2024).

Lastly, when Quinn’s ruminated on the development the development and future of fisheries stock assessment in 2008, the issue of non-stationarity was unlikely to be a big topic of contention. It is increasingly acknowledged that climate variation and non-stationary dynamics are important drivers of population productivity of a given stock. However, it still remains unclear how non-stationary dynamics should best be incorporated within harvest control rules and reference points, and whether the use of environmentally linked covariates to specific processes (e.g., recruitment, mortality) can predict future declines (Stock and Miller 2021), and the consequences of these relationships breaking down, if left undetected.

Stock assessment models and integrated population models that are commonly used in terrestrial ecology share some similarities, and cross-pollination between these two fields will likely benefit the development of fisheries stock assessment. In particular, Integrated models that are used in terrestrial ecology generally differ from stock assessment models in a variety of ways. In particular, methods from terrestrial ecology are typically hierarchical and model estimates are generally derived using a Bayesian framework. By contrast, stock assessment models often utilize tuning algorithms to estimate variance parameters and penalized maximum likelihood approaches to estimate process variation (Thorson 2019). This is in part due to the relative complexity of stock assessment models compared to integrated models from terrestrial ecology, but recent advancements in stock assessment methods have allowed for the objective estimation of variance parameters, which should be increasingly adopted in the coming years (i.e., weighting parameters for compositional likelihoods; Thorson et al. 2017; Fisch et al. 2022). Additionally, methods from terrestrial ecology commonly use a variety of tag-data, wherein multi-state capture-recapture data (i.e., Cormack-Jolly-Seber model; Schaub and Abadi 2011) are commonly integrated to estimate survival rates. However, these methods are seldom integrated in traditional single-area stock assessment methods – stock assessment methods could potentially benefit from fitting these data types and exploring the use of multi-state sub-models. A common difference between stock assessment models and integrated models in terrestrial ecology is that data in stock assessments are often aggregated up to a particular level (i.e., stratified). By contrast, integrated models in terrestrial ecology are generally fit to individual processes and are not aggregated, and thus, allow for improved inference on individual variation in demographic processes (Schaub et al. 2024). As such, stock assessment models should continue to strive towards fitting data on a finer spatial-scale, which may allow for improved inference on fine-scale demographic variation (Cao et al. 2020; Thorson et al. 2021).

I partially agree that we are seeing a paradigm shift that moves away from science-based management by de-emphasizing. In particular, the development of harvest control rules shifts reliance away from developing complex models to set catch advice towards a decision-making process that better addresses trade-offs in conservation, maximizing catch, and minimizing catch variability, that are not easily captured within complex models (Kvamsdal et al. 2016). Thus, it shifts from model-based decisions towards rule-based decisions that are more transparent, and further anchors decision-makers to a pre-defined set of rules and mitigate the influence of politics in this process. Furthermore, there has been recent developments and proposals of hybrid and empirical harvest control rules and reference points that do not explicitly rely on complex age-structured models that, but instead utilize metrics/indicators such as the proportion of high density areas, the relative change in survey biomass, or relative changes in absolute biomass to define target and limit reference points, which can then be used to define catch-limits for a given year (Berkson and Thorson 2015; Reuchlin-Hugenholtz et al. 2016; Goethel et al. 2023b). Furthermore, I agree with Quinn, 2008 that much of our contemporary management strategies aim to reconcile new and competing objectives for fisheries and resource management, which is in part, facilitated by the development of computational resources, making MSE simulation feasible (Punt et al. 2016). The development and advancements in MSE modelling has partially facilitated the de-emphasis of modelling, given that it is recognized that a biased stock assessment method does not necessarily lead to poor management advice, as long as the underlying harvest control rule is robust to uncertainties in the system (Punt et al. 2017; Goethel et al. 2023b). However, I do not necessarily agree (i.e., I partially agree but mostly disagree) with the fact that we are moving towards conservation strategies that are “feel good”, given that the development of harvest control rules is not entirely focused on conservation, but rather seek to provide trade-offs between variability in catch, the scale of catch, and preventing stock collapse and fishery closures. Such developments of harvest control rules thus attempt to reduce drastic economic and social consequences to harvesters, while balancing trade-offs with conservation. There are, however, some aspects of current fisheries management that could potentially be characterized as “feel good” conservation strategies, which I will play devil’s advocate to, just to cover my bases. In particular, *ad-hoc* adjustments to a given year’s level of catch (i.e., through risk tables), often attributed to uncertainties in climate and the prevailing environment, are sometimes made, and arguments for increasing uncertainty buffers towards harvest control rules that are already precautionary are sometimes made (Free et al. 2022), despite not having any quantitative basis behind these decisions. Moving beyond these “feel good” *ad-hoc* strategies, future advances in management strategies should include more explicit representations of uncertainty to adjust levels of catch, if model-based methods are used (i.e., the P-star approach; Free et al. 2022).

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