### Methods

Study Species

#### Data Sources

##### Juvenile abundance index

We use a juvenile Chum index based on NOAA’s Bering Arctic and Subarctic Integrated Survey (BASIS) to estimate survival from the spawner stage until when fish are captured and enumerated at the end of their first summer in the Bering Sea on the BASIS survey. The BASIS survey takes place annually in early Fall throughout the North and Southern Bering Sea (there are some spatially imbalanced years where the NBS or SEBS was not surveyed). Fish caught in this survey are allocated to genetic reporting groups, including western alaska Chum (Bristol Bay, Yukon Summer and Kuskokwim River) and Yukon Fall Chum.

[talk about index- not sure what I am using for the real index yet!] This index used Vector Autoregressive Spatio-Temporal modeling approach in creating an independent index of Yukon river fall chum salmon. [Insert summer methods – pat berry] The index spans brood years 2000-2023.

##### Catch and spawner index

Summer and fall run Chum spawner estimates for the Yukon River is provided by the Alaska Department of Fisheries and Game (ADFG) (Fleischman & Borba 2009, Hamazaki & Conitz 2009). We used run reconstructions to inform the stock-recruit transition functions used in this chapter. Run reconstructions typically use escapement, catch, and age composition data to estimate the number of fish returning to freshwater based on their brood year (the year they emerged from eggs in freshwater). Run reconstructions can vary significantly in complexity depending on the goal of the reconstruction and the system-specific data availability. The Yukon rivers is the longest river in Alaska, and a transboundary river with headwaters in Canada. The massive size of this system makes it difficult to fully account for salmon traveling across such remote regions and consequently, Chum salmon on these rivers have low-data availability relative to other systems. These age-structured run reconstructions use maximum likelihood estimates to minimize negative log likelihoods estimate total run size, spawner abundance, and harvest. These models are thoroughly documented in the associated publications (Fleischman & Borba 2009, Hamazaki & Conitz 2009).

##### Environmental Covariates

##### Population Process Model

The population model tracked cohorts of summer and fall Chum salmon by brood year, *t*, distinct life stages, *n*, and stocks, *s*.

The number of Chum salmon surviving from egg to ocean juveniles, *n = j*, which we consider year 0 fish that exited the river and have spent their first summer in the marine environment, depended upon the abundance of eggs that were spawned in brood year, *t*, and the population-specific survival rate from eggs to ocean juveniles, t,n=j,s.

Nt,n=j,s=t,n=j,s\* Nt,n=e,s

The survival rate, t,n=j,s, was estimated using a Beverton Holt Transition function (Moussalli & Hilborn 1986). It was calculated as

Where the productivity parameter represented time varying maximum survival rate without density dependence, and represented the maximum number of individuals that could survive past that life stage. The productivity parameter was estimated conditional on environmental covariates (Table XX) and estimated using an inverse logit function of basal productivity, , which is the mean survival rate at low density across the time series and the covariate effects

Eq. 4.2

Where covariate *c* values at time *t* were multiplied by coefficients which describe the relative influence on population specific survival rates.

I propose to develop a truncated life-cycle model based on a Beverton-Holt transition function that incorporates biological and physical environmental covariates to estimates of Chum salmon productivity to understand the relative influence of these process on changes in Chum salmon survival and abundance (Moussalli & Hilborn 1986). The model will be based on data from two life stages, a stage labeled FW which includes freshwater and early marine survival and is based on a marine juvenile survey, and a stage labeled S, which includes fish that survive from ocean-year 0 to spawn and is based on escapement and catch data (Figure 4.1). Model time-steps will be indexed based on calendar year; however, covariates will be matched based on brood-year which will inform the environmental conditions fish experienced during ocean entry. The stages are chosen based on stock-specific data availability throughout the lifecycle and to separate out early stage versus late-stage environmental effects on abundance. The Yukon River supports Chum salmon Summer and Fall runs, where the Fall runs tend to be larger and migrate to the ocean earlier than summer Yukon chum. Additionally, the marine genetic reporting groups can separate Yukon Fall chum from other Chum runs in the region, thus I will model two stock groups: Yukon Fall Chum, Yukon Summer Chum and Kuskokwim Chum salmon.

This model will focus on understanding processes in the early marine life stage, but also includes covariates for the secondary marine and spawner component. In this multistage model, the productivity and carrying capacity parameters for each stage , are estimated in a Beverton Holt transition function to calculate survival rate for each brood year t, stock s and stage, n, . This model takes the following form:

Eq. 4.1

Eq. 4.2

Eq. 4.3

Eq. 4.4

Eq. 4.5

Here, the relative number of spawning individuals is multiplied by the proportion of females in the spawning stock, , and the fecundity, to produce the total potential eggs, , for each calendar year, t and stock, s. Next, the survival rate for the freshwater/early marine stage, is multiplied by total potential eggs, , to yield EBS juvenile Chum abundance before their first winter at sea, . Fish estimated in this stage have survived to the first fall at sea where they are indexed by NOAA’s BASIS survey in Fall (termed Ocean Year-0). Next, survival rate for juvenile ocean year-0 to spawners, , is multiplied by the number of ocean age 0 fish, to yield relative number of spawning individuals . Productivity, is a function of the average survival rate across stocks, and the sum of environmental covariate effects, c. The coefficient for each stock s, life stage n and covariate c, will be multiplied by mean-scaled covariate time series within the covariate matrix, X (Hilborn and Walters 1992).

Prey Index and covariates

I will test multiple covariates at each life stage to understand relative contributions of physical and biological environmental processes to Chum salmon abundance (Figure 4.1). I intend to include nearshore degree days, mainstem river discharge, river ice break up timing and a marine prey index for the n = FW stage. I have described hypotheses and mechanisms in more detail for these covariates in table 4.1. I will develop a marine prey index for juvenile Chum during their first summer at sea within the juvenile Western AK Chum salmon spatial distribution (55°N to 64°N). These maps were developed by Cunningham et al. for the North Pacific Marine Fisheries Council. The marine prey index, as well as other FW stage covariates are represented within (Eq 4.2). This prey index will focus on relative abundance of copepods and amphipods that are abundant in juvenile Chum diets, such as Calanus spp and Themisto libellula as an indicator species for Chum salmon prey availability (Murphy et al. 2016). The species I will include are also diet for Chum prey, i.e. forage fish, when Chum become larger and piscivorous (Moulton 1997, Burril 2007). The initial intent was to use BEST-NPZ output to inform a hybrid Calanus spp prey index. However, conclusions from Chapter 1 indicate proceeding with caution when using BEST-NPZ as a temporal biomass index. Instead, I will utilize a zooplankton abundance dataset from the NBS collected by NOAA’s AFSC. This data set uses multiple gear types to survey the NBS zooplankton community in Fall from 2002 to 2023 (excluding 2020). Surveys used a vertically towed Juday net from 2002 to 2011 to capture smaller zooplankton and then they used paired bongo nets from 2011 to present. Most large zooplankton were collected using obliquely towed paired bongo nets; however, some samples were collected using an obliquely towed ring net from 2002 to 2011. Multiple surveys have tested the selectivity of these methods to understand potential data biases when switching between the two methods, they have concluded that they are comparable for Calanus spp (Gorbatenko & Dolganova 2007, Kimmel et al. 2023). Themisto libellula are only enumerated from the large zooplankton nets (60 cm diameter net using 333 μm and 505 μm mesh) in the dataset. To inform survival for the second life-stage component, n=Sp, I will include offshore degree days and hatchery origin Pink and Chum abundance within (Eq 4.3) (Table 4.1). Temperature can lead to stress and changes to metabolic rate as fish are staging to return to freshwater and spawn, this can negatively affect survival (Howard & von Biela 2023). Further, competition with hatchery fish can affect size and overall condition of returning fish (Tadokoro et al. 1996, Ohlberger et al. 2023).

Estimation and Likelihoods

I will fit the proposed model to stock-specific data using Bayesian methods, with a joint likelihood to allow the sharing of information between data rich and data limited stocks. This is advantageous as some AYK stocks are observed with greater precision than others (Schaub & Abadi 2011). The observation model will consist of two likelihood components using both life stage components (). Chum experience natural mortality across all life stages and they are also subject to subsistence and commercial fishing, in addition to pollock bycatch (Ianelli & Stram 2015). We assume this mortality is accounted for in estimates of . I will estimate model parameters within a Bayesian framework developed using STAN in R. I will evaluate convergence of the chains based on visual inspection of trace plots for each chain. I will use a posterior predictive check that estimates the Bayesian P-value to test whether the model can generate new observations that were similar or more extreme than the data. A Bayesian p-value between 0 and 1 indicates the model cannot generate new observations that properly resemble the data (Gelman 2005).

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