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Exploration of data and methods for developing estimates of a biologically-based spawning goal and biological benchmarks for Little Tahltan Chinook (Stikine River drainage)

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Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

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ABSTRACT

This paper evaluates the quantitative basis for establishing a biological frame of reference for spawner abundances of Chinook Salmon (*Oncorhynchus tshawytscha*) in the Little Tahltan River, which is a tributary of the Stikine River in northwestern British Columbia. Stikine River Chinook Salmon are a transboundary stock aggregate, and are managed cooperatively by Canada and the US under the Pacific Salmon Treaty.

The project originally focused on fitting various Spawner-Recruit (SR) models and estimating biological benchmarks for each model, but during the peer-review process for this work, hosted by DFO's Canadian Science Advisory Secretariat (CSAS), reviewers and participants raised serious concerns regarding the available data. The main concerns were

1. indications that the counting weir may have affected Chinook spawning distribution and increased mortality,
2. Little Tahltan may be an opportunistic spawning site in years with large abundance rather than a persistent spawning population, and
3. observed productivity dropped dramatically starting with the 2001 brood year.

Based on these concerns, the peer-review process discussed two alternative interpretations of the available data:

1. if one takes the weir counts at face value, then biological benchmark estimates are consistent with estimates published in 2000, and recent spawner abundances are substantially below various estimates of S_{MSY} and declining further.
2. Alternatively, if one considers the potential data concerns strong enough to invalidate recent weir counts, then biological benchmarks cannot be updated, current status of Little Tahltan is unknown, the current weir does not provide a useful indicator for total Stikine Chinook, and the drainage-wide assessment program needs to be reviewed.

After intensive debate, the consensus conclusion was that biological benchmarks based on spawner-recruit data cannot be estimated with the data currently available, but that it would be nevertheless informative for decision-makers to document our benchmark estimates and summarize the data concerns identified during the peer-review.

**Exploration des données et des méthodes concernant la mise au point
d'estimations d'un objectif de frai fondé sur des données et points de référence
biologiques pour le saumon quinnat de la rivière Little Tahltn (bassin versant de
la rivière Stikine)**

RÉSUMÉ

Le présent document évalue le fondement quantitatif de l'établissement d'un cadre biologique de référence pour l'abondance des saumons quinnat reproducteurs (*Oncorhynchus tshawytscha*) dans la rivière Little Tahltn, qui est un affluent de la rivière Stikine dans le nord-ouest de la Colombie-Britannique. Les saumons quinnat de la rivière Stikine sont un ensemble de stocks transfrontalier géré en collaboration par le Canada et les États-Unis dans le cadre du Traité sur le saumon du Pacifique.

Ce projet visait initialement à ajuster divers modèles reproducteurs-recrues (RR) et à estimer les points de référence biologiques pour chaque modèle, mais durant le processus d'examen par les pairs du Secrétariat canadien de consultation scientifique (SCCS) de Pêches et Océans Canada (MPO), les examinateurs et les participants ont soulevé de sérieuses préoccupations concernant les données disponibles. Les principales préoccupations étaient les suivantes :

1. Certains signes indiquaient que la barrière de dénombrement pourrait avoir nui à la répartition du frai du saumon quinnat et avoir fait augmenter le taux de mortalité;
2. La rivière Tahltn pourrait être un site de frai opportun durant les années où l'abondance est élevée plutôt que d'abriter une population reproductrice constante;
3. La productivité observée s'est effondrée à partir de l'année d'éclosion 2001.

En fonction de ces préoccupations, deux nouvelles interprétations des données disponibles ont été examinées lors du processus d'examen par les pairs :

1. Si l'on prend le dénombrement tel quel, les estimations des points de référence biologiques sont conformes aux estimations publiées en 2000, et l'abondance des reproducteurs est très en dessous des diverses estimations du nombre de reproducteurs nécessaires pour maximiser la valeur R_{RMS} et continue de diminuer.
2. Par ailleurs, si l'on juge que les préoccupations relatives aux données sont suffisamment solides pour invalider les dénombrements récents, alors les points de référence biologiques ne peuvent être mis à jour, l'état actuel de la rivière Little Tahltn est inconnu, le dénombrement actuel ne fournit pas d'indicateur utile du nombre total de saumons quinnat, et le programme d'évaluation de l'ensemble du bassin versant doit être revu.

Après un long débat, les participants ont convenu que les points de référence biologiques fondés sur les données reproducteurs-recrues ne peuvent pas être estimés à l'aide des données actuellement disponibles, mais qu'il serait néanmoins utile que les décideurs consignent nos estimations des points de référence et résumant les préoccupations concernant les données qui ont été soulevées durant l'examen par les pairs.

1 INTRODUCTION

1.1 SCOPE OF THIS PAPER

1.1.1 Purpose

The purpose of this paper is to evaluate the quantitative basis for establishing a biological frame of reference for spawner abundances of Chinook Salmon (*Oncorhynchus tshawytscha*) in the Little Tahltan River (step 1), which can then be considered by the Transboundary River Panel (TRP) of the Pacific Salmon Commission (PSC) to evaluate status and set management goals (step 2). Management goals adopted by the TRP then shape the annual harvest plans and in-season implementation of fisheries managed by Fisheries and Oceans Canada (DFO) and the Alaska Department of Fish and Game (ADFG).

This paper focuses on the first step, but includes a discussion of implications for the second step.

The specific objectives of this work were to:

1. Review Chinook production and escapement data for the Little Tahltan River;
2. Develop biological benchmarks including the number of spawning adults that would produce a maximum sustainable yield of Chinook salmon and use various models and contemporary methods to assess biological benchmarks of salmon stocks;
3. Examine and identify uncertainties and sensitivities in the data and methods;
4. Examine the models presented in the working paper and provide recommendations on applicability.

During the peer-review process for this work, hosted by DFO's Canadian Science Advisory Secretariat (CSAS), reviewers and participants raised serious concerns regarding some of the data used in our analyses. The CSAS discussions are documented in a Science Advisory Report (DFO 2016a) and proceedings (DFO 2016b).

After substantial debate, the consensus conclusion was to retain the quantitative results presented in this paper, but to refocus the paper on a treatment of data concerns and their implications (e.g. for the future operation of Little Tahltan weir). The final conclusion was that Objective 2 could not be addressed with the data currently available, but that it would be nevertheless informative for decision-makers to document the resulting benchmark estimates as well as the data concerns (i.e. Objectives 1, 3, and 4). Accordingly, the paper is organized in the standard format for presenting estimates of biological benchmarks, but disclaimers are included throughout, and readers are encouraged to read the discussion in Section 4.1 first, which summarizes the data concerns, conclusions, and unresolved questions.

1.1.2 Why Attempt to Develop a Spawning Goal for Little Tahltan Chinook?

Management of transboundary stocks under the Pacific Salmon Treaty (PST) focuses on the development of bilaterally agreed-upon escapement goals. In Alaska, for an escapement goal to be formally recognized, it needs to be biologically based, to provide sustained yield and be approved by the directors of Commercial Fisheries and Sport Fish divisions. In Canada, advice is sought through the CSAS process.

A drainage-wide escapement goal for managing large Stikine River Chinook salmon (i.e. Chinook salmon greater than 659 mm mid-eye to fork length) based on the objective of

maximizing sustainable yield was developed 15 years ago (Bernard et al. 2000) and then adopted by the TRP. The analysis by Bernard et al. (2000) also includes a range of 2,700 to 5,300 for corresponding counts of large Chinook (3-5 ocean age) through the Little Tahltan weir, but these were intended as indicator values for the whole drainage, not as a spawning goal specific to the Little Tahltan River.

Little Tahltan River Chinook have historically been major contributors to the total Stikine production, but have declined in recent years, both in abundance and relative contribution to the total Stikine Chinook run. Due to this concern, the Canadian caucus of the TRP initiated this project to explore specifically the population dynamics of Little Tahltan Chinook and develop quantitative estimates of reference points which can be used as the basis for a biological spawning goal.

As part of implementing Strategy 1 of the Wild Salmon Policy (WSP), DFO is required to identify biological benchmarks to assess the status of WSP Conservation Units (CUs) for Pacific Salmon. There are two Chinook Conservation Units (CU) identified for the Stikine River; early and late-run Chinook. Little Tahltan Chinook are considered part of the early-run CU and have served as an abundance index since 1975. WSP abundance benchmarks have not yet been identified for Stikine River CUs.

Our analysis complements earlier estimates of optimal Chinook production (Bernard et al. 2000) for the entire Stikine River. The Canadian caucus of the TRP identified the need for a review of the population dynamics and resulting management goals due to the following observations (see Section 2.1.2 for details):

- Productivity of Little Tahltan Chinook spiked in the 1999 and 2000 brood years, resulting in large returns and large catches in 2004 and 2005. However, in 2007 returns dropped dramatically to well below the long-term average and have not rebounded. This has resulted in escapements below the range 2,700 to 5,300 identified by Bernard et al. (2000) as corresponding to the total Stikine goal of 14,000 to 28,000.
- In late May 2014 a rockslide occurred at a site located approximately 800m upstream from the mouth of the Tahltan River. The rockslide introduced a seasonal migration barrier to a significant number of Little Tahltan Chinook and other upstream stock groupings; moreover, the slide drastically altered the age and size composition of Little Tahltan Chinook for the 2014 brood year, and preliminary observations for 2015 indicate this may be an on-going effect.
- Contribution of Little Tahltan to the total Stikine run has declined persistently over the last 15 years. Preliminary results from the 2015 radio telemetry project on the Stikine River located 55 radio tags above the landslide on the Tahltan River, however only one radio tag (2% of the radio tags located above the Tahltan landslide) was located in the Little Tahltan River. Approximately 200 radio tagged fish successfully spawned in the Stikine River in 2015 and only one radio tag (0.5%) was tracked to the Little Tahltan River. This is similar to the proportion of Stikine River spawning population counted at the Little Tahltan River weir (roughly 250 large spawners at weir / estimated 23,000 total Stikine \approx 1%)
- Age and size composition of Little Tahltan Chinook has changed over the last 30 years, shifting towards younger age-at-maturity (i.e. fewer age 6, more age 4 and 5) and smaller size (i.e. higher proportion of small adults with less than 660mm fork length). Note that estimates of % small adults vary across alternative assumptions, but most show a similar trend, Section 2.1.2)
- Total catch of Stikine Chinook salmon has been substantially reduced in the last 10 years, but observed exploitation rate (ER) is still in the 30-40% range due to the decline in

abundance. Note that ER estimates are based on coded-wire tag (CWT) estimates for the total Stikine, and adjusted to account for the Upper Stikine First Nations Food Fishery. The long-term average catch is roughly 1,000 Upper Stikine Chinook, with less than half from the Little Tahlitan)

All of these observations have implications for the assumptions we make about population dynamics (i.e. capacity, productivity, density dependence), which in turn affects the spawner-recruit models we fit (e.g. Ricker or Beverton-Holt) and thereby influence our estimates of biological benchmarks and the considerations that shape management goals.

1.1.3 Analytical Approach

Chinook salmon spawning in the Little Tahlitan River, in the Stikine drainage, are part of a transboundary stock group managed cooperatively by Canada and the US under the Pacific Salmon Treaty (PST). The methods we use to develop biological benchmarks cover recent practice by both Fisheries and Oceans Canada (DFO) and Alaska Department of Fish & Game (ADFG). We follow the approach developed by Pestal & Johnston (2015) for Taku River Coho, which was peer-reviewed through CSAS.

In this paper, we compare the results from alternative approaches recently applied in similar reports (Section 1.3), provide science advice for interpreting the results, and discuss implications for using the results. Note, however, that the peer-review process raised concerns with the available data (Sec. 2.1), and the estimates we present need to be considered in the broader context of previous analyses (Bernard et al. 2000) and probable implications of issues with the recent spawner-recruit data (Sec. 4.1).

We apply 2 alternative approaches to establish a reference range for spawner abundance of Little Tahlitan River Chinook Salmon:

- *Percentile Method*: Based on some percentiles of observed spawner abundance. ADFG has a step-wise algorithm based on contrast in the data (e.g. Table on p6 of Volk et al. 2009), while DFO has used 25th and 75th percentiles as the default (English et al. 2014). Both implementations refer back to Bue and Hasbrouck¹ and label the resulting range a Sustainable Escapement Goal (SEG);
- *Spawner-Recruit (SR) Model Method*: Based on fitting spawner-recruit (SR) models and estimating biological benchmarks for each model (SMSY, SMAX, SGEN, SEQ). Two estimation approaches can be used for this:
 - Maximum Likelihood Estimate (MLE) estimates (e.g. McPherson et al. 2010, Holt and Ogden 2013);
 - Bayesian estimates using Markov Chain Monte Carlo (e.g. production model of Eggers and Bernard 2011, Grant et al. 2011, Holt and Ogden 2013);

Alternative SR models include:

- *Ricker*: characterized by a density-dependent drop in recruitment at larger spawner abundances;
- *Ricker AR1*: Ricker with a 1-year autoregression term to correct for patterns over time (i.e. good years tend to follow good years, so that residuals are not independent);

¹ Bue, B.G. and J.J. Hasbrouck. Escapement goal review of salmon stocks of Upper Cook Inlet. Alaska Department of Fish and Game, Report to the Alaska Board of Fisheries, November 2001 (and February 2002), Anchorage. Unpublished Report.

-
- *Beverton-Holt*: characterized by approaching a fixed production limit at larger spawner abundances (i.e. a maximum number of recruits), rather than a density-dependent decline in production.

We explore whether results are robust by:

- Using alternative data assumptions:
 - a) alternative age/size composition assumptions resulting in alternative estimates of adult recruits by brood year;
 - b) alternative catch reconstruction assumptions.
- Evaluating different time windows (i.e. retrospective evaluation);
- Evaluating the effect of dropping individual data points (i.e. jackknife evaluation)

Note that the project originally focused on fitting alternative SR models and estimating biological benchmarks for each model, because a long time series of spawner-recruit data is available for Little Tahltan Chinook (Little Tahltan weir counts, Lower Stikine mark-recapture program with genetic stock identification, radio telemetry studies; see Sec 2.1). We also present results for the percentile method, usually applied in data-poor systems, as a consistency check, because they are more widely applicable and account for the majority of spawning goals for Pacific Salmon currently in use by DFO and ADFG. Note, however, that potential data concerns identified during the peer-review process (DFO 2016a) affect both of these methods, as well as the interpretation of their results (Sec 2.1.2, 4.1).

Our analytical approach is conceptually similar to the methods in Bernard et al. (2000), but there are some key differences to keep in mind when comparing the results:

- Estimates based on SR data for Little Tahltan, rather than for the whole Stikine system;
- Use weir data since 1985, rather than infill 1977-1984 based on aerial counts, and recruit data up to 2007 brood year, rather than 1991 which was the most current brood year available at the time of Bernard et al. (2000) analysis. Overall, our analysis uses 23 brood years, compared to the 15 observations available at the time;
- Test three alternative SR models (Ricker, Ricker with autoregression correction, Beverton-Holt), rather than just the classic Ricker fit;
- Bayesian parameter estimates, rather than deterministic estimates with bootstrap intervals;
- Note that Bernard et al. (2000) formally quantify uncertainty in estimates of spawner abundance and recruitment, and sample for these distributions as part of the bootstrapping. In contrast, we qualitatively explore uncertainty in the input data and do some simple sensitivity tests (e.g. infill missing catch data with either a median or resampled observations).

1.2 LITTLE TAHLTAN RIVER CHINOOK SALMON

1.2.1 Brief Overview of the Stikine River Watershed and the Little Tahltan River

This section adapted from Pahlke and Etherton (1999).

The Stikine River originates in British Columbia and flows to the sea approximately 32 km south of Petersburg, Alaska (Figure 1). The drainage covers about 52,000 km² of which about 90% is inaccessible to anadromous fish due to natural barriers and velocity blocks. The Stikine River's principal tributaries include the Tahltan, Chutine, Scud, Iskut, and Tuya rivers.

The lower river and most tributaries are glacially occluded (e.g. Chutine, Scud, and Iskut rivers).

Only 2% of the Stikine River drainage is in Alaska (Beak Consultants Limited 1981), and most of the identified Chinook salmon spawning areas in the Stikine River are located in British Columbia, Canada in the mainstem Tahltan and Little Tahltan rivers (including Beatty Creek). However, Andrew Creek, in the lower Stikine River, supports a significant run of Chinook salmon. The upper drainage of the Stikine is accessible via the Telegraph Creek Road.

The Little Tahltan River drains an area of approximately 314 km² and flows into the Tahltan River, a major tributary of the Stikine River. The river length is 40 km and drains a significant section of the southwest quadrant of Level Mountain. The confluence of the Little Tahltan and Tahltan Rivers is approximately 32 km northwest of the community of Telegraph Creek, British Columbia (BC).

1.2.2 Transboundary Chinook Salmon

Many Southeast Alaska and transboundary river Chinook salmon stocks were depressed in the mid- to late 1970s, relative to historical levels of production (Kissner 1982). The Alaska Department of Fish and Game (ADFG) developed a program in 1981 to rebuild southeast and transboundary Chinook salmon stocks over a 15-year period (roughly 3 life cycles; ADFG 1981²). In 1979, the Canadian Department of Fisheries and Oceans (DFO) initiated commercial fisheries on the transboundary Taku and Stikine Rivers. The fisheries primarily targeted sockeye salmon and were structured to limit the harvest of Chinook salmon to incidental catches. In 1985, the Alaskan and Canadian programs were incorporated into a comprehensive coastwide rebuilding program under the auspices of the U.S./Canada Pacific Salmon Treaty (PST). The rebuilding program has been evaluated, in part, by monitoring trends in escapement for important stocks. Escapements in 11 rivers in Southeast Alaska and Canada are directly estimated or surveyed annually: the Situk, Alsek, Chilkat, Taku, King Salmon, Stikine, Unuk, Chickamin, Blossom, and Keta rivers, and Andrew Creek. Total escapements of Chinook salmon have been estimated at least once in all 11 key index systems, providing expansion factors for index counts to estimate actual escapement of large Chinook salmon. Escapements in the Stikine River have rebounded since initiation of the rebuilding program (Pahlke et al. 2000).

The Pacific Salmon Commission (PSC) Chinook Technical Committee (CTC) began incorporating the inriver abundance of Stikine River Chinook salmon into the PSC Chinook Model in 2013, which, among other things, produces preseason forecasts of abundance for setting annual quotas for fisheries under the jurisdiction of the PST. Hence, data from annual assessments are not only essential for management of this stock, but may serve in the management of other coastwide stocks as well. Specifically, the drainage-wide abundance estimate for Stikine River Chinook population (based on mark-recapture since 1996) is currently used for international management under the PST. Canada has curtailed Total Allowable Catch (TAC) of Stikine Chinook recognizing the downward trends in escapement at Little Tahltan.

1.2.3 Population Structure of Stikine River Chinook Salmon

Holtby and Ciruna (2007) developed the initial delineation of conservation units (CU) for Pacific Salmon under Canada's Wild Salmon Policy (WSP). Since then, the CU list has been reviewed

² ADFG (Alaska Department of Fish and Game). 1981 Proposed management plan for Southeast Alaska Chinook salmon runs in 1981. January 1981. Region Unpublished Report 1J81-3, Juneau.

and updated for Fraser River Sockeye (Grant et al. 2011), Southern BC Chinook (Brown et al.³), and Interior Fraser Coho (Chuck Parken, DFO, Kamloops, B.C., pers. comm.). CUs for transboundary stock groups, including Stikine Chinook have not been reviewed yet. The summary in this section is based on Holtby and Ciruna (2007).

Chinook salmon originating in the Stikine drainage are part of the Stikine/Taku genetic cluster and enter the ocean in the Transboundary Fjords marine adaptive zone.

Holtby and Ciruna (2007) identified 2 Chinook CUs for the Stikine River, based on run timing and habitat use:

- Early Stikine Chinook: 6 distinct spawning sites (Beatty Creek; Christina Creek; Little Tahltan River; Shakes Creek; Stikine River; and Tahltan River)
- Late Stikine Chinook: 3 distinct spawning sites (Craig River; Katete River; Verrett River)

As noted, Little Tahltan Chinook are considered part of the early-run CU and have served as an abundance index since 1975.

Chinook Salmon spawning in the Little Tahltan River have been numerically one of the most significant single stocks contributing to the Stikine River Chinook population (based on radio telemetry surveys in 1997 and 2005, mark-recapture studies from 1996 to 2015, and weir projects from 1985 to 2015; see Section 2.1.1 for details).

Little Tahltan Chinook enter the Stikine in late May and start to enter the Little Tahltan River in late June. Observations by weir staff and from aerial survey indicate that spawning occurs from mid to late July until mid to late August, with peak spawning in early August.

An unknown number of juveniles rear in the stream before migrating downstream to rear at sites along the Stikine River and may immigrate into non-natal streams for food and cover. Each year since 2000, Little Tahltan Chinook smolts have been coded-wire tagged as part of the drainage-wide aggregate on the lower Stikine River ~200 km downstream from Little Tahltan.

There may be interspecific competition between Little Tahltan Chinook and Stikine Coho during the rearing phase at locations along the mainstem; however, differences in rearing habitat preferences in general should minimize the effects.

Adults are vulnerable to bear predation. There appears to be a lightly exploited grizzly bear population in the Little Tahltan drainage; bears fish near the weir site (electric fence used since 2007). Predation rates are unknown but may be significant in years of low spawner abundance, i.e. predation may be constant and not responding to reduced prey. Predation may actually increase over time due to habituation.

1.2.4 Fisheries Harvesting Stikine River Chinook Salmon

Chinook salmon returning to the Stikine River are caught incidentally to sockeye salmon in the U.S. marine gillnet fishery (District 108) and in the in-river Canadian commercial fishery, as the run timing of sockeye salmon overlaps the latter component of the Chinook salmon migration. Stikine River Chinook salmon are also caught in marine recreational fisheries near Wrangell and Petersburg, in the commercial troll fishery in Southeast Alaska, and in Aboriginal, recreational, and commercial fisheries in Canada (Pahlke et al. 2010).

³ Brown, G.S., S.J. Baillie, R.E. Bailey, J.R. Candy, C.A. Holt, C.K. Parken, G.P. Pestal, M.E. Thiess, and D.M. Willis. 2014. Pre-COSEWIC review of southern British Columbia Chinook salmon (*Oncorhynchus tshawytscha*) conservation units, Part II: Data, analysis and synthesis. DFO Can. Sci. Advis. Sec. Working Paper. In revision.

Harvests of Little Tahltan Chinook in these fisheries are assumed to be proportional to the stock composition of Stikine-origin Chinook.

1.2.5 Harvest Management of Stikine River Chinook Salmon

In February 2005, an agreement was negotiated between the United States and Canada by the Transboundary Rivers Panel and approved by the PSC for directed harvest of wild Chinook salmon returning to the Stikine River (Annex IV, Paragraph 3). The agreement allows for harvest sharing of above-border Stikine-origin Chinook salmon caught by the U.S. and Canada in fisheries operating in Southeast Alaska Management District 108 and Canadian fisheries on the Stikine River. During years of directed fishing, U.S. harvests in excess of escapement needs and base level catches do not count towards the Southeast Alaska (SEAK) Aggregate Abundance Based Management (AABM) harvest limit set annually by the PSC. Escapement needs are tied to the existing escapement goal and base level catches are predicated on the average catches seen in the pre-existing sport and commercial fisheries from 1985-2003. U.S. base level catches count toward the AABM harvest limit and during years of no directed fishing, all U.S. harvest counts toward the AABM harvest limit.

For the total Stikine, the escapement goal that produces maximum sustained yield (S_{MSY}) has been estimated at 17,368 based on spawner-recruit data from the 1977 to 1991 brood years (Bernard et al. 2000). Based on the estimate of S_{MSY} , an escapement goal range of 14,000 to 28,000 adult spawners (age-.3, -.4, and -.5 fish), was chosen. Bernard et al. (2000) also indicated that the total Stikine S_{MSY} of 17,386 large Chinook corresponds to 3,300 through the Little Tahltan weir). Similarly, the range of 14,000 to 28,000 large Chinook corresponds to a range of 2,700 to 5,300 through Little Tahltan weir.

This range was recommended to and accepted by the CTC and an internal review committee of ADFG in spring 1999. The Pacific Scientific Advice Review Committee of DFO declined to pass judgment on this range in deference to a decision by the Transboundary Technical Committee (TTC) of the PSC; the TTC accepted the range in March 2000.

1.2.6 Fishery Contributions of Little Tahltan Chinook Salmon

The section briefly summarizes the estimated Little Tahltan harvest contributions to the various fisheries. Sections 2.1.1.5 and 2.1.1.6 describe the catch estimates in detail.

Little Tahltan Chinook are a key source of fish for Food, Social, and Ceremonial (FSC) purposes for the Tahltan First Nations (Thompson 2007) and have been so for centuries. Based on two radio tagging studies, it is estimated that Little Tahltan Chinook account for 30-40% of the Tahltan First Nations Chinook harvest. It is assumed that they account for similar proportions of the Upper River recreational and commercial fisheries.

The contribution of Little Tahltan Chinook to the lower Stikine commercial fishery is assumed to be proportional to stock composition estimate from the ratio of weir returns to lower river (drainage-wide) mark-recapture estimates (i.e. no differential harvest for different timing groups). This amounts to a median estimate of 16% and range of 3% to 34% over the years 1996-2013. 2014 was an outlier of 0.7% due to the rock slide. Note, however, that the rock slide and resulting mortality occurred above the commercial fishery in the lower river and below the weir, confounding the ratio-based stock composition estimate for 2014 and likely again for 2015.

Troll fisheries in SEAK intercept a mix of many different stocks, and catches of Stikine Chinook likely contribute less than 5% to the average total annual Chinook harvest in those fisheries. Applying the same stock composition estimates as in the lower river, this results in a Little Tahltan contribution to those fisheries of likely well below 1%.

US fisheries in District 108 target fewer stocks in more terminal approach areas, and catches of Stikine Chinook contribute roughly 40%-60% to the average total annual Chinook harvest in those fisheries (total catch excluding hatchery production and Andrew Creek).

However, in terms of exploitation rate on Little Tahltan Chinook these catches can be substantial. In most years since 1985, total exploitation rate (ER) has been in the 20-40% range, but it peaked up to 60%-70% in 2005-2007.

1.3 BENCHMARKS FOR PACIFIC SALMON

Stikine River Chinook Salmon, including Little Tahltan Chinook, are managed cooperatively by Canada and the US under the Pacific Salmon Treaty. The two agencies responsible for salmon management operate under similar policy frameworks and recent work related to biological benchmarks is conceptually consistent. However, there are important differences in both methodological details and how the results are used. Section 1.3 of Pestal and Johnston (2015) compares the concepts and definitions of Alaska's *Sustainable Salmon Policy* and Canada's *Wild Salmon Policy*, as well as the methods used in recent applications.

In each case the chosen approach depended on available data and the institutional frame of reference. The analysis for this paper was shaped by three considerations:

1. Where methods diverged (e.g. bias correction), we chose the approach taken for other transboundary stocks as the base case (i.e. McPherson et al. 2010 for Taku Chinook, Bernard et al. 2000 for Stikine Chinook, Eggers and Bernard 2011 for Alsek Sockeye, Bernard and Jones 2010 for Alsek Chinook)
2. Given the transboundary management system for Little Tahltan Chinook, we present the information required by both agencies for their individual and joint planning processes.
3. We chose to also present the percentile-based proxies typically used for data-poor systems (e.g. of Volk et al. 2009, English et al. 2014) in order to check whether the results are roughly consistent with our spawner-recruit modelling.

2 METHODS

2.1 DATA

2.1.1 Data Sources

We constructed a spawner-recruit data set for Little Tahltan Chinook for brood years 1985 to 2007 using the following steps:

1. Start with Chinook counts at Little Tahltan weir.
2. Remove estimated proportion of small fish to get "large" Chinook at weir.
3. Estimate Stikine-origin Chinook catch in marine fisheries based on CWT.
4. Sum marine catches and lower river catches, and then calculate the proportion of Little Tahltan based on observed ratio between mark-recapture estimates of total Stikine run and the weir counts.
5. Sum upper river catches and apply an adjusted stock composition derived from radio tagging (Little Tahltan/Tahltan).
6. Estimate Little Tahltan run as the sum of weir returns plus all catches.

7. Use annual estimates of age composition to convert runs into brood year recruits.

Each step required a set of assumptions, and we tested sensitivity of the run reconstruction to alternative assumptions (e.g. using long-term median or resampled values to infill missing observations at the beginning of the time series for catch by the US troll fishery).

The CSAS peer-review process raised serious concerns regarding the available data, specifically:

1. indications that the counting weir may have affected Chinook spawning distribution or increased mortality;
2. Little Tahltan may be an opportunistic spawning site in years with large abundance rather than a persistent spawning population; and
3. observed productivity dropped dramatically starting with the 2001 brood year.

These issues are discussed throughout the paper. Observed effects of various Chinook counting weirs are summarized in Table 1, and Appendix A lists weir-by-weir details.

Note that catches included here are all considered to be in-bound or terminal, so that adjustments for adult equivalents are not required.

Table 2 lists the main components in the run reconstruction. Table 3 summarizes the run reconstruction estimates. Table 4 describes the alternative spawner-recruit data sets used for sensitivity analysis, and Table 5 lists the corresponding annual estimates.

The rest of this section briefly describes the data and each of the processing steps. Appendices B and C show all the input data.

2.1.1.1 Spawner Abundance

Estimates of total annual Chinook returns to the Little Tahltan watershed are based on a fish counting weir operated by DFO and Tahltan First Nation at the mouth of the Little Tahltan River since 1985.

Daily Chinook counts at Little Tahltan weir are available each year since 1985. Weir counts are assumed to give a complete census of passing Chinook, and there are no harvests above the weir. Therefore, the weir counts are a direct estimate of total spawning abundance in the Little Tahltan watershed.

The weir is operational from mid/late June to early/mid August using a tripod-based picket fence style barrier to fish migration. Fish are corralled to a counting chamber and trap located on river left. A second trap from which to collect samples is incorporated between two tripods on the downstream side of the structure. The total length of the weir is 21m; the counting chamber is 1.4m by 2m, and the trap 3m by 3m.

The weir is monitored from ~0800 to 2300 hrs, with sampling effort adjusted based on observed and projected fish activity (e.g. if fish are holding at the mouth of the river).

In most years, Chinook counts are 0 or very small during the very beginning of the weir counts and during the last few days of weir operation, indicating good coverage in terms of the timing window.

Table B 1 lists the total weir counts. Total estimates are then adjusted to exclude small adults, because they are considered to not contribute to the total production. For transboundary Chinook salmon, small adults are defined as adults with fork length less than 660mm. In practice the estimates are typically adjusted based on age composition, but the details differ among previous analyses. For example, the definition "EU age 1.3 and older" was used by

Bernard et al. (2000) for Stikine Chinook and by McPherson et al. (1999) for Taku Chinook, but Bernard and Jones (2010) used "all ages (1.1-1.5)".

We use a combination of age and size data to develop alternative estimates for annual proportion of small adults in the weir returns (next section).

ADFG helicopter surveys of the Little Tahltan River started in 1975, and ran in parallel with the weir operation from 1985 to 2009. Discontinuation of aerial surveys was recommended by Bernard et al. (2000), however they continued until 2009 when ADFG budgets became restricted. Sufficient data are available to establish a relationship between the weir count and the helicopter survey data, but we chose not to include re-scaled estimates from the aerial surveys to extend the time series back from 1985 to 1979, opting instead to focus our analysis on the observations collected with consistent methods since 1985. In contrast, Bernard et al. (2000) did a double expansion to get total Stikine spawner estimates for 1979 to 1984, first expanding aerial counts to "virtual weir counts", then expanding the virtual weir counts to a total Stikine abundance.

Bernard et al. (2000) found that age composition estimates from carcass surveys (1981-1988) were similar to weir samples (1985-1988). They recommended continuation of the weir counts as part of the Stikine stock assessment program, which also included a mark-recapture (MR) survey in the lower Stikine. They also found high correlation between Little Tahltan weir counts and Beatty Creek aerial-based index, but poor correlation with Tahltan River aerial-based index (frequent poor water clarity due to glacial source). They concluded that weir counts had sufficient quality to serve as the basis for Stikine-wide spawning goal estimate, and recommended that both the weir and the MR program in the lower river should continue. Bernard et al. (2000) did not mention potential weir effects on Chinook spawning distribution or mortality.

However, The CSAS peer-review process identified strong concerns with the weir counts, debating two alternative interpretations of recent counts of large Chinook at Little Tahltan weir:

- Consider the recent weir counts as invalid, due to the sudden, dramatic change in spawner counts (Figure 2), the recent disconnect between weir counts and lower Stikine MR-based estimates (Sec 2.1.1.3), the unusual age and size composition (Sec 2.1.1.2) and experience with other Chinook counting weirs (Table 1).
- Consider the recent weir counts as reflecting a real signal, consistent with a recent large-scale drop in size and age of Chinook salmon in Alaska and the Yukon (next section, Lewis et al. 2015).

Participants in the peer-review process considered it probable that weir effects and a large-scale productivity decline interacted to result in the observed pattern of spawner counts: Smaller, younger fish would be less productive, and might be more susceptible to weir effects. Any weir effects on spawning distribution or mortality would then become amplified during low-abundance brood years, especially if the Little Tahltan is only one of several opportunistic spawning areas within the Tahltan watershed.

Section 2.1.2 summarizes the observed patterns and Section 4.1 discusses implications for interpreting the results of our quantitative analyses. Table 1 summarizes observed effects of various Chinook counting weirs, which are described in more detail in Appendix A.

2.1.1.2 Age and Size Composition

Age and size data are collected annually at Little Tahltan weir, with sampling throughout the entire weir operation, and annual sample sizes ranging from 75 to 804 for age data and from 140 to 1,413 for size data over the period 2000-2013. Estimates of age composition at the weir

are available since 1985, but the size distribution (i.e. proportion of fish smaller than 660mm fork length) has only been worked up back to 1999. Note that we use the Gilbert-Rich age designations throughout the text, but also include the conversion to European-style age designations in the tables (e.g. GR 5.2/EU1.3).

A sampling target of 700 fish was established to assess the age and gender profile of the Little Tahltan return (Thompson 1987). In addition, a goal to observe/handle an additional 1,300 Little Tahltan Chinook was set with the objective of assessing the tag fraction (spaghetti and CWT) for the spawning population including both the small and large component. To note: all sampled fish, including fish sampled for age and size information, are assessed for tag presence.

Chinook are sampled throughout the entire weir operation, and samples are weighted by statistical week based on observed abundance.

Some migrating fish enter one of the two fish traps under their own volition. It was assumed that the traps are not size selective. Fish are extracted from the traps on a daily basis and sampled for age (five scales), size, presence of a spaghetti tag and secondary mark associated with the application of a spaghetti tag, and presence of a CWT as indicated by an excised adipose fin. Fork length is taken from all the fish; mid-eye-fork (MEF) and post-orbital-hypural (POH) length were alternately taken in units of ten. A linear regression relationship was generated to provide a proxy measurement for samples lacking either a MEF or POH measurement.

Table B 2 lists the available age composition estimates from 1985-2014. Annual age composition is estimated as the weighted average of weekly proportion of each age class in the scale samples.

Table B 3 lists size composition by age class for 2000-2013, expressed as the proportion of fish smaller than 660mm fork length observed in biosampling at the weir.

As the base case we chose to use the overall proportion (i.e. for each age class, we took the cumulative sample size of small fish / total), which implies the assumption that size composition is stable over time, but also uses the largest possible sample size.

As a sensitivity test, we resampled observed size proportions from the 14 years of available data, but note that some years have very small sample sizes. For example, in 2007 the total sample size was 67 large Chinook and 8 small fish, spread over 13 age classes.

We use this information to develop 3 alternative time series of estimated spawner abundance, defined as the number of large Chinook passing the weir:

- *WeirRet_AdjAge*: Apply annual age proportions to the total weir count, and for each age class apply the observed proportion of small fish (overall proportion in samples from 2000 to 2013). This is used in the base-case data set.
- *WeirRet_5&6*: Apply the annual proportion of age 5 and 6. This captures most of the weir counts in most of the years (median=90%, range=71-98%).
- *WeirRet_M3+*: Apply the annual proportion of all age class with 3 years in the ocean (i.e. GR: 4.1, 5.1, 5.2, 6.2, 6.3, 7.2, 7.3, 8.2, 8.3). This captures most of the weir counts in most of the years (median=95%, range=73-100%).

Table B 1 lists the total weir counts for 1985 to 2014, and shows the effect of the alternative approaches for estimating % small fish on estimated spawner abundance. Figure B 1 shows the pattern in observed spawner estimates from 1985 to 2014. Figure B 2 shows the range resulting from alternative definitions and resampling of the % small fish by age class, and Figure B 3 shows the change in estimated proportion of small fish over time for each of these alternative approaches. Figure B 4 summarizes age composition and Figure B 5 visualizes the small fish

ratios described in Table B 3. All 3 variations result in similar time series (Figure B 1), but there are differences in some years, most notably for 2004 which had the largest observed weir returns. Given that individual points on the recruit vs. spawner scatter plot can exert a disproportionate pull on the SR model fits, we tested all 3 variations.

Visual counts of small fish at the weir are also available since 1985, but note that the visual counts differ significantly from the proportion of 2-ocean fish (Figure B 3).

Some participants in the peer-review process considered the size and age composition of Chinook at Little Tahltan weir to be extremely unusual (i.e. proportion of small fish far lower than expected) and interpreted this as an indication that either weir counts are inaccurate or that the weir is having some effect on the population.

Section 2.1.2 summarizes the observed patterns and Section 4.1 discusses implications for interpreting the results of our quantitative analyses.

2.1.1.3 Proportion of Little Tahltan in Stikine Returns

In 1995, DFO, in cooperation with the Tahltan First Nation (TFN), ADFG, and the U.S. National Marine Fisheries Service (NMFS) instituted a project to determine the feasibility of a mark-recapture (MR) experiment to estimate abundance of Chinook salmon spawning in the Stikine River above the U.S./Canada border. Since 1996 a revised, expanded MR study has been used to estimate annual spawning escapement abundance (Pahlke and Etherton 1997, 1999, 2000; Pahlke et al. 2000; Der Hovanisian et al. 2003, 2004, 2005; Der Hovanisian and Etherton 2006; Richards et al. 2008, 2012). In 1997 and 2005, radio-telemetry was used in concert with the mark-recapture experiment to estimate the distribution of spawners (Pahlke and Etherton 1999; Richards et al. 2008).

Briefly summarizing the methods described in Pahlke and Etherton (1999):

- *Marking Step:* Chinook are sampled, tagged, and released near Kakwan Point in the lower river from early May to early July. Two drift gillnets are fished daily, unless high water or staff shortages occur. Nets are watched continuously, and captured fish are removed from the net as soon as they are observed. Sampling effort is as constant as practical across the full migration period. If fishing time is lost due to entanglements, snags, cleaning the net, etc., the lost time (processing time) is added at the end of the day to bring fishing time to 4 hours per net.
- *Recapture Step:* Pre- and post spawning fish are sampled at the Little Tahltan River weir. Post spawning fish are speared at Verrett and Shakes Creeks, and samples are collected from Canadian gillnet fisheries in the lower river.

The M-R estimate included samples (tag fractions) from the weir as part of a metric to generate a run size. Other sources of tag fraction are from the Lower Stikine River commercial fishery (major) and the Verrett Creek spawning site. In addition, the weir counts and Verrett Creek data are used to determine the proportion of small adults for the total aggregate.

Estimates of Little Tahltan contribution to the total Stikine run are based on the ratio of weir counts to mark-recapture estimates from the lower river, and are available since 1996. This proportion is applied to catch estimates for Stikine-origin Chinook in marine fisheries and lower river fisheries. We infill stock composition prior to 1996 using the median for 1996 to 2013. 2014 is excluded due to the rockslide.

To get an adjusted proportion for Upper Stikine catches, we scaled up the annual proportion observed in the lower river based on the average proportion of Little Tahltan vs. Tahltan Chinook observed in telemetry studies conducted on the Upper Stikine in 1997 and 2005

(Pahlke and Etherton 1999, Smith et al. 2007). The scalar for Upper Stikine catches is 2.28 when using the median telemetry proportion compared to the median lower river proportion, but ranges from 1.66 (2005) to 1.97 (1997) when using the annual estimates.

We considered using expansion of aerial surveys for 1985 to 1998 to get total Tahltan estimate and Little Tahltan contribution, but decided that the expansion based on Little Tahltan weir is applicable only to Beatty Creek, and does not reflect estimates for Tahltan River. Figure B 7 compares the patterns in aerial survey estimates and weir counts.

2.1.1.4 Coded Wire Tagging Program

In 2000, a program to capture Chinook salmon smolt in the lower Stikine River and mark them with adipose-clips and coded wire tags was initiated. Marked fish recovered as adults in fisheries and on the spawning grounds are used to estimate smolt production and harvest by brood year (Pahlke et al. 2010, Richards et al. in prep⁴).

2.1.1.5 Canadian Catches

Catches of Little Tahltan Chinook in Canadian in-river fisheries are estimated based on total catches and observed stock composition. All catch estimates are for large Chinook, determined based on age composition or size samples.

Five fisheries harvest Little Tahltan Chinook in the Canadian portion of the Stikine drainage (Figure C 1):

- *Lower river commercial fishery*: Total catches of all stocks were stable from 1979 to 2003, then spiked during the large runs and directed fishing in 2005/2006 and dropped again by 2009. Median catch is about 1,700 large Chinook, and catches were below 3,000 for most years before 2004 (except 1997), then reached 20,000 in 2005 and dropped back to 8,000 in 2008. Up to 19 licences participate; mesh size limited to 204 mm and up to two nets/licence permitted.
- *Lower river test fishery*: test fisheries occurred in years where there was no or limited TAC. The test fishery was capped at 1,400 large Chinook salmon taken from early May to the third week in June (statistical week 25). The commercial fleet served as the test fish fleet. Up to 19 licences participated; mesh size was limited to 204 mm and only one net permitted per licence. The fishing time varied from 4 hrs to three days per week.
- *Upper river Food, Social and Ceremonial (FSC) fishery*: Total catch of all stocks has been stable since 1979, with a median of about 900 and ranging from about 600 to about 2,000, with up to 30 licences fishing by members of the Tahltan First Nations and their designates. There are no gear or area restrictions, but most participants use a 15-20m net affixed to a boom pole extended into select river eddies. Most members have Chinook gear (large mesh up to 204 mm) and sockeye gear (small mesh 140-160mm)
- *Upper river sport fishery*: Total catch of all stocks has been stable since 1979, with a median of about 150 and ranging from 0 to about 500. Two Chinook permitted per day with an annual bag limit of 10 large Chinook.
- *Upper river commercial fishery*: Total catch of all stocks has been stable since 1979, with a median of about 40 and ranging from 0 to about 200. Up to two nets may be used. Only four parties are licensed to fish commercially in the upper Stikine River; only one license has been active in the recent past.

⁴ Richards, P.J., T.A. Jaecks, P. Etherton. Production of Chinook salmon from the Stikine River, 2002-2008. Alaska Department of Fish and Game, Fishery Data Series, Anchorage. In prep.

Estimated stock composition in the different fisheries is based on the observed ratio of weir counts to mark-recapture estimates for the lower river, and the same proportion is applied to marine fisheries. Upper river stock composition is re-scaled based on telemetry studies in 1997 and 2005 (see Section 2.1.1.3). For example, applying the median scalar gives the following estimates of Little Tahltan Chinook catch for 2009:

- *Lower river Canadian commercial fishery*: Total catch = 2,085, % Little Tahltan = 17.5%, Little Tahltan catch = 366
- *Upper river Canadian FSC fishery*: Total catch = 632, % Little Tahltan = 17.5% * 2.28 = 39.9%, Little Tahltan catch = 275

2.1.1.6 US Catches

Estimates of US catches of large-sized Stikine-origin Chinook salmon are derived from data collected through the large-scale coded wire tagging (CWT) program. Our analysis focuses on interceptions in the commercial gillnet fishery in Clarence and Sumner Straits, the recreational fishery near Petersburg and Wrangell, and the commercial troll fishery in Southeast Alaska (SEAK). For year classes with tagged fish, CWTs recovered during catch sampling in the 3 fisheries were expanded for the fraction of the catch inspected and the estimated fraction of each year class marked as per procedures described in Bernard and Clark (1996).

Our analysis covers following components:

- Troll fisheries (TROLL)
- Sport and gillnet fisheries outside District 108 (GN&SP-OUTER)
- Gillnet fisheries in District 108 (GN-108)
- Sport fisheries in D108 (SP-108)

The general approach is the same for each of these fisheries, but the details differ by fishery and time period. For example, all estimates are for large Chinook only, but the proportion of small fish is estimated based either on age classes (GR:5.2/ EU:1.3 and 6.2/1.4) or size data (>659mm). This matches the approach taken for spawner estimates and Canadian catches. Similarly, most of the individual time series require some infilling, but infilling is done either using all available data (e.g. 2003 to 2013 for GN&SP-OUTER) or using a subset of the available data (e.g. 2008 to 2013 for TROLL) to account for changes in fishing pattern.

In addition, Little Tahltan Chinook are intercepted in US in-river subsistence fisheries, but total Chinook catches are small (max = 64 fish). With a median proportion of 15.6%, these translate into less than 12 Little Tahltan Chinook at the high end. These values fall well within the rounding errors on the other catches, and Alaska subsistence fisheries are therefore not explicitly incorporated in the Little Tahltan run reconstruction.

SEAK troll fishery

This is a large-scale, multi-species fishery with high rates of sampling and CWT recovery averaging 40-45% for Chinook salmon. The recent (1986-2010) history and management of spring troll fisheries in SEAK can be found in Skannes and Hagerman (2011) and Stopha (1999). This fishery has undergone large-scale changes in management; the fishery has been closed most of the spring troll period (April 16 to June 30) since 1981, when Stikine-origin fish would have been harvested (McPherson et al. 1999). Additionally, there were no Stikine-specific CWT estimates for the calendar years prior to 2002, but we estimated troll harvests during this period using the average seen from 2008 to 2013. Age composition was estimated from CWT recoveries.

CWT recoveries indicate that >90% of Stikine Chinook harvests occur during spring troll fisheries in SEAK (Pahlke et al. 2010, Richards et al. in prep4). Given the magnitude of the harvest and the high sampling rate, the likelihood of recovering CWTs from this fishery is higher than for the other fisheries covered in our analysis.

Harvests of Stikine-origin Chinook salmon in the commercial troll fishery in SEAK were estimated directly from CWT recoveries.

Troll catch estimates of Stikine-bound Chinook are available for 5yr-old fish (GR: 5.2/EU:1.3) from 2003 to 2013 and for 6yr-old fish (GR: 6.2/EU:1.4) from 2004 to 2014. Troll harvest by age is listed in Table C 2. These estimates also include standard errors, developed through bootstrapping. Estimates of 4yr-old fish (GR: 4.2/EU:1.2) are available for some years, but these are assumed to be small adults with less than 660mm fork length and are excluded from our analyses. As a cross-verification, catch estimates based on GSI are also listed. Estimates of total Stikine-origin catch are available since 2003, and show a steep decline over that period, from a high of about 14,000 in 2005, which was a year with high abundance and directed troll fisheries in D108 to a low of 1,100 in 2013, which was a year with low abundance and no directed troll fishery in D108 (Figure C 2).

We infilled earlier years using the average for 2008-2013 for 5yr-olds and 2008 to 2014 for 6yr-olds, because these are years without directed Chinook harvest in the troll fishery, and we assume that they reflect the long-term level of harvest in the mixed-stock fishery (similar methods to McPherson et al. 2010).

The estimated magnitude and pattern of total Stikine interceptions based on CWT are confirmed by GSI-based estimates (Table C 2). Figure C 2 shows that the two alternative estimates track closely in terms of overall pattern, but can be quite different in some years (e.g. 2010). We use the CWT-based estimates in the run reconstruction.

The troll harvest of Stikine Chinook is also similar Taku Chinook, which have nearly identical marine life history, genetic makeup, and population size (McPherson et al. 2010).

To get the troll catch of Little Tahltan Chinook (bottom panel Figure C 2) we applied the estimated annual stock composition based on the ratio between Little Tahltan weir counts and mark-recapture estimates of total Stikine returns, as described in Section 2.1.1.3).

Gillnet, sport, and purse seine fisheries outside District 108

CWTs originally released in the Stikine River have been recovered in sport, gillnet, purse seine, and high seas trawl fisheries throughout SEAK, the gulf of Alaska, and northern British Columbia, however harvest estimates are very low. Estimates of total Stikine-origin catch are available since 2003, and have been low and stable (i.e. below 1,500), except for a spike in 2005 where catch was almost 4,000 Stikine Chinook (a year with extremely high abundance). We infilled earlier years using the average for 2003-2013.

Where Stikine-origin CWTs were found, these harvests were estimated from expansions of CWTs. Incidental mortality of Chinook salmon in marine fisheries was ignored in this analysis. Only the recreational fishery near Petersburg and Wrangell is known to cover the migration window of Chinook salmon returning to the Stikine River on an annual basis. Some fish caught in this fishery are most likely released and some of these released fish most likely die. However, the number of released, legal-sized Chinook salmon in this fishery is known to be minor, from annual creel sampling (Hubartt et al. 1999). Hence, the number of these incidentally killed Chinook salmon is negligible relative to the abundance of returning adults.

Catches outside District 108 are listed in Table C 3. Figure C 3 shows the pattern over time (upper panel). Gillnet and Sport catch estimates of Stikine-bound Chinook outside of District 108

are available for 5yr-old fish (GR: 5.2/EU:1.3) from 2003 to 2013 and for 6yr-old fish (GR: 6.2/EU:1.4) from 2004 to 2014. These estimates also include standard errors, based on bootstraps. Estimates of 4yr-old fish (GR: 4.2/EU:1.2) are available for some years, but these are assumed to be small adults with less than 660mm fork length and are excluded from our analyses.

To get the sport and gillnet catch outside District 108 of Little Tahltan Chinook (bottom panel of Figure C 3), we applied the estimated annual stock composition based on the ratio between Little Tahltan weir counts and mark-recapture estimates of total Stikine returns, as described above.

Gill net fisheries inside District 108

Prior to 2005, Chinook harvest in District 108 was low and restricted to by-catch in the directed sockeye fishery. In February 2005, an agreement was negotiated between the United States and Canada by the Transboundary Rivers Panel and approved by the PSC for directed harvest of wild Chinook salmon returning to the Stikine River (Annex IV, Paragraph 3). The gillnet fishery in District 108 accounts of the majority of the harvest in years of directed fishing.

Gillnet catch estimates of Stikine-bound Chinook inside of District 108 are available from different sources for three time periods:

- Calendar years 1981 to 1997 adopted from Table B4 in Bernard et al. (2000).
- Calendar years 1987 to 2004 from base level harvest of Stikine River Chinook salmon.
- Calendar years 2005 to 2014 from genetic stock identification (GSI) estimates (PSC 2015)

These estimates were adjusted to exclude hatchery-origin fish from 1981 to 2004. Bernard et al. (2000) state that this approach probably over-estimates catch, because it assumes that all the remaining catch is Stikine-bound (i.e. small harvests of Northern BC and Columbia River stocks are not removed).

Catches were low and stable up to 2003 (less than 1,800), then spiked from 2004 to 2008 (up to 21,000), and dropped to below 1,000 after 2008 (Figure C 4).

Age composition of harvests of Stikine-bound Chinook salmon in the commercial gillnet fishery offshore of the river mouth (U.S. District 108) from early May until mid July (stat weeks 19-29) was estimated by first discounting catches for hatchery production (1981 to 2004) and by genetic stock identification (2005 to 2014). Estimated harvests of hatchery-produced Chinook salmon from Alaska ranged from 310 to 850 since 1989. Prior to that year, harvests of all fish were small. Catch sampling for coded-wire tags began in 1994 and showed that on average 32.6% of harvests through 1997 were hatchery-origin. Catches from 1990 through 1993 were reduced by this fraction to develop estimates of naturally produced Chinook salmon in the harvest. For 1994-2004 direct estimates of harvests of hatchery produced salmon were subtracted from the District 108 gillnet harvest to estimate the contribution of Stikine River Chinook salmon. For 2005 to 2014, genetic stock identification was used to estimate the contribution of Stikine River-bound Chinook salmon in the D 108 gillnet fishery in statistical weeks (SW) 19-29. Gillnet harvest by age inside D108 is listed in Table C 4.

Although some Stikine-origin Chinook salmon are undoubtedly caught later than SW 29 (evidenced by CWT recoveries in some years), some harvest of other age-1.X stocks (non-Stikine River origin) is also included in our estimates and we expect these differences to be approximately equal and cancel out.

Estimated marine gillnet harvests in District 108 were apportioned among year classes by applying the lower river Canadian commercial age composition.

Sport fisheries inside District 108

Estimates of total Stikine-origin catch are available back to 1981 through a combination of data for 3 distinct time periods. Catches were stable and larger than gill net catches up to 2003 (ca. 1,500 to 4,500), then stayed at that level while gillnet catches spiked, and dropped to below 700 after 2008 (Figure C 4). These estimates were adjusted to all exclude hatchery-origin fish from 1981 to 2004. Genetic stock identification was used to estimate Stikine Chinook contribution from 2005 to 2014.

Sport catch estimates of Stikine-bound Chinook inside of District 108 are available from different sources for three time periods:

- Calendar years 1981 to 1997 adopted from Table B5 in Bernard et al. (2000).
- Calendar years 1987 to 2004 from base level harvest of Stikine River Chinook salmon.
- Calendar years 2005 to 2014 from genetic stock identification (GSI) estimates (PSC 2015)

Age composition of harvests of Stikine-bound Chinook salmon in the recreational fishery near Petersburg and Wrangell (District 108) was also estimated by first discounting catches for hatchery production from 1981 to 2004. Hatchery contributions to the harvest were estimated from catch sampling for CWTs since 1981 (see Hubartt et al. 1999 for details). Estimated hatchery contributions were subtracted from estimated harvest, with the remainder considered to have been bound for the Stikine River. Bernard et al. (2000) state that this approach probably over-estimates catch, because it assumes that all the remaining catch is Stikine-bound. The longstanding size limit for retaining Chinook salmon in this fishery has been 710 mm (28 inches) total length, so the numbers of age 1.2 fish in the harvest were considered nil and were not estimated.

From 1981 until 1997 age composition of recreational harvests was estimated as the product of the harvest of naturally produced salmon (as determined by CWT) and the relative age composition among large Chinook salmon spawning in the Stikine River. From 1998 to 2014 the recreational harvest was estimated as the product of the harvest of naturally produced salmon (determined by GSI) and the relative age composition among large Chinook salmon in the Canadian lower river commercial harvest.

Sport harvest by age inside D108 is listed in Table C 5. Some of these estimates also include standard errors based on bootstrapping. Estimates of 4yr-old fish are available for some years, but these are assumed to be small adults with less than 660mm fork length and are excluded from our analyses.

2.1.1.7 Total Run Size and Alternative Brood Tables

Estimated annual total run size of Little Tahltan Chinook is calculated as the sum of spawner abundance plus Canadian catches and US catches, with early years for relying on infilling for one or more component data sets (e.g. total Stikine-origin troll catch, % Little Tahltan)

Estimated recruitment by brood year is then calculated based on the observed annual age composition.

As for the spawner abundances above, we test two alternative age composition assumptions.

- *Rec5&6*: Apply the annual proportion of age 5 and 6 (i.e. GR:5.2 and 6.2). This captures most of the weir counts in most of the years (median=90%, range=71-98%).
- *RecM3+*: Apply the annual proportion of all age class with 3 years in the ocean (i.e. GR: 4.1, 5.1, 5.2, 6.2, 6.3, 7.2, 7.3, 8.2, 8.3). This captures most of the weir counts in most of the years (median=95%, range=73-100%).

Throughout this analysis, we compare 4 alternative combinations of spawner data and recruit data (Section 2.3.1). The base case data set uses weir returns which exclude small adults based on the observed average proportion of small adults for each age class (AdjAge) and 5-6 year old recruits (Rec5&6).

The next section summarizes observed patterns in the reconstructed spawner-recruit data set for Little Tahltan Chinook.

2.1.2 Exploratory Data Analysis (EDA) for Little Tahltan Chinook

Figure 2 shows the alternative time series used for the spawner-recruit analyses presented in this report. Figure 3 shows the base-case time series rescaled to isolate the underlying signal using ranked deviations from the median (Section 13.2) and comparing the ranks by brood year. Brood years 2001, 2004, and 2005 are flagged as having spawner abundances near the upper end of the observed range associated with recruitment near the lower end of the observed range. The 3 largest spawner abundances (1993, 2001, and 2004) all had low recruitment.

Figure 4 shows scatter plots of the spawner-recruit data. The pattern is very similar across all 4 alternative data sets. Most of the spawner abundances are between about 3,000 and 6,000, and the resulting recruitment from this range of spawners has been extremely variable, from about 2,000 to about 23,000 (corresponding to a range of 0.5 – 5 recruits/spawner). Spawner abundances above 6,000 have consistently resulted in poor to very poor recruitment.

At first glance, this could be interpreted as a strong signal of density-dependent effects (i.e. spawner abundance above capacity resulting in reduced recruitment). However, the fact that production remained low in subsequent years despite declining spawner abundance (2006, 2007) points to a potential larger-scale issue, such as marine or freshwater survival, or some issue with the recent weir counts (discussed below).

Figure 5 shows patterns in total run, total ER, and harvest rate by country, as well as the observed relationship between run size and exploitation rate.

Total runs have stayed low in the years since 2007, for which brood year recruit estimates are not yet available (Figure C 8). Note, however, that the total Stikine abundance has not declined to the same extent as Little Tahltan (i.e. Little Tahltan proportion has dropped, Figure B 6). Production of Little Tahltan Chinook spiked in the 1999 and 2000 brood years, resulting in large returns and large catches in 2004 and 2005, then dropped rapidly by 2007 and stayed substantially below long-term average.

Total exploitation rate has been roughly in the 20%-40% range with US harvest rate about 19% (8%-41%) and Canadian harvest rate about 14% (4%-30%) over the period 1985 to 2013. Exploitation rate peaked at 60%-70% in 2005-2007, with 2004 and 2005 having a large run and large catch, and both catch and run dropping steeply over the next 2 years.

These observed patterns in the spawner-recruit data need to be interpreted in the context of the patterns in the components of the run reconstruction, with details in Appendices B and C:

- Total weir returns since 1985 averaged around 5,000, but spanned a very wide range from 209 in 2014 (with the rockslide) to 16,631 in 2004 (Table 2). There has been a pronounced pattern in weir returns, which was stable or slightly increasing from 1985 to 2004, then declined sharply and stayed low. Eight of the 10 lowest returns occurred in the last 10 years (Figure B 1)
- Age and size composition of Chinook salmon sampled at Little Tahltan weir has changed persistently over the last 30 years (Figure B 3 to Figure B 5), shifting towards younger age-at-maturity (i.e. fewer age 6, more age 4 and 5) and smaller size (i.e. higher proportion of

small adults with less than 660mm fork length). Lewis et al. (2015) identified broad-scale declines in average size and age of Chinook salmon in Alaska and the Yukon. Figure B 4 shows the same pattern for Little Tahltn Chinook, with the proportion of 6yr olds dropping steadily and the proportions of 4yr and 5yr olds increasing. The rockslide in 2014 has further drastically altered the age and size composition of Little Tahltn Chinook for the 2014 brood year (see last data point in Figure B 3 to Figure B 5), and preliminary observations for 2015 indicate this may be a persistent effect.

- Estimated proportion of Little Tahltn Chinook in the Stikine run has been highly variable, but shows an overall declining trend (Figure B 6), ranging from 13% to 34% over the period 1996-2009 (except for 4% in 2007), from 3% to 7% over the period 2010 to 2013, and only 0.7% after the rockslide in 2014.
- Productivity of Little Tahltn Chinook spiked in the 1999 and 2000 brood years, resulting in large returns and large catches in 2004 and 2005. However, in 2007 returns dropped dramatically to well below the long-term average and have not rebounded. This has resulted in escapements below the range 2,700 to 5,300 identified by Bernard et al. (2000) as corresponding to the total Stikine goal of 14,000 to 28,000.

During the peer-review process, three alternative explanations for the observed patterns were discussed (DFO 2016a):

- *Hypothesis 1:* Inaccuracies in recent weir counts
- *Hypothesis 2:* Changing productivity regimes
- *Hypothesis 3:* Stock collapse

Figure 6 summarizes the 3 key pieces of this puzzle:

- Little Tahltn weir counts and lower-river Mark-Recapture estimates for the total Stikine initially followed a similar pattern but diverged starting in the 2007 return year.
- Estimated productivity dropped precipitously in the 2001 brood year and stayed below replacement until the 2007 brood year, which had the lowest spawner abundance in the time series.
- Estimates of recruits and spawners fall into two distinct 2 time periods: An early period (1985-2000) with stable spawner abundances and highly variable recruitment, and the recent period (2001-2007) with highly variable spawner abundances and very poor recruitment.

As a comparison, Figure 7 shows the patterns in SR data used by Bernard et al. (2000) to develop biological benchmarks for total Stikine Chinook. Estimates used by Bernard et al. (2000) were based on the same weir counts as our base case for the period 1985 to 1997, but they expanded weir counts to estimate total Stikine spawners, whereas we scaled down catch estimates to get a data set for Little Tahltn. In addition, they included estimates based on aerial surveys from 1977 to 1985, which we did not include. Figure B 7 shows that aerial and weir counts tracked each other closely, and Bernard et al. 2000 reported a Pearson correlation coefficient of 0.86. Overflights were discontinued soon after. Table B 5 lists their estimates. At the time, the data showed annual variability, but nothing like the sudden and persistent drop observed in recent years, and the two alternative observations (weir vs. aerial) showed similar patterns, unlike the discrepancy between recent weir counts and mark-recapture estimates. Finally, the SR scatter plot of their estimates does not show any obvious clustering of earlier and later observations.

In addition to the patterns highlighted in Figure 6, participants also offered examples of other Chinook counting weirs that were discontinued due to observed effects on spawning distribution or mortality. Following the meeting, we compiled a summary of implementation experience for Chinook counting weirs using three complementary approaches:

- Informal e-mail survey of Chinook stock assessment experts conducted between November 2015 and March 2016.
- Review of stock assessment reports published by DFO and ADFG.
- Review of most recent annual CTC report on catch and escapement data (PSC 2015).

Observed effects of various Chinook counting weirs are summarized in Table 1, and Appendix A lists weir-by-weir details. All contributors and sources are identified in Appendix A.

The intent was to verify the anecdotal weir-related concerns that were brought up during the CSAS review in November 2015. Appendix A lists information for different weirs, and Table 1 summarizes the key points. Section 4.1 discusses implications for interpreting the weir counts of Little Tahltan Chinook.

Based on the observed patterns and experiences with other Chinook counting weirs in similar settings (Nahlin River, Kitwanga River, several Upper Fraser systems listed in Table A 3), participants in the peer-review process considered it probable that weir effects and a large-scale productivity decline interacted to result in the observed pattern of spawner counts: Smaller, younger fish would be less productive, and might be more susceptible to weir effects. Any weir effects on spawning distribution or mortality would then become amplified during low-abundance brood years, especially if the Little Tahltan is only one of several opportunistic spawning areas within the Tahltan watershed.

After intensive debate, the consensus conclusion was that biological benchmarks based on spawner-recruit data cannot be estimated with the data currently available, but that it would be nevertheless informative for decision-makers to document our benchmark estimates and summarize the data concerns identified during the peer-review.

Sections 2.2 to 3.2 of this report focus on the methods and results for quantitative analyses of the available data, assuming that the spawner and recruit estimates in Figure 4 are reasonably accurate and can be used to update and expand the biological benchmark estimates developed by Bernard et al. (2000). Section 4.1 then discusses the data concerns described above and their implications for interpreting the quantitative estimates.

2.2 PERCENTILE METHOD FOR DATA-POOR SYSTEMS

Note that this section carries over text from Pestal and Johnston (2015).

This method identifies a biological reference range based on some percentiles of observed spawner abundance. ADFG has a step-wise algorithm based on contrast in the data (e.g. Table on p6 of Volk et al. 2009), while DFO has used 25th and 75th percentiles as the default (e.g. English et al. 2014). Both implementations refer back to work by Bue and Hasbrouck² and label the resulting range a Sustainable Escapement Goal (SEG).

This approach has been widely used for stocks that have a time series of spawner abundance but lack the information to estimate either juvenile production (e.g. smolt survey) or total adult returns (e.g. stock-specific catch estimates based on coded-wire tag recoveries)

Recent examples include:

- Volk et al. (2009) present 73 escapement goal recommendations for salmon stocks in the Arctic-Yukon-Kuskokwim region in Alaska: 59 of these (80%) are SEG based on the percentile method and 14 are BEG based on S_{MSY} estimates from a SR model fit.
- Most of the spawning goals reported as part of the ecocertification of BC Chum Salmon are SEG based on the percentile method (English et al. 2014).
- Pestal and Johnston (2015) tested 2 alternatives of the percentile method for the data-rich Taku Coho stock aggregate, and found that the percentile-based SEG ranges were cautionary and robust approximations of S_{MSY} estimates derived from spawner-recruit models.

Section 13.3 documents our implementation of the steps described by Volk et al. (2009) using the statistical package R (R Core Team 2013). First, round up spawner estimates to 2 significant figures, then choose the appropriate percentile range to calculate, based on the observed contrast in the data according to the following criteria, attributed to Bue and Hasbrouck²:

- if contrast <4 , then use 15% and largest observed;
- if contrast is ≥ 4 and <8 , then use 15% and 85%; or
- if contrast is > 8 , then use 75% for the upper bound and 15% for the lower bound if ER is low, or use 25% for the lower bound if ER is moderate to high. Volk et al. (2009) do not specify a cut-off between low and moderate ER, so our code in Section 13.3 calculates and reports both lower bounds.

A recent simulation study (Clark et al. 2014) recommends using the percentile method only for stocks with low to moderate harvest levels. Clark et al. (2014) also propose a different set of break-points, as follows:

- Not applicable if ER $> 40\%$, or if contrast ≤ 4 and measurement error = high;
- if contrast > 4 and < 8 , then use 5% and 65%;
- if contrast >8 and measurement error = low, then use 15% and 65%;
- if contrast >8 and measurement error = high, then use 20% and 60%.

We apply all 3 alternative sets of criteria (DFO, ADFG using Volk et al. 2009, and ADFG2 using Clark et al. 2014) to alternative spawner time series to test sensitivity, and check all these variations in over different subsets of data (retrospective, jackknife; see section 2.4). We round up spawner observations to 2 significant figures, as done by Volk et al. (2009).

2.3 BIOLOGICAL BENCHMARKS BASED ON SPAWNER-RECRUIT ANALYSIS

Note that this section carries over text from Pestal and Johnston (2015).

2.3.1 Spawner-Recruit (SR) Models

When estimates of adult recruitment are available in addition to spawner data, we can go beyond the approximate methods described in the previous section and use the observed interaction between spawner abundance and productivity to determine biological benchmarks.

The basic steps are to first choose a candidate model for the relationship between spawners and recruits, then estimate the model parameters from the observed data (i.e. fit a line through

the scatter plots in Figure 4). By testing alternative model forms we can find out whether the conclusions are robust, or whether different starting assumptions produce widely differing results.

We fitted three alternative SR models (equations in Table 7)

- Standard Ricker model with density-dependence and log-normal errors (e.g. Bernard et al. 2000, McPherson et al. 2010, Grant et al. 2011, Holt and Ogden 2013);
- Extension to the standard Ricker Model to account for autocorrelation in residuals (i.e. series of good years and series of bad years) (e.g. Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al. 2011, Hamazaki et al. 2012);
- Beverton-Holt model characterized by approaching a fixed production limit at larger spawner abundances (i.e. a maximum number of recruits), rather than a density-dependent decline in production (e.g. Korman and Tompkins 2014)

We fitted the three alternative SR models to four alternative data sets (Table 4):

- *Base Case*: Weir returns which exclude small adults based on the observed average proportion for each age class (AdjAge) and 5-6 year old recruits (Rec5&6), covering brood years from 1985 to 2007 ;
- *RecM3+*: Same spawner abundance as base case, but including recruits for all age classes with 3 years in the ocean, covering brood years 1985 to 2005;
- *Only 5&6*: Using 5 and 6 year old age classes for both weir returns and recruits, covering brood years from 1985 to 2007.
- *Only M3+*: Using all age classes with 3 years in the ocean for both weir returns and recruits, covering brood years 1985 to 2005.

Appendices D and E document the computer code used to calculate the SR model fits and associated benchmarks, which we implemented in the statistical package R (R Core Team 2013). The rest of this section briefly summarizes each step.

Figure C 10 shows QQnorm plots of log-transformed observations for each of the five time series (Figure 2) that are used in the four alternative SR data sets listed above. QQnorm plots plot the percentiles in an observed data set against the percentiles of a normal distribution, resulting in a linear pattern along the diagonal if the 2 distributions are similar. All are roughly log-normal, and we assume log-normal errors in all the SR model fits described below. Note, however, that the more recent observations of very low spawner abundance introduce a strong deviation from the log-normal distribution (Figure C 11), identified in the lower left corner of the 3 QQNorm plots for spawner data. Recruit estimates for those years are not yet available. These deviations will need to be taken into account in future updates of the SR fits, once additional recruit estimates can be incorporated.

2.3.2 Simple estimates of SR model parameters

Several recent studies include simple deterministic Ricker fits as a first step before exploring other models (e.g. McPherson et al. 2010) or more complex estimation methods (e.g. Holt and Ogden 2013, Pestal and Johnston 2015). We expand on this approach by testing alternative model forms and alternative estimation approaches.

As a first consistency check, we estimated maximum-likelihood (MLE) parameters for the linear Ricker form, $\ln(R/S) = \ln(a) - bS$, with the simple linear regression function $lm()$ in R (code in Section 13.4). To check for residual autocorrelation in each of the 4 alternative data sets, we

applied the Durbin-Watson test using the `dwtest()` function of the linear model testing package `lmtest` in R.

As a second consistency check, we fitted the Ricker and Beverton-Holt models (Table 7) in MS Excel using either the `slope()` and `intercept()` functions or MS Solver with the GRG Nonlinear algorithm to minimize the sum of squares. We explored the following variations:

- Ricker: Linear regression of $\ln(R/S) = \ln(a) - bS$.
- Beverton-Holt V2: Linear regression of $1/R = d + c(1/S)$
- Ricker, Beverton-Holt V1, Beverton-Holt V2: minimize either sum of squared errors (SSE) or the sum of squared log errors (SSLE).

Holt and Ogden (2013) point out that SR-based benchmarks may not be appropriate for populations with very low productivity, and recommend Ricker $a < 1.5$ (i.e. $\ln(a) < 0.4$) as the criterion. We adopted their approach, and used the simple linear regression fits to verify whether Bayesian SR model fits are appropriate.

2.3.3 Bayesian MCMC Method to fit SR models

The main analyses for this report are based on Bayesian estimates using Markov Chain Monte Carlo (MCMC). This is the approach taken in most recent work on biological benchmarks for Pacific Salmon by ADFG and DFO (e.g. Brown et al.³, Eggers and Bernard 2011, Grant et al. 2011, McPherson et al. 2010)

We implemented the MCMC using the R2OpenBUGS package in R in combination with OpenBUGS (Sturtz et al. 2005) but also cross-checked the results using R2jags package in R in combination with JAGS (Su and Yajima 2014).

Our approach to MCMC estimation follows the methods described by Grant et al. (2010), and our BUGS code grew out of their long-evolving library of functions (Cass et al. 2006, Grant and MacDonald 2011, Grant and MacDonald 2012, MacDonald and Grant 2012). BUGS code for the Beverton-Holt model was adapted from an example provided by Mike Hawkshaw (DFO).

Appendix D documents the BUGS/JAGS model code and Appendix E documents the associated R code, including key function calls from the R2OpenBUGS() and R2jags() packages.

Table 9 summarizes the priors and settings used for each SR model variation. Table 10 summarizes the diagnostics we used to assess MCMC convergence and model fit.

2.3.4 Benchmark Estimation

For each deterministic estimate or MCMC sample of spawner-recruit parameters, we calculated the estimated value of biological benchmarks S_{MSY} , S_{MAX} , and S_{EQ} based on the equations in Table 8 which are derived from the simplified calculation developed by Hilborn (1985). Benchmark definitions are listed in Table 6 and illustrated in Figure 8.

When calculating biological benchmarks, ADFG analyses typically apply a bias correction to the productivity parameter (e.g. Bernard et al. 2000, McPherson et al. 2010, Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al. 2011, Hamazaki et al. 2012), but this has not been applied for the WSP benchmarks (Grant et al. 2011, Brown et al.³) and is not part of the WSP Software toolkit (Holt and Ogden 2013).

We used the bias correction as the base case in our analyses to stay consistent with other Transboundary analyses (i.e. McPherson et al. 2010 for Taku Chinook Salmon, Bernard et al.

2000 for Stikine Chinook Salmon, Eggers and Bernard 2011 for Alek Sockeye Salmon), but present uncorrected estimates as part of the sensitivity analyses.

2.4 OVERVIEW OF SENSITIVITY ANALYSES

In addition to four alternative spawner-recruit data sets and three alternative SR model forms (Sec 2.3.1), we also tested the sensitivity of SR model fitting approaches and resulting benchmark estimates.

The base case for all SR model fits was to use:

- all available years of data (1987 to 2009 brood years for adult recruits, 1990 to 2010 brood years for smolts);
- Bayesian MCMC estimates using `r2OpenBUGS()` and `OpenBUGS`;
- Derived benchmarks based on the equations in Table 8 with bias correction on the productivity parameter.

Sensitivity analyses cover variations in the data set and variations in the estimation approach (Table 11).

We tested the effect of two resampling approaches:

- Retrospective: increase the time window used to fit the model starting with the 1985-1996 period and increasing it up to 1987-2007.
- Jackknife: drop each observation and use the rest to fit the model

We compared the results from the following 4 alternative approaches to estimating derived biological benchmarks:

- Bayesian estimates using `R2OpenBUGS()` and `OpenBUGS`;
- Bayesian estimates using `R2jags()` and `JAGS`;
- Deterministic estimates using linear regression
- Deterministic estimates using MS Solver
- Using the software package developed by Holt and Ogden (2013) to estimate WSP benchmarks and metrics, which includes 80% S_{MSY} . Calculations are done in BUGS linked to the `PBSModelling()` Package in R. For now it includes only the standard Ricker model.

Finally, we checked derived S_{MSY} estimates against values calculated directly based on the largest median difference between recruits and spawners for 500 increments over the range $[0, 1.5 * \text{largest observed Spn}]$.

2.5 PRESENTATION OF RESULTS

We present the results in various formats relevant to the two institutional frames of reference currently applied by ADFG and DFO. The concepts are described in Section 1.3 of Pestal and Johnston (2015) and implementation details are summarized in their Section 2.5. This approach was reviewed and accepted by CSAS in the fall of 2015, and we apply it the same way here.

BM ranges, non-parametric measures of precision

We summarize posterior distributions of SR parameters and biological benchmarks with the percentiles p_{10} , p_{25} , p_{50} , p_{75} , p_{90} . In our notation, $p_{\#}$ is the proportion of samples smaller than a particular value, such that, for example, $p_{90} = 3,100$ means that 90% of the samples are

smaller than 3,100 and 10% of the samples are larger than 3,100. Therefore p90 captures the upper tail of the benchmark distribution, with a high probability that this value meets or exceeds the true benchmark.

We also report three simple measures to summarize the spread in sample distributions: Non-parametric Coefficient of Variation (NPCV), Standardized Interquartile Range (SIQR), and Standardized Median Absolute Deviation (SMAD). Section 13.5 in Appendix E lists the definition of these measures and includes the R code used to calculate them. Of these three variations, we use NPCV in subsequent comparisons (e.g. to rank by precision), because it is the only one with a published threshold (25%; Clark et al. 2009). Note that NPCV and SIQR are only valid if the sample range does not span zero.

Yield profiles

Recent ADFG reports with spawning goal recommendations (Section 1.3.5 of Pestal and Johnston 2015) include yield profiles that capture the notion of “pretty good yield” (PGY) as defined by Hilborn (2010).

We implement two versions of this:

- PGY: plot the probability of meeting overall MSY, based on comparing the distribution of expected yields across parameter samples for each spawner abundance to the overall median MSY.
- OY: plot the probability of meeting MSY for each parameter sample, based on comparing the distribution of expected yields across parameter samples for each spawner abundance to the sample-specific MSY

The OY version is consistent with recent ADFG publications (e.g. Figure 10 in Eggers and Bernard 2011)

Recovery profiles

Recent DFO reports with status assessments include estimates of S_{GEN} as a key piece of information (definition in Table 6). In status assessments under Canada’s *Wild Salmon Policy*, S_{GEN} is used as the lower benchmark for one of the status metrics. Refer to Section 1.3.5 of Pestal and Johnston 2015 for a brief overview of the status metrics, and to Grant et al. (2011) for the details.

We show information relating to the lower benchmark for the *Relative Abundance* metric in a plot equivalent to the yield profiles described above. At each increment of spawner abundance, we compare the distribution of recruits across parameter samples to the median S_{MSY} and count the proportion that is larger. The resulting profile shows the probability of rebuilding to S_{MSY} in 1 generation in the absence of fishing, which is the basis for formal estimates of S_{GEN} .

Summary reference points (SRP)

Yield and recovery profiles capture a lot of relevant information (e.g. shape of the curves), but are difficult to interpret across many sensitivity analyses.

Pestal and Johnston (2015) proposed a suite of Summary Reference Points (SRP) that extract key information from these plots into a simple summary of biological reference ranges, capturing plausible interpretations of the benchmark distributions, yield profiles, and recovery profiles. For example, if S_{MSY} has 10th percentile at 2,500 and 90th percentile at 3,800 (Table 15, basic Ricker, base case data set, bias correction), these bookends reflect the same tail end of the distribution, but mean different things for status assessment and fisheries planning. A spawner

abundance (or goal) at 2,500 has a 90% probability of falling short of S_{MSY} , while 3,800 has a 90% probability of meeting or exceeding S_{MSY} .

The notation is Label#, with # indicating a percentile or probability level.

We propose the following SRP:

- SMSY50 = Median of MCMC posterior or bootstrap distribution of S_{MSY} ;
- LBM90 = the lowest spawner abundance that has a 90% or more probability of rebuilding to SMSY50 in one generation in the absence of fishing, $\text{Prob}(\text{Rec} \geq \text{SMSY50})$, which is the point where the recovery profile crosses the 90% threshold, so that it reflects a 90% probability that this spawner abundance meets or exceeds the Lower WSP BM for *Relative Abundance*;
- UBM90 = 90th percentile of distribution for 80% SMSY50, which reflects a 90% probability that this spawner abundance meets or exceeds the Upper WSP BM for *Relative Abundance*;
- PGY7070 = range of spawner abundances with 70% or more probability that the yield meets or exceeds 70% of MSY (median yield at SMSY50), which correspond to the segment of the yield profile above the 70% threshold.

As an illustration, we also report three arbitrary alternatives to PGY7070, showing the range of spawner abundances with 60% probability of 70 % MSY, 80% MSY, or 90% MSY.

Note that these proposed SRP are not intended to be management reference points as defined by Holt and Irvine (2013); they are used only to compare a large number of sensitivity analyses side-by-side in a simplified summary that addresses both ADFG and DFO frames of reference.

3 RESULTS

Note: The results presented in this section are based on the assumption that the spawner and recruit estimates in Figure 4 are reasonably accurate and can be used to update and expand the biological benchmark estimates developed by Bernard et al. (2000). Refer to Section 4.1 for a summary of data concerns identified during the peer-review process and their implications for interpreting the quantitative results.

3.1 PERCENTILE METHOD FOR DATA-POOR SYSTEMS

Table 12 shows percentile-based SEG ranges calculated for large Chinook based on all years with weir counts (1985-2013). 2014 was excluded due to the rockslide.

The approach used by ADFG in recent years and the DFO approach produce an identical range of 2,800 to 6,400 Chinook Salmon for the base case data set, based on the 25th-75th percentiles because contrast in the spawner observations is very large ($\gg 8$) according to the ADFG criteria (see Section 2.2, and Fair et al. 2011). The revised criteria recommended by Clark et al (2014) result in a lower range of 1,800 to 5,420 based on the 15th-65th percentiles.

Results are similar for 4 of the 5 alternative abundance time series, but percentile-based SEG come out much lower if only years with size-based estimate of % small adults are included and data are limited to 2000-2013.

Figure 9 shows that percentile-based SEG ranges are wide, but stable over time and insensitive to individual observations. Stable over time also means that SEG ranges smooth out the signal from highly variable time series, but lag behind any persistent change. This is highlighted for the

period 2005 to 2013, where the SEG range is declining gradually while weir counts had a drastic and persistent drop.

3.2 BIOLOGICAL BENCHMARKS BASED ON SPAWNER-RECRUIT ANALYSIS

3.2.1 Deterministic SR Fits – Alternative SR Models and Data Sets

Note that these estimates are intended as a diagnostic check for the Bayesian estimates, and should not be used for setting spawning goals.

Table 13 lists results for regression-based point estimates of parameters for the basic Ricker model for each of the 4 alternative data sets and corresponding tests for serial autocorrelation. All 4 SR data sets have high intrinsic productivity ($\ln(a) > 0.4$, $a > 1.5$), so biological benchmarks can be calculated (Holt and Ogden 2013). Neither of the data sets shows strong autocorrelation in residuals from the basic Ricker model.

Table 14 summarizes deterministic estimation cross-check using simple methods. All estimates are for the base case data set. Ricker model fits are identical across 3 different estimation methods, but are affected by assumptions about the error structure. Ignoring the common log-normal shape of SR residuals (i.e. using MS Solver to minimize SSE rather than SSLE) results in a higher estimate of productivity (larger a parameter) and a larger S_{MSY} estimate. Beverton-Holt fits are identical for the 2 alternative model forms, but are strongly influenced by the estimation method. The productivity parameter ($'b'$ = spawner abundance that achieves half of the maximum recruitment) is more sensitive than the capacity parameter ($'a'$ = max recruits). S_{MSY} estimates for the Ricker fits are substantially higher than for the Beverton-Holt fits (Ricker: 2,600 to 2,800 / Beverton Holt: 1,500 to 1,800).

Figure 10 shows the recruitment and yield curves corresponding to the alternative estimates listed in Table 14. The plot highlights the fundamental difference between the standard Ricker fits with density-dependent decline in production at larger spawner abundances (i.e. curves drop down on right side of the plot) and the Beverton-Holt model which approaches a maximum production (i.e. curve flattens out on right side of the plot). Dropping the assumption of log-normal error structure has the opposite effect for the 2 alternative models. The Ricker curve jumps up and shifts left, estimating a higher productivity (steeper slope at origin) and larger production (higher peak of the curve). The Beverton-Holt curve drops down and shifts right, estimating a lower capacity (i.e. lower max Rec) and lower productivity (i.e. larger $'b'$ parameter means that more spawners are required to achieve half of the max Rec). The inverse linear regression estimate shifts the Beverton-Holt curve even further down and right. Despite these shifts in fitted curves, resulting estimates of S_{MSY} are similar within each model type. For an illustration, see the two different Beverton-Holt fits illustrated in the yield plot in the bottom panel of Figure 10.

3.2.2 Bayesian SR Fits – Alternative SR Models and Data Sets

The results in this section are all based on Bayesian MCMC estimation using r2OpenBUGS() and OpenBUGS. Model forms are listed in Table 7. Prior assumptions and MCMC settings are listed in Table 9.

Figure 12 to Figure 15 show the three alternative SR fits for the base-case data set ($S_{pn} = AdjAge$, $Rec = 5 \& 6$). Each figure has four panels, showing the recruitment curve as well as the resulting yield curve and two alternative probabilistic yield profiles (see Section 2.5 for definitions of PGY and OY). Figure 12 to Figure 14 show posterior distributions of fitted values for the Ricker, Ricker AR1 and Beverton-Holt models. Figure 15 compares the median fits across model forms.

Table 15 lists percentile values for posteriors of S_{MSY} , S_{MAX} , and S_{EQ} , as well as simple indicators of precision for 3 SR model variations fitted to the base-case data set (Spn= AdjAge, Rec=5&6). Table 16 lists corresponding model fit, precision, and Summary Reference Points (SRP) for all 12 model-data combinations that we tested.

Figure 16 plots model fit (DIC) vs. precision (NPCV) for the 12 combinations of SR model variations and data sets.

Figure 17 shows the shape of posterior parameter distributions for 3 variations of the Ricker model fitted to the base-case data set.

All three SR model variations fit the base-case data well, and resulting posterior distributions are fairly precise (Figure 15, Table 15), with all NPCV < 25% (Clark et al. 2009). Median S_{MSY} (SMSY50) estimates are similar across data sets, but differ among the three alternative SR models. SMSY50 for Ricker AR1 is slightly higher than for the basic Ricker (2,800 to 3,100 vs. 2,700 to 2,900), but both Ricker fits produce estimates substantially above the Beverton-Holt fit (1,900 to 2,000). All the other reference points follow the same pattern.

The Deviance Information Criterion (DIC), summarized in Table 16 and plotted in Figure 16, measures statistical fit based on the MCMC sample distributions as a combination of spread in the posteriors of all the model parameters and a penalty for additional parameters (See definition in Table 10). Models with better fit have lower DIC.

For Little Tahltan Chinook, the Beverton-Holt model clearly has the best statistical fit (lowest DIC values) across alternative data sets, while both Ricker variations have similar, poorer DIC.

DIC values have a consistent pattern across data sets with M3+ (more age classes, fewer brood years in the data set) having lower DIC than 5&6. This can be explained by the 2 extra data points in the 5&6 data sets, especially the extreme observation from 2007. However, the two additional years of recent data are consistent with subsequent spawner observations for 2008 to 2013, which cannot be captured in any of the SR fits (recruit estimates not yet available). Essentially, data points for 2006 and 2007 provide an initial signal of recent changes, affect the SR model fit, and change the resulting benchmark estimates (the additional data points reduce productivity estimates and increase productivity-based reference points like SMSY50 and LBM90)

Statistical fit and the estimate precisions are typically correlated, such that better fits (lower DIC) should also produce more precise estimates (lower NPCV). Pestal and Johnston (2015) observed that this expectation roughly held up for Taku River Coho. In our results, this pattern holds among Ricker-type models, but not for comparisons between Ricker and Beverton-Holt fits. The Beverton-Holt fits have better statistical fit, but wider posteriors (Figure 16). The likely cause of this unexpected pattern is the shape of the posterior distributions, which are more skewed for the Ricker models (Figure 15). The middle part of the distribution is narrower, but the overall range is wider, resulting in larger residuals at the tail ends, and consequently a poorer DIC score.

Observed autocorrelation in the residuals is weak (see Durbin-Watson test in Table 13), and the resulting autoregression parameter ϕ in the Ricker AR1 model is small with a median of 0.23 for the base case data set (Figure 17).

3.2.3 Sensitivity Analyses - Alternative Calculation Approaches

We implemented the base-case analysis (Ricker, Spn= AdjAge, Rec=5&6) with several alternative calculation approaches to check robustness of the benchmark estimates. Table 17

summarizes the results. We also tested deterministic estimates the basic Ricker model and two alternative forms of the Beverton-Holt model (Table 14).

3.2.3.1 BUGS vs. JAGS

As previously noted by Pestal and Johnston (2015), the choice of alternative software packages for MCMC sampling has little effect on S_{MSY} estimates. Comparing row 1 to row 3 and row 2 to row 4 in Table 17 shows that results are very close, but not identical (i.e. within rounding to the nearest 100), except for the upper tail end of the posterior distribution (75th and 90th percentile), which affects the estimate of UBM90, the reference point with a 90% probability of meeting or exceeding 80% of S_{MSY} .

3.2.3.2 Bayesian vs. Deterministic Estimates

Parameter and benchmark estimates are very stable across estimation methods, with linear regressions, MS Excel Solver, and alternative Bayesian fits all producing very similar values. Results for the Beverton-Holt fits were more sensitive to the choice of estimation method (see Table 14 and Figure 10). The Bayesian fits produced parameter and benchmark estimates similar to the MS Excel Solver minimized the SSLE.

3.2.3.3 Bias Correction

Bias correction on the SR parameters (Table 8) increases the S_{MSY} estimates. However, the magnitude of increase is substantially larger for Little Tahltan Chinook than in an earlier analysis of Taku River Coho salmon (Pestal and Johnston 2015), with bias-corrected S_{MSY} estimates 10-20% larger (comparing “corr” with “raw” in Table 14, e.g. row 1 vs. 2). The bias correction also changes the shape of the posterior distribution by stretching out the upper tail.

3.2.3.4 Holt and Ogden (2013) Toolkit

Holt and Ogden (2013) developed a software package (denoted H&O below) for estimating status metrics under Canada’s WSP, which produces estimates of 80% S_{MSY} as the upper benchmark for the *Relative Abundance* metric and S_{GEN} as the lower benchmark. Using the base case data set, the H&O deterministic point estimates of $S_{MSY}=2,600$ and $S_{MAX}=4,700$ are identical to our deterministic results without bias correction, and the Bayesian estimates are very close to our results, but have a narrower posterior distribution (i.e. p75 and p90 are lower). Overall, H&O confirms our results for the subset of variations that match up (basic Ricker model, no bias correction).

H&O estimates of S_{GEN} have a median of 800 (p10=500, p90=1,100), which is much lower than our estimates of LBM90=1,600 for the same model and data (Ricker, base case). Note that our estimates of LBM90 are anchored on rebuilding to the bias-corrected S_{MSY} , which is 10-20% larger for Little Tahltan Chinook. In order to achieve the same probability of rebuilding to this larger S_{MSY} estimate, a larger spawner abundance is required, and the benchmark estimate goes up.

3.2.4 Sensitivity Analyses – Retrospective, Jackknife

Figure 18 to Figure 20 show the effect of including additional data points. Basically, the figures show how estimates would have evolved if this analysis had been updated each year with the latest available information.

Figure 18 shows the change in parameter estimates for the two alternative Ricker models. For both model forms the productivity parameter increases throughout the 1990s as the large recruit years are incorporated, then drops in the 2000s as low return years are added into the data set. For both models the median capacity parameter is roughly stable throughout the 1990s, then

shows pronounced drop when the 2001 brood year is added to the data set and stays stable at that lower number for the rest of the time period (i.e. maximum recruits occurs at a lower spawner abundance in the later estimates). Also note that uncertainty in the capacity estimate is drastically reduced after this point. 2001 had the 3rd-largest spawner abundance in the data set combined with the 2nd-lowest recruitment. The Ricker fit interprets this as a strong signal of density-dependent decline in production, and the capacity parameter drops. At the same time, this is the first year that has a clear signal of density dependence, so the previously wide uncertainty band around the capacity parameter narrows considerably. The autoregression parameter ϕ in the Ricker AR1 model is close to zero for most of the retrospective evaluation (i.e. last year's deviation from the fitted value has little effect on this year's fitted value). Note however that the autoregression parameter increases as 2006 and 2007 are added, which extend a string of below-average recruitment years.

Figure 19 shows the change in parameter estimates for the Beverton-Holt model. The capacity parameter ($a = \text{max Rec}$) follows a similar patterns as the Ricker 'a' parameters, increasing throughout the 1990s, and declining steadily throughout the 2000s. The productivity parameter ($b = S$ at $a/2$) declines slightly for most of the retrospective evaluation, then picks up as 2006 and 2007 are added. The 2007 brood year, with the lowest observed spawner abundance in the data set, strongly pulls the Beverton-Holt curve to the left, resulting in a steeper slope at lower spawner abundances (i.e. fewer spawners needed to get to half the maximum recruits). Figure 20 tracks the changes in reference points resulting from these retrospective patterns in parameter estimates. Differences between the alternative SR fits are consistent across different reference points. Median S_{MSY} estimates are similar for the two Ricker fits, with the Ricker AR1 estimate slightly higher, and much lower for the Beverton-Holt fit. All three S_{MSY} estimates decline as data from the 2000s is added, but the change is drastic for the Ricker fits and gradual for the Beverton-Holt fit.

Figure 21 and Figure 22 show the same information for jackknife testing of the Ricker and Beverton-Holt model fits, where individual data points are dropped from the sample. For both models the capacity parameter is very stable (i.e. no single data point on its own has a strong influence on the estimate on its own), which is a stark contrast to the effect of adding 2001 into the data set in a retrospective analysis. When using the whole data set except for one point, the information in the scatter plot is generally sufficient to produce stable estimates. The only clear signal is the effect of the last two brood years (2006 and 2007) on the productivity parameters in both models. As in the retrospective analysis these two observations are flagged as influential. The Ricker AR1 model requires a continuous sequence of observations, and the jackknife test is therefore not applicable.

4 DISCUSSION

4.1 DATA CONCERNS AND INTERPRETATION OF SR MODEL RESULTS

4.1.1 Alternative Interpretations of Available Information

This project originally focused on fitting various Spawner-Recruit (SR) models and estimating biological benchmarks for each model, but during the peer-review process for this work, hosted by DFO's Canadian Science Advisory Secretariat (CSAS), reviewers and participants raised serious concerns regarding the available data. The CSAS discussions are documented in a Science Advisory Report (DFO 2016a) and proceedings (DFO 2016b). This section summarizes data concerns, documents the relevant conclusions of the peer-review process, outlines some unresolved questions, and offers different views on the weight of evidence for choosing among 2 alternative interpretations:

-
- **Interpretation 1: Consider the recent weir counts as invalid.** If one considers the potential data concerns strong enough to invalidate recent weir counts, then biological benchmarks cannot be updated, current status of Little Tahltan is unknown, the current weir does not provide a useful indicator for total Stikine Chinook, and the drainage-wide assessment program needs to be reviewed.
 - **Interpretation 2: Consider the recent weir counts as a real signal.** If one takes the weir counts at face value, then biological benchmark estimates are consistent with estimates published in 2000, and recent spawner abundances are substantially below various estimates of S_{MSY} and declining further.

4.1.2 Pieces of the Puzzle

The main concerns regarding weir counts were:

1. indications that the counting weir may have affected Chinook spawning distribution and increased mortality;
2. Little Tahltan may be an opportunistic spawning site in years with large abundance rather than a persistent spawning population; and
3. observed productivity dropped dramatically starting with the 2001 brood year.

Clues pointing towards problems with recent weir counts include:

1. the recent disconnect between weir counts and lower Stikine MR-based estimates (Figure 6);
2. experiences with other Chinook counting weirs in similar settings (Nahlin River, Kitwanga River, several Upper Fraser systems listed in Table A 3); and
3. some participants in the peer-review process considered the size and age composition of Chinook at Little Tahltan weir to be extremely unusual (i.e. proportion of small fish far lower than expected)

Evidence in support of using the weir data includes:

1. long-running consistency between weir counts and mark-recapture estimates in the lower Stikine (Figure 6):
2. high correlation between weir counts and aerial surveys (Figure B 7, Bernard et al. 2000);
3. similarity in age composition estimates from carcass surveys and weir samples in the 1980s (Bernard et al. 2000):
4. recent large-scale drop in size and age of Chinook salmon in Alaska and the Yukon (Lewis et al. 2015); and
5. large number of published reports stating that Chinook weirs have high quality data (Table 1)

In addition to questions regarding the weir counts, there was also some debate regarding the details of our run reconstruction, especially the catch estimates and stock composition assumptions used in Appendix C. These were not pursued in our revisions of this paper, due to the more fundamental concerns with the weir counts. But if future work revisits the SR models for Little Tahltan Chinook or total Stikine Chinook, the analysis needs to seek closer consistency with the most recent approach adopted by the Chinook Technical Committee of the PSC.

During the CSAS review, habitat-based estimates of biological reference points were suggested as a potential alternative to the estimates that rely on weir counts. In subsequent discussions,

the Transboundary Technical Committee and the Transboundary River Panel agreed that this could be informative, but does not offer a short-term solution because unresolved questions regarding population structure (i.e. Little Tahltan vs. Total Tahltan) also affect the habitat-based estimates. The Transboundary Technical Committee identified the following required steps for a long-term effort to develop habitat-based estimates, if they are identified as a funding priority:

1. resolve population structure (e.g. spawning behaviour) of Tahltan Chinook;
2. compile available habitat information for each population unit;
3. conduct field surveys to verify spawning distribution and habitat characteristics;
4. develop habitat-based estimates, using the methods established by Parken et al. (2006).

4.1.3 Views on the Weight of Evidence

CSAS process in November 2015

Participants in the peer-review process reached a consensus (DFO 2016a) and considered it probable that weir effects and a large-scale productivity decline interacted to result in the observed pattern of spawner counts: Smaller, younger fish would be less productive, and might be more susceptible to weir effects. Any weir effects on spawning distribution or mortality would then become amplified during low abundance brood years, especially if the Little Tahltan is only one of several opportunistic spawning areas within the Tahltan watershed.

This consensus was based on a combination of observed patterns (Figure 6) and experiences with other Chinook counting weirs in similar settings (Nahlin River, Kitwanga River, several Upper Fraser systems listed in Table A 3).

After intensive debate, the consensus conclusion was that biological benchmarks based on spawner-recruit data cannot be estimated with the data currently available, but that it would be nevertheless informative for decision-makers to document our benchmark estimates and summarize the data concerns identified during the peer-review.

Authors' Commentary

The survey of Chinook weirs conducted after the CSAS meeting in November 2015 showed that experiences in the field have varied greatly by system, but that there are some regional patterns (Table 1). Stock-assessment experts working on transboundary rivers and the interior Fraser watershed reported several Chinook weirs that were discontinued due to observed effects on spawning distribution. Conversely, observed weir effects in Northern BC and Vancouver Island were generally minor, and weirs there are still active. Suggested hypotheses to explain these differences tended to focus on the specific type of weir (e.g. fish handling vs. video counter) and the setting of the weirs (e.g. distance from the ocean, distance from the spawning grounds, availability of alternative spawning habitat, and co-migrating species). In contrast, published commentary consistently rates Chinook weir counts as high-quality data (Table 1).

We interpret this discrepancy between personal communications of current thinking and the previously published record as strong evidence that Chinook weir counts need to be assessed carefully for each individual system. For weir counts of Little Tahltan Chinook, there are several indirect clues pointing to possible weir effects, but using the large amount of published statements as a qualitative prior, the weight of evidence is not as clear-cut as the consensus at the CSAS meeting suggests. In addition, the observed patterns are consistent with a recent large-scale drop in size and age of Chinook salmon in Alaska and the Yukon (Lewis et al. 2015).

In our view, both possible interpretations remain plausible (i.e. recent counts are invalid vs. stock has declined), and should be considered in planning harvests as well as stock

assessment activities for Stikine Chinook over the next few years until the current spawner distribution in the Tahltan watershed and the quality of the weir counts can be confirmed.

The crucial issue here is not a disagreement over analytical methods, but conflicting clues regarding the quality of available information. These potential data concerns then affect all subsequent analysis, from simple percentile-based calculations of a SEG range to estimates of biological benchmarks based on Bayesian SR model fits (but note that SEG based on percentiles are less sensitive to recent observations; Table 18). If standard SR models are fitted to the spawner and recruit estimates we reconstructed from available data, then the results match the estimates by Bernard et al. (2000), but readers need to keep in mind the model-fitting challenges caused by the two distinct time periods identified in the SR scatter plot (Figure 6) as well as the minor adjustments of the run reconstruction proposed by some participants in the CSAS process. The first issue could be addressed by exploring time-varying SR models. CSAS consensus regarding the second issue was that changes to the data would likely be minor, and that updates of the catch estimates are less important than resolving the questions around the weir counts. Consequently, these tasks were not done as part of the revisions for this paper. However, any future analysis of population dynamics of Little Tahltan Chinook should explore these questions.

4.2 PERCENTILE METHOD

Approximate goal calculations, such as the percentile method (Section 2.2), are used for data-poor populations which constitute the majority of Pacific salmon stocks (e.g. Volk et al. 2009, English et al. 2014). Stocks with additional information can be used to check whether these simple proxies are valid and provide background for the more complex analyses.

Assuming that weir-based spawner estimates for Little Tahltan Chinook reflect a real pattern for a persistent population or subpopulation, our results show that:

- 25th percentile of spawner abundance is 2,800 (i.e. $\frac{1}{4}$ of observations are smaller, $\frac{3}{4}$ are larger), which is close to the median bias-corrected estimate of SMSY and a bit higher than the uncorrected SMSY (Table 12 vs. Table 16). Two of the three alternative versions of the percentile method produce the 25th percentile as the lower bound on the Sustainable Escapement Goal (SEG), and therefore define a range that is consistent with the objective of roughly capturing SMSY plus a cautionary buffer.
- ADFG2, the revised percentile method by Clark et al. (2014) uses the 15th percentile, given that contrast in the data is high and measurement error is low, and produces a lower bound of 1,800, which is close to the median SMSY estimate for the Beverton-Holt model and similar to the estimates of LBM90 (lower WSP BM) and the lower end of the yield-based range (70% probability of 70% MSY).
- ADFG also produces an upper bound for the SEG of 5,400 (65th %ile) which is close to SMAX for the Ricker models, while the earlier ADFG approach and DFO approach use 6,400 (75th %ile), which is above the Ricker SMAX, but roughly corresponds to the abundance where observed values start to fall below the replacement line (Figure 4).
- All 3 variations of the percentile method give reasonable SEG ranges for Little Tahltan Chinook, and produces estimates that are consistent with one of the biological benchmark estimates (i.e. either Ricker or Beverton-Holt, either S_{MSY} or S_{MAX}).

The SEG range is wide, but stable over time and insensitive to individual observations (Figure 9). In fact, SEG ranges are less variable over time than the SR-based estimates and have less lag-time in response to changes in the system. Table 18 compares estimate ranges for the period 1998 to 2007, for which both percentile-based and SR-based estimates are

available. Figure 23 shows the pattern, and that percentile-based updates are available for 6 additional years (2007 vs. 2013).

In summary, the percentile method produces reference ranges that are generally consistent with the SR-based estimates of biological benchmarks for Little Tahltan Chinook using the available data. If recent data, however, are invalid due to weir effects (see previous section), then the percentile-based estimates are affected, and should not be used for assessing status assessment or setting management goals.

4.3 BIOLOGICAL BENCHMARKS BASED ON SPawner-RECRUIT ANALYSIS

The discussion in this section assumes that the spawner and recruit estimates in Figure 4 are reasonably accurate and can be used to update and expand the biological benchmark estimates developed by Bernard et al. (2000).

S_{MSY} estimates, which are the main anchor point for developing reference points under both Canada's *Wild Salmon Policy (WSP)* and Alaska's *Sustainable Salmon Policy (SSP)*, are highly consistent across estimation methods and alternative data sets, which is reassuring, but differ substantially between types of the spawner-recruit model, which creates a dilemma when choosing a spawning goal. The Ricker estimates of median S_{MSY} cluster around 3,000, but the Beverton-Holt estimates are about 30% lower, clustering around 1,900 (Table 16).

Figure 24 shows the benchmark ranges compared to observed spawner abundances. Spawner abundances from 1985 to 2005 were at or above the current estimate for S_{MSY} across 3 alternative R models. Many years exceeded the current estimate of S_{MAX} , and the 3 largest brood years were well above the estimated S_{EQ} .

S_{MSY} estimates for both model forms are strongly influenced by the time period used. The 2001 brood year turned out to be the break point (Figure 20), resulting in a roughly 25% drop in the median S_{MSY} estimate from around 4,000 to around 3,000. The Beverton-Holt model also picks up a drop in S_{MSY} when adding 2001 brood year, but less pronounced (2,600 to 2,300). However, the Beverton-Holt estimate continues to decrease as data up to 2007 brood year are added, while the Ricker fit stabilizes after 2001. By 2007, both model forms have an S_{MSY} estimate about 30% lower than the pre-2001 estimate.

Lack of contrast is a common challenge when fitting spawner-recruit models (e.g. Collie et al. 1990). In the case of Little Tahltan Chinook Salmon, contrast is very high in both abundance (Table 12) and exploitation rate (Table 5).

Our analyses are based on spawner-recruit data from 1985 to 2007. A few more years could be infilled at the beginning of the time series based on the ratio of weir counts to aerial surveys, as was done by Bernard et al. (2000). These observations would likely fall into the range of 800 to 9,000 spawners (using the aerial indices in their Table 2 and the expansion factors in their Table 5), matched up against a range of 4,000 to 10,000 recruits from our brood table. Most of these points would fall into the middle of the SR scatter in Figure 4, and would probably not add much contrast to the overall fits. Given the effect of the 2 most recent observations, and the likely pattern in the 2008-2011 brood years, it would be a more interesting extension of our work to infill these recent years based on partial age classes and a projected age composition.

If the available data are taken at face value, then updated biological benchmark estimates for Little Tahltan Chinook are consistent with the estimates presented by Bernard et al. (2000) when based on the same time period and SR model, and about 30% lower if recent low abundances are included in the data set. If, however, recent estimates are invalid due to weir effects that have increased in recent years (e.g. due to low abundance, low productivity), then the Bernard et al. (2000) estimates cannot be updated at this time.

4.4 CONSIDERATIONS FOR CHOOSING A SPAWNING GOAL

The final step of sifting through all the alternative estimates, summarized in Table 16 and Table 18), and choosing a spawning goal range for Little Tahlitan Chinook Salmon needs to combine practical, biological, and statistical considerations.

Among the model-data variations we tested, the biggest difference in estimates is between the Ricker and Beverton-Holt models. Considerations for choosing between these 2 models include:

1. *Statistical goodness-of-fit*: No clear picture emerges using this criterion. For the Bayesian estimates, the Beverton-Holt model has a better fit using the standard criterion of lower DIC, but it also has wider posterior distributions. This inconsistency is probably due to the shape of the posteriors, which is more skewed for the Ricker estimates. For the deterministic estimates, on the other hand, the Ricker models have a better fit in terms of a lower sum of squared log errors.
2. *Stability*: Again, no clear picture emerges. The Bayesian Beverton-Holt estimates are more stable over the course of the retrospective evaluation than the Bayesian Ricker estimates, both in terms of median S_{MSY} estimate and spread of the posterior distribution (top 2 panels of Figure 20). However, the deterministic Beverton-Holt parameter estimates are much more sensitive to alternative estimation methods than the Ricker parameters (Table 14).
3. *Biological context*: The alternative model forms have different implicit biological assumptions. The classic mechanism for producing Beverton-Holt-type SR curves is strong juvenile competition linked to limited capacity of the rearing habitat (Hilborn and Walters 1992). In terms of observed data, the Beverton-Holt model is a good candidate model to test if the R vs. S scatter plot shows recruit estimates of similar magnitude over a wide range of spawner abundances. The Beverton-Holt then fits a horizontal line through these points and sets this as the asymptote for the SR curve. However, the picture for Little Tahlitan Chinook is very different (Figure 4, Section 2.1.2). Most of the spawner abundances are between about 3,000 and 6,000, and the resulting recruitment from this range of spawners has been extremely variable, from about 2,000 to about 23,000 (corresponding to a range of 0.5 – 5 recruits/spawner). Spawner abundances above 6,000 have consistently resulted in poor to very poor recruitment, indicating a density-dependent effect consistent with a Ricker fit.
4. *Management implications*: Both model forms produce benchmark estimates and reference points that could be used to set annual spawning goals. However, they differ in terms of the expected consequences of large spawner abundances as well as the assumed inherent potential for rebuilding from a low-abundance period. The Beverton-Holt fits tend to have a steeper slope at the origin, implying a higher productivity and lower spawner abundance required for rebuilding (e.g. LBM90)

Once a model form has been selected, there are additional factors to consider when choosing the spawning goal:

1. *Changes over time – Production regimes*: There are two major break-points in the data set, the first one in the 2001 brood year, which was the first in a series of years with high spawner abundance and poor recruitment, and the second one in 2006/2007, which are an initial signal of a period with very low spawner abundance and recruitment. Spawner abundances (Figure 2) and run sizes (Figure 5) have stayed low since then. Quantitative recruitment estimates are not yet available for more recent brood years, but based on the low runs and low catches (Figure C 1 to Figure C 4) they will be low as well. Given that Little Tahlitan is in a low-abundance period, one option could be to set an interim rebuilding goal (e.g. at LBM90) and a longer-term goal based on long-term average population dynamics

(e.g. at S_{MSY}). An alternative approach would be to choose a wider goal range that encompasses both.

1. *Changes over time – Population Characteristics:* Over the last 30 years, Little Tahltan Chinook have been steadily shifting towards lower age-at-maturity and smaller size (Section 2.1.2). Older, larger fish typically contribute more to recruitment (i.e. higher fecundity), so that this change hints at a long-term, persistent reduction in productivity. This is indirectly reflected in the changing estimate of S_{MSY} as data points are added in the retrospective evaluation (Figure 20). Note that our estimates are for large Chinook, so that corrects for part of this pattern (i.e. if proportion of small adults increases, then the same goal translates into a larger required total return to the weir. However, this does not account for the fact that a spawner abundance of 3,000 large Chinook in the 1990s would have been predominantly age 6 and would now be predominantly age 5, and would have had larger average size (Figure B 4).
2. *Extreme events:* The 2014 rock slide resulted in large mortality drastically altered the age and size composition and preliminary observations from 2015 indicate this effect may persist. At this point we have no quantitative data to gauge how this will affect the long-term status and productivity of Little Tahltan Chinook. In practice, this means that any goals based on long-term SR dynamics will likely not be achieved in the near future. One option would be to choose an interim rebuilding goal and focus on studying the effects of the slide.

All of these considerations, however, are built upon the fundamental assumption that the available recent spawner and recruit estimates for Little Tahltan Chinook are reasonably accurate and reflect a real pattern for a stable population or subpopulation. If, however, the recent spawner estimates are invalid due to weir effects, then biological benchmarks cannot be updated at this time, and the management process by default continues to use the estimates by Bernard et al. (2000).

4.5 SOURCES OF UNCERTAINTY

We evaluated the following sources of uncertainty:

- *Observation error:* Little Tahltan Chinook Salmon have a long time series of data collected with consistent methods (i.e. have more than 30 years of weir counts, coupled with 15-20 years of mark-recapture and CWT data). Weir counts are generally considered to yield a complete census of passing fish, but there may still be biases that affect the benchmark estimates, and future analyses could incorporate a more formal exploration of observation error by adding a Bayesian run reconstruction (e.g. Eggers and Bernard 2011, Fleischman and Evenson 2010).
- *Alternative data assumptions:* The analyses included 4 data variations capturing alternative assumptions about age and size composition. Results were consistent across data variations for each model form.
- *Alternative model forms:* The analyses included two variations of the Ricker model and the Beverton-Holt model. Both Ricker models assume that productivity declines at large spawner levels, but they differ in how they interpret observed productivity patterns. Results were robust across these model variations. The Beverton-Holt model, which has no density-dependent decline in production at larger spawner levels, gives much lower estimated benchmarks and reference points.
- *Alternative estimation approaches:* Benchmark estimates were confirmed using different estimation approaches and software tools (e.g. comparison with output from WSP software package by Holt and Ogden 2013).

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- *Policy interpretation and variations in technical details:* For a given set of results (e.g. a single model-data combination and estimation approach), the numerical estimates were sensitive to the alternative policy interpretations and technical details of summary calculations (e.g. yield profiles, summary reference points). Future analyses could be streamlined with clear guidelines for methodological details.

In addition, the peer-review process identified potential data concerns as a major source of uncertainty, specifically:

1. indications that the counting weir may have affected Chinook spawning distribution and increased mortality;
2. Little Tahltan may be an opportunistic spawning site in years with large abundance rather than a persistent spawning population.

These sources of uncertainty were not evaluated quantitatively, but the eventual consensus among participating experts was that the weight of evidence points towards not using the currently available data to develop updated estimates of biological benchmarks. The rationale for this consensus was a combination of the observed patterns in Figure 6 and experiences with Chinook counting weirs in other systems (Table 1).

4.6 SUMMARY OF PROJECT OUTCOMES BY OBJECTIVE

Section 1.1 lists the 4 objectives for this project as identified in the original request for science advice. In this section we briefly summarize the outcomes for each objective.

Objective 1: Review Chinook production and escapement data for the Little Tahltan River & Objective 3: Examine and identify uncertainties and sensitivities in the data and methods.

We addressed these objectives in two ways:

- *Quantitatively:* Exploratory data analysis summarized in Section 2.1.2, which highlights the key features in the data to watch out for when interpreting the results, and the sensitivity analysis based on carrying 4 data set variations through the whole suite of SR analyses. Table 16 lists results for 12 sensitivity analyses (i.e. alternative model-data combinations).
- *Qualitatively:* Documenting the data concerns and alternative interpretations of the observed patterns (e.g. weir effect on spawning distribution or population decline).

Objective 2: Develop biological benchmarks including the number of spawning adults that would produce a maximum sustainable yield of Chinook salmon and use various models and contemporary methods to assess biological benchmarks of salmon stocks.

The scope of our analysis was based on the approach taken by Pestal and Johnston (2015) for Taku River Coho salmon, which was previously reviewed by CSAS and produced estimates that were then adopted by the TRP.

The main results of the work are estimates of standard biological benchmarks (S_{MSY} , S_{MAX} , S_{EQ}) for 3 alternative SR models, but we also present a variety of reference points relevant to policy consideration in Canadian and Alaskan planning processes (e.g. lower and upper bounds for various yield-based ranges).

Our analysis focuses on Bayesian estimates of SR parameters, but we cross-check the results with deterministic estimates (i.e. regression fit of Ricker model) as well as an approximate approach for data-poor systems.

The analysis includes extensive sensitivity analyses for key assumptions in the development of spawner estimates and run reconstructions (i.e. age composition, catch) for Little Tahltan Chinook, as well as alternative SR models, estimation approaches, and subsets of the available data.

However, the peer-review process concluded data quality concerns confound the results of the stock-recruitment analyses. The potential productivity changes for Little Tahltan Chinook violate one of the assumptions for stock-recruitment analyses. It is also possible that the fish counting weir may have influenced the apparent spawner abundance used in the datasets.

Therefore, science advice for the establishment of an escapement goal cannot be provided based on the results of our analyses, and Objective 2 could not be addressed.

Objective 4: Examine the models presented in the working paper and provide recommendations on applicability.

This objective is addressed through the discussion in Chapter 4 and the recommendations in Chapter 5.

5 CONCLUSIONS

5.1 BIOLOGICALLY-BASED SPAWNING GOAL FOR LITTLE TAHLTAN CHINOOK SALMON

5.1.1 Quality of Information

Relative to the majority of salmon stocks (see Section 2.2 and references cited there), the spawner and recruit data for Little Tahltan Chinook appears to be of high quality. Consistent weir counts are available since 1985, and DFO's nuSEDS database assigns the highest quality ranking to weir counts. In-river catch estimates are also of high quality, given the scale of the fisheries. However, marine catch estimates are more uncertain, due to the challenge of identifying Stikine-origin fish in the mixed-stock fisheries. The two major marine fisheries in terms of harvest rate are the SEAK troll fishery and the fisheries inside District 108. In the troll fishery, two independent estimates of Stikine contributions give similar numbers (CWT vs. GSI; Table C 2). In District 108, the main uncertainty arises from separating out the hatchery-origin and the slight overestimate due to interception of passing stocks.

Using the available data, estimates of biological benchmarks and summary reference points are remarkably consistent across many alternative definitions and data sets, with significant differences found only between the alternative SR model forms (Table 16).

However, the peer-review process identified concerns with the available estimates (Sec 4.1), and the eventual consensus was that the recent weir counts cannot be used as the basis for updated biological benchmarks. As a result, the management process defaults back to the estimates by Bernard et al. (2000), which are similar to ours, but not affected by the recent data issues.

5.1.2 Choosing a Model-Data Combination and Spawning Goal

This section illustrates how the results of our quantitative analyses could be used, if one assumes that the spawner and recruit estimates in Figure 4 are reasonably accurate.

Pestal and Johnston (2015) summarize the review process for a project similar in scope and method to the one presented here. The Salmon Subcommittee of CSAS first reviewed a draft working paper. As part of the review, CSAS recommended 1 of 18 model-data combinations as

the most appropriate for developing management goals for Taku River Coho salmon, but did not choose specific benchmark or reference range as the spawning goal. The Transboundary Technical Committee then reviewed the paper, and recommended a spawning goal range, which was later adopted by the Transboundary Rivers Panel.

In this section we describe one approach to interpreting the results, consistent with the eventual outcome of the Taku Coho process. Note, however, that this is not intended as a formal recommendation for a specific spawning goal.

1. The first step is to choose between Ricker and Beverton-Holt model fits, or to combine estimates from both in some way. Based on the opposing clues listed in Section 4.4, we will have to rely on our understanding of the life history of Little Tahltan Chinook. Given that juveniles disperse through the mainstem, we consider the limited rearing capacity implied in the Beverton-Holt model to be less of a factor than spawning capacity limitations implied in the Ricker fit. The observed pattern of large recruitments at medium spawner abundances and low recruitment at high spawner abundances also points in that direction, but is confounded by the low production period. Therefore, choose the Ricker model form over the Beverton-Holt model form. (Drop four of 12 model-data combinations)
2. Among the Ricker model forms, the default practice in recent ADFG reports has been to use the Ricker AR1 model with autocorrelation correction, and for Taku Coho this was the better-fitting model. For Little Tahltan Chinook, however, the degree of autocorrelation is weak, the estimate autoregression parameter is close to zero for most years in the retrospective test, and the model fit is also slightly poorer in terms of statistical fit, mainly because the models have a similar fit but the Ricker AR1 has an extra parameter, which incurs a penalty in the goodness-of-fit measure (DIC in Table 16). Therefore choose the basic Ricker model over the Ricker AR1 model (Drop four of the remaining eight model-data combinations).
3. Differences between the remaining four data variations are small. However, estimates based on only 5 and 6 year old recruits differ from the estimates using all the marine age 3+ age classes, because brood years 2006 and 2007 are included, and provide an important signal of more recent changes. (Drop two of the remaining variations).
4. Results for the remaining two model-data combinations are basically identical, and no further elimination is required. The median S_{MSY} estimate is 2,900, with an associated range of 1,700 to 3,600 for a good chance of pretty good yield (70% probability of 70% MSY or more). Corresponding estimates of benchmarks consistent with WSP criteria are 1,600 (LBM90) to 3,000 (UBM90). Note, however, that Little Tahltan is not a distinct conservation unit under Canada's WSP, but a part of the Early Stikine Chinook CU.
5. For Taku Coho, the spawning goal range was selected using a combination of alternative estimates and reference points, and ended up at roughly $S_{MSY} \pm 30\%$. Applying $\pm 30\%$ to an S_{MSY} of 3,000 for Little Tahltan Chinook would result in a range of 2,000 to 4,000 fish.

Once a goal is chosen, it needs to be re-assessed on a regular basis. For example, Bernard et al. (2000) developed a goal, but the very next year the system changed (see influence of 2001 brood year data on S_{MSY} estimate in Figure 20). Even with frequent updates it would have still taken until 2008 before this signal could have been detected. The SR fits and resulting benchmarks should be revisited at least once every generation for Chinook salmon (i.e. 5-6 years for Little Tahltan Chinook).

5.2 STATUS OF LITTLE TAHLTAN RIVER CHINOOK SALMON

A formal status assessment under either Canada's WSP or Alaska's SSP is outside the scope of our project, but several concerns emerged from the data review and SR analysis:

- Long-term gradual changes in age and size, shifting towards younger, smaller fish;
- A persistent decline in estimated abundance and production since 2000. With respect to spawner abundance over the last ten years (2005 to 2014), 6 years were below all 12 alternative estimates of S_{MSY} , 8 years were below the 8 alternative Ricker estimates of S_{MSY} , and a least 5 years were below the LBM90 reference point intended to flag potential status concern for the relative abundance metric under the Wild Salmon Policy.
- In addition, there are unknown effects of the 2014 rockslide, but preliminary observations from 2015 indicate that the slide has created an on-going migration challenge for larger Chinook.

All together, these observations point to the need for a formal status assessment, and subsequent considerations of management implications.

If one takes the weir counts at face value, then biological benchmark estimates are similar to earlier estimates published in 2000, and recent spawner abundances are substantially below various estimates of S_{MSY} and declining further. Alternatively, if one considers the potential data concerns strong enough to invalidate recent weir counts, then biological benchmarks cannot be updated, current status of Little Tahltan is unknown, the current weir does not provide a useful indicator for total Stikine Chinook, and the drainage-wide assessment program needs to be reviewed.

A third possible interpretation is that the available data are reasonably accurate, and that the observed drastic drop in abundance is due to external factors, such as a shift to a persistent regime of poor marine survival. In this case, it is not appropriate to fit the models described in Section 2.3.1 to all years of data, but alternative models could be explored. Pending these additional analyses, the previous benchmark estimates by Bernard et al. (2000) would still apply, and current status would be assessed as very poor.

However, the peer review process did not recommend expanded sensitivity analyses to cover time varying SR models or environmental covariates, due to the broader concerns regarding the weir counts.

Therefore, current status of Little Tahltan Chinook is unknown, and cannot be assessed until the questions regarding weir counts are resolved. The starting point for any future status assessment will be to clarify the population structure of Stikine Chinook and determine the appropriate units of assessment (e.g. a review of conservation units under Canada's *Wild Salmon Policy*).

5.3 FUTURE DATA REQUIREMENTS

During our review of available data for Little Tahltan Chinook salmon, we identified the following priority areas for future work:

- Study rock slide effects before and after mitigation measures, particularly estimates of total mortality and changes in size composition.
- Explore plausible causes for the observed long-term changes in abundance, age and size (e.g. weir effects on spawning distribution and mortality, winter temperatures, spring flow regimes, predation)

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- Complete the genetic base line for Stikine River Chinook, including better representation of Little Tahltan.
 - Review the Wild Salmon Policy Conservation Unit delineations for Stikine
 - Consider alternative assessment approaches to estimating salmon abundance in the Tahltan watershed (e.g. move weir location to mouth of Tahltan, change to video monitoring, or explore the feasibility of acoustic counters.
 - The current public record does not explicitly reflect the weir effects described by stock assessment experts for some systems (Appendix A, Table 1). The anecdotal evidence shared by participating experts was the deciding factor in the peer-review consensus that the recent data should not be used to fit SR models, and a formal peer-reviewed synthesis of counting weir operations would be very useful for future work.

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7 TABLES

Table 1: Overview of Observed Effects of Chinook Counting Weirs. This overview is based on the information compiled in Appendix A. Sources are listed there.

	Little Tahltan	Transboundary Rivers	Northern BC	Fraser River	Vancouver Island
Pers. Comm.	Potential shift in spawning distribution and increased bear predation, but no direct evidence. Indirect clues include recent disconnect between weir counts and MR survey.	Nahlin River weir removed due to fish refusing to pass the weir and fish spawning below the weir, where spawning had not been observed before (poor habitat).	1 weir with effects on distribution and timing. 3 weirs affecting timing. 1 weir with no observed effect. All 5 still active.	6 Chinook weirs discontinued due to observed changes in spawning distribution (not passing the fence). 1 weir still in use for brood stock, but often have passage issues.	1 weir used to cause passage delays, but has been modified (site, design). 7 weirs with no observed effect.
ADFG and DFO Reports	Bernard et al. (2000) evaluated weir counts relative to overflights and checked against MR program Recommended continuing the weir and using it as basis for Stikine-wide spawning goal estimate. Parken et al. (2006) rated quality as “excellent”.	DFO Research Documents include 22 with Chinook in title, and 7 of those explicitly mention weir or fence counts. ADFG Fishery Manuscript Series includes 53 with Chinook in keywords, and 38 of those related to escapement estimation or spawning goals based on title. Throughout, weir counts are typically rated as high-quality data (e.g. Riddell et al. 2002; Parken et al. 2006; Fair et al. 2010)			
CTC Report	No comment on weir data quality or weir effects. States that spawner estimates “have met US CTC data standards since 1996” and cite highly stable weir/MR ratio.	States that Stikine (including Little Tahltan) meets data standards. No mention of weir effects or quality of weir data for other systems.			

Table 2: Run Reconstruction of Little Tahltan Chinook Salmon (large Chinook > 659mm FL). Using medians for weighting and infilling, as per section 2.1.1. Summary statistics in Table 3.

Brood Year	Total Stikine Catch				Little Tahltan Run Reconstruction							
	Marine and Lower River			Upper	% Little Tahltan		Catch					
	US MAR	Cdn LR	Total	River (UR)	MAR & LR	UR	US	CDN	Total	Spn	Run	ER
1979	-	775	-	934	15.6%	35.5%	-	453	-	-	-	-
1980	-	1,488	-	897	15.6%	35.5%	-	551	-	-	-	-
1981	6,323	664	6,987	981	15.6%	35.5%	987	452	1,440	-	-	-
1982	8,002	1,693	9,695	899	15.6%	35.5%	1,249	584	1,833	-	-	-
1983	6,345	922	7,267	1,184	15.6%	35.5%	991	565	1,556	-	-	-
1984	5,925	0	5,925	796	15.6%	35.5%	925	283	1,208	-	-	-
1985	6,772	347	7,119	1,053	15.6%	35.5%	1,057	428	1,486	3,301	4,787	31.0%
1986	6,185	1,171	7,356	1,845	15.6%	35.5%	966	839	1,804	3,419	5,223	34.5%
1987	5,311	1,151	6,462	1,650	15.6%	35.5%	829	766	1,595	4,895	6,491	24.6%
1988	6,266	1,208	7,474	1,827	15.6%	35.5%	978	838	1,816	7,478	9,295	19.5%
1989	6,712	1,694	8,406	1,414	15.6%	35.5%	1,048	767	1,815	4,785	6,600	27.5%
1990	8,170	2,249	10,419	1,106	15.6%	35.5%	1,276	744	2,020	4,456	6,475	31.2%
1991	7,907	959	8,866	1,358	15.6%	35.5%	1,235	632	1,867	4,544	6,411	29.1%
1992	7,496	962	8,458	1,322	15.6%	35.5%	1,170	620	1,791	6,649	8,440	21.2%
1993	8,687	994	9,681	1,555	15.6%	35.5%	1,356	708	2,064	11,443	13,507	15.3%
1994	7,028	1,174	8,202	1,213	15.6%	35.5%	1,097	614	1,712	6,384	8,096	21.1%
1995	5,897	1,666	7,563	961	15.6%	35.5%	921	602	1,522	2,751	4,273	35.6%
1996	6,860	1,929	8,789	1,147	16.7%	38.1%	1,149	760	1,909	4,487	6,397	29.8%
1997	8,556	3,469	12,025	1,513	20.7%	47.1%	1,770	1,430	3,201	5,417	8,617	37.1%
1998	5,221	1,942	7,163	832	18.9%	43.0%	987	725	1,712	4,756	6,468	26.5%
1999	7,886	2,916	10,802	1,452	23.9%	54.5%	1,887	1,489	3,375	4,283	7,658	44.1%
2000	6,839	2,210	9,049	1,760	25.4%	57.9%	1,740	1,582	3,322	5,878	9,200	36.1%
2001	5,923	885	6,808	911	15.4%	35.1%	913	456	1,369	9,661	11,030	12.4%
2002	6,752	642	7,394	1,764	14.8%	33.7%	1,000	690	1,691	7,361	9,051	18.7%
2003	14,282	1,367	15,649	1,299	13.8%	31.4%	1,972	597	2,569	5,309	7,878	32.6%
2004	15,539	4,551	20,090	2,032	33.8%	76.9%	5,249	3,100	8,350	13,991	22,341	37.4%
2005	42,636	20,251	62,887	1,041	18.2%	41.4%	7,763	4,119	11,881	7,188	19,069	62.3%
2006	28,108	17,053	45,161	800	15.8%	36.0%	4,446	2,985	7,431	3,780	11,211	66.3%
2007	15,987	11,600	27,587	632	3.9%	8.8%	617	503	1,120	542	1,662	67.4%
2008	8,867	7,959	16,826	1,014	14.5%	33.0%	1,287	1,490	2,777	2,670	5,446	51.0%

Brood Year	Total Stikine Catch				% Little Tahltan		Little Tahltan Run Reconstruction					
	Marine and Lower River			Upper			Catch					
	US MAR	Cdn LR	Total	River (UR)	MAR & LR	UR	US	CDN	Total	Spn	Run	ER
2009	4,818	2,085	6,903	689	17.5%	39.9%	845	641	1,486	2,149	3,635	40.9%
2010	7,743	1,907	9,650	858	7.0%	15.9%	541	270	811	1,128	1,939	41.8%
2011	4,595	2,997	7,592	825	7.3%	16.6%	336	356	692	1,629	2,321	29.8%
2012	5,759	5,097	10,856	753	3.2%	7.3%	186	220	405	747	1,152	35.2%
2013	2,931	1,901	4,832	1,375	5.2%	11.9%	153	263	417	879	1,295	32.2%
2014	-	1,407	-	1,173	0.7%	1.6%	-	28	-	158	-	-

Table 3: Summary Statistics for Run Reconstruction of Little Tahltan Chinook Salmon. This table summarizes the data shown in Table 2.

Statistic	Total Stikine Catch				% Little Tahltan		Little Tahltan Run Reconstruction					
	Marine and Lower River			Upper River			Catch					
	US MAR	Cdn LR	Total	(UR)	MAR & LR	UR	US	CDN	Total	Spn	Run	ER
Average	9,162	3,091	12,423	1,191	15.1%	34.3%	1,483	893	2,426	4,737	7,447	34.2%
Min	2,931	0	4,832	632	0.7%	1.6%	153	28	405	158	1,152	12.4%
p25	5,925	986	7,267	899	15.3%	34.7%	921	455	1,486	2,690	4,787	26.5%
Median	6,839	1,680	8,458	1,127	15.6%	35.5%	1,048	626	1,791	4,516	6,491	32.2%
p75	8,170	2,416	10,802	1,424	15.7%	35.7%	1,287	785	2,064	6,258	9,051	37.4%
Max	42,636	20,251	62,887	2,032	33.8%	76.9%	7,763	4,119	11,881	13,991	22,341	67.4%

Table 4: Overview of alternative SR data sets used in sensitivity analyses. Section 2.1.1 describes each data set. Appendices B and C list all of the data. The base case data set is marked with green shading. Table cells list the short label used for each combination of spawner and recruit data.

Spawners	Recruits	
	Rec5&6	RecM3+
WeirRet_AdjAge	Base Case	Rec M3+
WeirRet_5&6	Only 5&6	--
WeirRet_M3+	--	Only M3+

Table 5: Alternative Spawner-Recruits Data Sets for Little Tahltan Chinook Salmon. Section 2.3.1 describes the estimates included in each data set.

Year	Total Catch	Base Case					Only 5&6					Only M3+			
		WeirRet AdjAge	Total Run	Total ER	Rec 5&6	Rec M3+	WeirRet 5&6	Total Run	Total ER	Rec 5&6	WeirRet M3+	Total Run	Total ER	Rec M3+	
1985	1,486	3,301	4,787	31%	4,345	4,178	3,204	4,690	32%	4,196	3,289	4,776	31%	4,164	
1986	1,805	3,419	5,224	35%	9,222	9,470	3,314	5,120	35%	9,139	3,453	5,258	34%	9,482	
1987	1,596	4,895	6,492	25%	14,073	14,585	4,474	6,070	26%	13,757	4,875	6,472	25%	14,616	
1988	1,817	7,478	9,296	20%	8,320	8,063	7,314	9,132	20%	7,714	7,467	9,284	20%	8,045	
1989	1,816	4,785	6,601	28%	4,121	3,659	3,833	5,649	32%	3,697	4,816	6,632	27%	3,571	
1990	2,021	4,456	6,476	31%	2,958	2,954	4,136	6,156	33%	2,830	4,376	6,397	32%	2,927	
1991	1,868	4,544	6,411	29%	11,319	11,376	4,337	6,205	30%	11,175	4,530	6,398	29%	11,381	
1992	1,791	6,649	8,441	21%	6,803	6,854	6,650	8,441	21%	6,649	6,670	8,461	21%	6,850	
1993	2,065	11,443	13,508	15%	6,023	6,094	11,095	13,160	16%	5,838	11,474	13,540	15%	6,026	
1994	1,713	6,384	8,097	21%	8,495	8,284	5,727	7,440	23%	8,193	6,378	8,090	21%	8,137	
1995	1,523	2,751	4,274	36%	6,188	6,213	2,280	3,803	40%	6,062	2,614	4,137	37%	6,184	
1996	1,910	4,487	6,397	30%	16,212	16,101	4,489	6,399	30%	16,135	4,509	6,419	30%	16,170	
1997	3,202	5,417	8,619	37%	4,028	4,060	5,229	8,431	38%	3,870	5,403	8,605	37%	3,928	
1998	1,713	4,756	6,468	26%	13,476	13,569	4,606	6,319	27%	12,990	4,759	6,471	26%	13,168	
1999	3,377	4,283	7,659	44%	20,504	20,583	4,026	7,403	46%	20,128	4,169	7,546	45%	20,326	
2000	3,324	5,878	9,202	36%	22,744	22,575	5,540	8,864	38%	22,671	5,695	9,019	37%	22,594	
2001	1,369	9,661	11,030	12%	1,869	1,834	9,747	11,116	12%	1,855	9,887	11,256	12%	1,832	
2002	1,692	7,361	9,052	19%	4,444	4,494	7,184	8,875	19%	4,433	7,232	8,924	19%	4,503	
2003	2,570	5,309	7,879	33%	3,824	3,794	4,901	7,471	34%	3,784	4,956	7,526	34%	3,793	
2004	8,352	13,991	22,344	37%	2,733	2,705	13,421	21,773	38%	2,673	13,554	21,906	38%	2,691	
2005	11,882	7,188	19,070	62%	2,061	2,098	7,153	19,035	62%	1,989	7,252	19,134	62%	2,061	
2006	7,432	3,780	11,212	66%	1,901	NA	3,724	11,155	67%	1,806	3,751	11,183	66%	NA	
2007	1,120	542	1,662	67%	1,133	NA	520	1,641	68%	1,098	546	1,667	67%	NA	

Table 6: Definition of Biological Benchmarks

Label	Definition
S_{MAX}	Spawner abundance that maximizes recruits
S_{MSY}	Spawner abundance that maximizes sustainable yield (Rec-Spn)
S_{EQ}	Long-term equilibrium spawner abundance in the absence of harvest
U_{MSY}	Harvest mortality rate at MSY
S_{GEN}	Spawner abundance with a high probability of rebuilding to S_{MSY} in 1 generation in the absence of harvest

Table 7: Alternative Spawner-Recruit (SR) Models

Model	SR Function	Description
Ricker	$\ln(R) = [\ln(\alpha) - \beta S] + \ln(S)$	Standard Ricker model with density-dependence and log-normal errors (e.g. Bernard et al. 2000, McPherson et al. 2010, Grant et al. 2011, Holt and Ogden 2013)
RickerAR1	$\ln(R) = [\ln(\alpha) - \beta S + \phi \varepsilon_{y-1}] + \ln(S)$	Extension to the standard Ricker Model to account for autocorrelation in residuals (i.e. series of good years and series of bad years) (e.g. Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al 2011, Hamazaki et al. 2012)
Beverton-Holt	V1: $R = \frac{aS}{b+S}$ V2: $R = \frac{S}{c+dS}$	Standard Beverton-Holt model which approaches a maximum recruitment, rather than a density-dependent decline (e.g. Korman and Tompkins 2014). Two alternative forms are commonly used. Version 1 was used in the Bayesian estimation. Versions 1 and 2 were used in the simple cross-checks using linear approximations and the <i>Solver</i> function MS Excel

Note: the Function column shows the model form used in the Bayesian estimation code (Appendix D).

Table 8: Derived Estimates of Biological Benchmarks. Biological benchmarks are calculated for each parameter set (MCMC or bootstrap) based on the derived equations below. In addition, Table 17 compares these derived BM estimates to calculated benchmark estimates based on a brute-force computation (Section 2.3.4). Note: for Ricker AR1 and Ricker Kalman the bias correction occasionally results in a negative S_{MSY} (typically less than 10 out of a 1000 MCMC samples). These are discarded from subsequent analyses.

Model	S_{MAX}	S_{EQ}	S_{MSY}	U_{MSY}	Bias Correction	Source
Ricker	$\frac{1}{\beta}$	$\frac{\ln(\alpha)}{\beta}$	$S_{eq} (0.5 - 0.07 \ln(\alpha))$	$\frac{S_{msy}}{\beta}$	$\ln(\alpha') = \ln(\alpha) + \frac{\sigma^2}{2}$	With Bias Correction: McPherson et al. (2010), Bernard et al. 2000 / Without bias correction: Grant et al. 2011, Holt and Ogden 2013
RickerAR1	$\frac{1}{\beta}$	$\frac{\ln(\alpha)}{\beta}$	$S_{eq} (0.5 - 0.07 \ln(\alpha))$	$\frac{S_{msy}}{\beta}$	$\ln(\alpha') = \ln(\alpha) + \frac{\sigma^2}{2(1-\phi^2)}$	Fleischman and Evenson (2010)
Beverton- Holt (v1)	NA		$a\sqrt{\frac{b}{a}} - b$	$1 - \sqrt{\frac{b}{a}}$	$a' = ae^{\sigma^2/2}$	Hilborn and Walters (1992)

Table 9: Priors and MCMC Settings for Bayesian Estimates. Priors are implemented in the BUGS/JAGS code in Appendix D. Settings are used in the R2OpenBUGS and R2jags function calls as illustrated in Appendix E.

Model	Priors	Settings	Sources
Ricker	$\alpha \sim \text{lognormal}(0,0.0001)$ $\beta \sim 1/\text{lognormal}(0,0.1)$ $\sigma \sim 1/\text{sqrt}(\tau)$ $\tau \sim \text{gamma}(0.001,0.001)$	2 chains with 100,000 burn-in and 40,000 retained MCMC samples each. Thinning =2 for diagnostics and 40 for extracted MCMC samples used in subsequent calculations (i.e. n= 2,000)	Adapted from code used by Grant et al. (2010)
RickerAR1	$\alpha \sim \text{lognormal}(0,0.0001)$ $\beta \sim 1/\text{lognormal}(0,0.1)$ $\sigma \sim 1/\text{sqrt}(\tau)$ $\tau \sim \text{gamma}(0.001,0.001)$ $\phi \sim \text{normal}(0,0.0001) \text{ I}(-1,1)$	2 chains with 100,000 burn-in and 40,000 retained MCMC samples each. Thinning = 2 for diagnostics and 40 for extracted MCMC samples used in subsequent calculations (i.e. n= 2,000)	Adapted from a combination of two BUGS implementations: Code used by Grant et al. (2010) and Appendix A2 of Fleishman and Evenson (2010)
Beverton-Holt*	$\ln a \sim \text{normal}(9,2)$ $\ln b \sim \text{normal}(7.5,2)$ $\sigma \sim 1/\text{sqrt}(\tau)$ $\tau \sim \text{gamma}(0.001,0.001)$	2 chains with 100,000 burn-in and 40,000 retained MCMC samples each. Thinning = 2 for diagnostics and 40 for extracted MCMC samples used in subsequent calculations (i.e. n= 2,000)	Adapted from code provided by Mike Hawkshaw.

* Priors for Beverton-Holt model chosen to roughly center on the range of values produced by simple approximations using linear regression and the solver function in MS Excel (Table 14), and then tested for sensitivity.

Table 10: Checklist of MCMC diagnostics. The following standard diagnostics were used to assess MCMC sampling and model fit.

Consideration	Diagnostic	Thresholds	Examples
Parameter estimates	Shape of posteriors	Check whether posterior distributions are smooth and whether they bump up against the limits imposed by the priors (i.e. appear cut off)	-
Convergence	Trace plot (sequence of sampled values) for each variable	Visual assessment of overlaid pattern for the 2 chains (check for adequate mixing)	-
Convergence	Change in Brooks-Gelman-Rubin statistic BGR (Brooks and Gelman 1998) with additional MCMC samples	Check whether initial conditions for the 2 chains are different from each other (large BGR) and then converge before the end of the burn-in, such that BGR over the length of the retained sample is between 0.9 and 1.1. Visually check plots and check numeric values over 50 bins on the thinned samples.	Grant et al. (2011)
Convergence	Geweke statistic G (Geweke 1992)	Check whether G falls within the range $[-2, 2]$. If not, then the earlier part of the MCMC chain differs from the later part and the samples didn't converge (G is a z score and values in this range indicate that early and late sample means fall within 2 standard deviations).	Grant et al. (2011)
Relative model fit	Deviance Information Criterion DIC (Spiegelhalter et al. 2002, Gelman et al. 2004)	Check relative difference in DIC to compare alternative model fits. Lowest DIC indicates best fit among the models considered, but does not show whether any of the models fit well or poorly.	Grant et al. (2011), Korman and Tompkins (2014)

Table 11: Overview of SR Model Fitting Sensitivity Analyses. Base case for all SR model fits is to use all available years of data (1985-2007 for Rec5&6, 1985-2007 for RecM3+). Sensitivity analyses cover variations in the data set and variations in the estimation approach. Abbreviations are as follows: LS/Solver= Simple linear regression and Solver in MS Excel, BUGS = MCMC using r2OpenBUGSand OpenBUGS, JAGS = MCMC using r2jags and JAGS, H&O = Holt and Ogden (2013) software package.

Model	RESAMPLING		ESTIMATION			
	Incr. Time Window (Retrospective)	Drop 1 Observation (Jackknife)	LS/Solver	BUGS	JAGS	H&O
Ricker	X	X	X	X	X	X
RickerAR1	X	NA*	--	X	X	--
Beverton-Holt	X	X	X	X	X	--

* Ricker AR1 requires complete time series, preventing a direct jackknife evaluation.

Table 12: SEG Ranges for Little Tahltan Chinook based on Percentiles of Observed Spawner Abundance. Estimates include only years with weir counts (starting in 1985) and exclude 2014 due to the rockslide. The data series based on size samples only goes back to 2000. The 3 alternative methods have different criteria for choosing the percentile range, which are documented in Section 13.3. ER for Little Tahltan Chinook has been below 40% most years, and measurement error is very low in the weir counts.

	Size only		Age only		Age and Size	% used	
	Total	Visual	Sample	M3plus	5n6		Adj Age
Min (Obs) excl 2014	580	570	470	550	530	550	
Max(Obs) excl 2014	17,000	17,000	15,000	14,000	14,000	14,000	
Contrast (Max/Min)	29	30	32	25	26	25	
n obs	29	29	14	29	29	29	
ADFG							
SEG_L_LowER	2,080	1,900	750	1,720	1,620	1,800	15%
SEG_L	3,300	2,900	1,225	2,700	2,700	2,800	25%
SEG_H	6,800	6,700	6,800	6,400	5,800	6,400	75%
ADFG2							
SEG_L	2,080	1,900	750	1,720	1,620	1,800	15%
SEG_H	5,880	5,760	5,790	5,100	5,060	5,420	65%
DFO							
SEG_L	3,300	2,900	1,225	2,700	2,700	2,800	25%
SEG_H	6,800	6,700	6,800	6,400	5,800	6,400	65%

Table 13: Point estimates of Linear Regression Ricker Parameters (MLE). Note that these SR fits are intended as a quick diagnostic check, and should not be used for setting spawning goals. DW = Durbin-Watson test of autocorrelation. Data sets as defined in Table 4. Note that the 'a' parameter is for the log-transformed Ricker model.

Data Set	Years	a	σ_a	$b*10k$	σ_b	Adj r^2	DW Stat	DW p value	Serial autocorrelation
Base Case	1985-2007	1.36	0.341	2.13	0.530	0.41	1.40	0.0613	Moderate (<0.1)
RecM3+	1985-2005	1.66	0.374	2.50	0.560	0.49	1.76	0.266	Weak (>>0.1)
Only 5&6	1985-2007	1.38	0.333	2.23	0.538	0.42	1.38	0.0551	Moderate (<0.1)
Only M3+	1985-2005	1.68	0.373	2.55	0.564	0.49	1.74	0.254	Weak (>>0.1)

Table 14: SR estimation cross-check using simple methods. Note that these estimates are intended as a quick diagnostic check and should not be used for setting spawning goals. Beverton-Holt estimates used to bound the priors for the Bayesian estimation. Model forms as per Table 7. All estimates are for the base case data set (AdjAge2Rec5&6) described in Section 2.3.1 and do not include the bias correction for log-normal error structure. SSE=Sum of squared errors of the raw data and fitted values, SSLE = Sum of squared log residuals. Beverton Holt V2 parameters converted back to V1 format for interpretation. Figure 10 shows the curve fits for each set of parameter estimates. Note that the Ricker a' parameters are for the log-transformed model.

Model	Method	Parameters	S_{MSY}	SSE	SSLE	SSLE Rank
Ricker	Lin regr. R	a= 1.36 / b=2.13E-4	2,578	7.78E8	11.0	1
Ricker	Lin regr. Excel	a= 1.36 / b=2.13E-4	2,578	7.78E8	11.0	1
Ricker	Excel Solver (min SSE)	a= 1.79/ b=2.41E-4	2,781	6.82E8	12.8	2
Ricker	Excel Solver (min SSLE)	a= 1.36 / b=2.13E-4	2,578	7.78E8	11.0	1
Bev-Holt V1&2	Excel Solver (min SSE)	a=8,556 / b= 464	1,529	7.91E8	15.7	5
Bev-Holt V1&2	Excel Solver (min SSLE)	a=7,478 / b= 1,358	1,829	8.85E8	13.2	3
Bev-Holt V2	Inverse lin regr. Excel	a=6,955 / b=2,524	1,665	10.4E8	14.7	4

Table 15: Biological Benchmark Estimates – Base Case Data (MCMC). Benchmark estimates are for SR models fitted to large weir returns, infilled run reconstruction, and brood year recruits calculated based on 5-6 year old returns, using the code in Appendices D and E with OpenBUGS and the r2OpenBUGS() function in R. These results are for all available years of data, capturing 1985 to 2007 brood years. S_{MAX} , S_{EQ} , and S_{MSY} are based on the equations in Table 8, either excluding or including bias corrections on the productivity parameter. p_{10} to p_{90} are percentiles of the posterior distribution (e.g. p_{25} means that 25% of the MCMC samples result in estimates below this number, and 75% of the MCMC samples result in larger BM estimates). The range from p_{10} to p_{90} captures 80% of the posterior distribution. p_{50} is the median. NPCV, SIQR, and SMAD are nonparametric measures of benchmark precision to summarize the spread of the posterior distributions (Section 2.5). For all three measures, a smaller value means higher precision. Benchmark values rounded to the nearest 100.

Bench- mark	Raw Estimates			Bias-corrected Estimates		
	Ricker Basic	Ricker AR1	Beverton- Holt	Ricker Basic	Ricker AR1	Beverton- Holt
S_{MAX}						
p10	3,600	3,800	--	3,600	3,800	--
p25	4,100	4,400	--	4,100	4,400	--
p50	4,900	5,200	--	4,900	5,200	--
p75	5,900	6,700	--	5,900	6,700	--
p90	7,300	8,800	--	7,300	8,800	--
NPCV	23%	26%	--	23%	26%	--
SIQR	38%	43%	--	38%	43%	--
SMAD	19%	20%	--	19%	20%	--
S_{EQ}						
p10	5,400	5,200	--	6,700	6,700	--
p25	5,900	5,800	--	7,100	7,200	--
p50	6,400	6,500	--	7,700	8,000	--
p75	7,000	7,200	--	8,500	9,100	--
p90	7,600	8,100	--	9,500	10,800	--
NPCV	11%	12%	--	12%	14%	--
SIQR	17%	21%	--	18%	23%	--
SMAD	9%	10%	--	9%	11%	--
S_{MSY}						
p10	2,200	2,200	1,400	2,500	2,600	1,400
p25	2,400	2,400	1,600	2,700	2,800	1,600
p50	2,500	2,600	1,900	2,900	3,100	2,000
p75	2,800	2,900	2,200	3,300	3,600	2,300
p90	3,100	3,300	2,600	3,800	4,400	2,600
NPCV	11%	13%	19%	13%	14%	19%
SIQR	17%	21%	31%	21%	25%	33%
SMAD	8%	10%	16%	10%	11%	16%

Table 16: Summary Reference Points (SRP) for large Chinook on the Little Tahltan River – Alternative SR Models and Data Sets (MCMC). The reported Deviance Information Criterion (DIC) is total DIC from OpenBUGS output. $\Delta DIC = DIC - \min(DIC)$. NPCV is a non-parametric coefficient of variation and proposed SRP are intended to summarize reference points used in recent ADFG and DFO reports (definitions in Section 2.5). All empty cells in PGY90 indicate that yield profile never exceeds 90% (it still has a clear peak, just doesn't meet the 90% cut-off. See Figure 14). All estimates include bias correction.

SR Model	Data Set	DIC (Fit)	ΔDIC	NPCV (S_{MSY})	SMSY50	WSP		PGY7070		60% Prob of		
						LBM90	UBM90	L	H	70% MSY	80% MSY	90% MSY
Ricker	Base Case	449	400	13%	2,900	1,600	3,000	1,700	3,600	1.3-4.2k	1.6-3.7k	
Ricker	Rec M3+	413	364	10%	2,800	1,200	2,900	1,700	3,800	1.3-4.2k	1.6-3.7k	2.4-2.9k
Ricker	Only 5&6	448	399	13%	2,900	1,600	3,000	1,500	3,700	1.2-4k	1.5-3.7k	2.1-3k
Ricker	Only M3+	413	363	10%	2,700	1,000	2,600	1,600	3,700	1.3-4.2k	1.6-3.6k	2.3-2.8k
Ricker AR1	Base Case	458	409	14%	3,100	1,900	3,500	1,900	3,500	1.4-4.2k	1.8-3.7k	
Ricker AR1	Rec M3+	424	374	13%	2,900	1,400	3,100	1,800	3,700	1.3-4.2k	1.8-3.7k	
Ricker AR1	Only 5&6	457	407	16%	3,000	1,900	3,400	1,700	3,500	1.3-4.1k	1.7-3.6k	2.7-2.7k
Ricker AR1	Only M3+	423	374	12%	2,800	1,300	2,900	1,800	3,600	1.3-4.2k	1.7-3.7k	
Bev Holt	Base Case	55	5	19%	2,000	900	2,100	1,100	2,900	0.8-3.5k	1.1-2.9k	1.6-2.2k
Bev Holt	Rec M3+	50	0	19%	1,900	800	2,100	1,000	3,100	0.8-3.6k	1-3k	
Bev Holt	Only 5&6	55	6	20%	1,900	900	2,100	1,000	2,900	0.8-3.4k	1.1-2.9k	
Bev Holt	Only M3+	50	0	19%	1,900	800	2,100	1,000	3,100	0.8-3.6k	1-3.1k	
	Min(All)	50	0	10%	1,900	800	2,100	1,000	2,900			
	Max(All)	458	409	20%	3,100	1,900	3,500	1,900	3,800			
	%Diff				63%	138%	67%	90%	31%			
	Min(Ricker)	413	363	8%	2,700	1,000	2,600	1,500	3,500			
	Max(Ricker)	458	409	13%	3,100	1,900	3,500	1,900	3,800			
	%Diff				15%	90%	35%	27%	9%			
	Min(BevHolt)	49	0	19%	1,900	800	2,100	1,000	2,900			
	Max(BevHolt)	55	6	20%	2,000	900	2,100	1,100	3,100			
	%Diff				5%	13%	0%	10%	7%			

Table 17: Sensitivity of Ricker S_{MSY} Estimates to alternative calculation methods – Base Case Data Set. Derived S_{MSY} estimates use the equations in Table 8. Calculated S_{MSY} is the spawner abundance with largest median difference between recruits and spawners for 500 increments over the range $[0, 1.5 \times \text{largest observed Spn}]$. MCMC are results from Bayesian fits using Markov Chain Monte Carlo methods (Section 2.3.3). MLE+B are results for maximum likelihood estimates of a simple regression on the linear form of the basic Ricker model combined with bootstrap distribution (Section 2.3.2). H&O is the software toolkit developed by Holt and Ogden (2013). Point estimates are only available for the regression-based estimates, using point estimates of Ricker parameters. Percentiles summarize either the posterior distribution of MCMC samples or the bootstrap distribution for regression-based estimates.

Row	Model	Class	Method	R Pack	BM Var	Point Estimate	Percentiles				
							p10	p25	p50 (Median)	p75	p90
1	Ricker	Derived	MCMC	R2OpenBUGS	Corr	--	2,500	2,700	2,900	3,300	3,800
2	Ricker	Derived	MCMC	R2OpenBUGS	Raw	--	2,200	2,400	2,500	2,800	3,100
3	Ricker	Derived	MCMC	r2JAGS	Corr	--	2,500	2,700	2,900	3,400	3,900
4	Ricker	Derived	MCMC	r2JAGS	Raw	--	2,200	2,400	2,600	2,800	3,100
5	Ricker	Derived	MLE+B	lm()	Corr	2,600	--	--	--	--	--
6	Ricker	Derived	MLE+B	lm()	Raw	2,600	--	--	--	--	--
7	Ricker	Derived	MLE	H&O	--	2,600	--	--	--	--	--
8	Ricker	Derived	MCMC	H&O	--	--	2,200	2,400	2,600	2,700	2,900
9	Ricker	Calculated	MCMC	R2OpenBUGS	--	2,600	--	--	--	--	--
10	Ricker AR1	Derived	MCMC	R2OpenBUGS	Corr	--	2,600	2,800	3,100	3,600	4,400
11	Ricker AR1	Derived	MCMC	R2OpenBUGS	Raw	--	2,200	2,400	2,600	2,900	3,300

Min
Max
% Diff

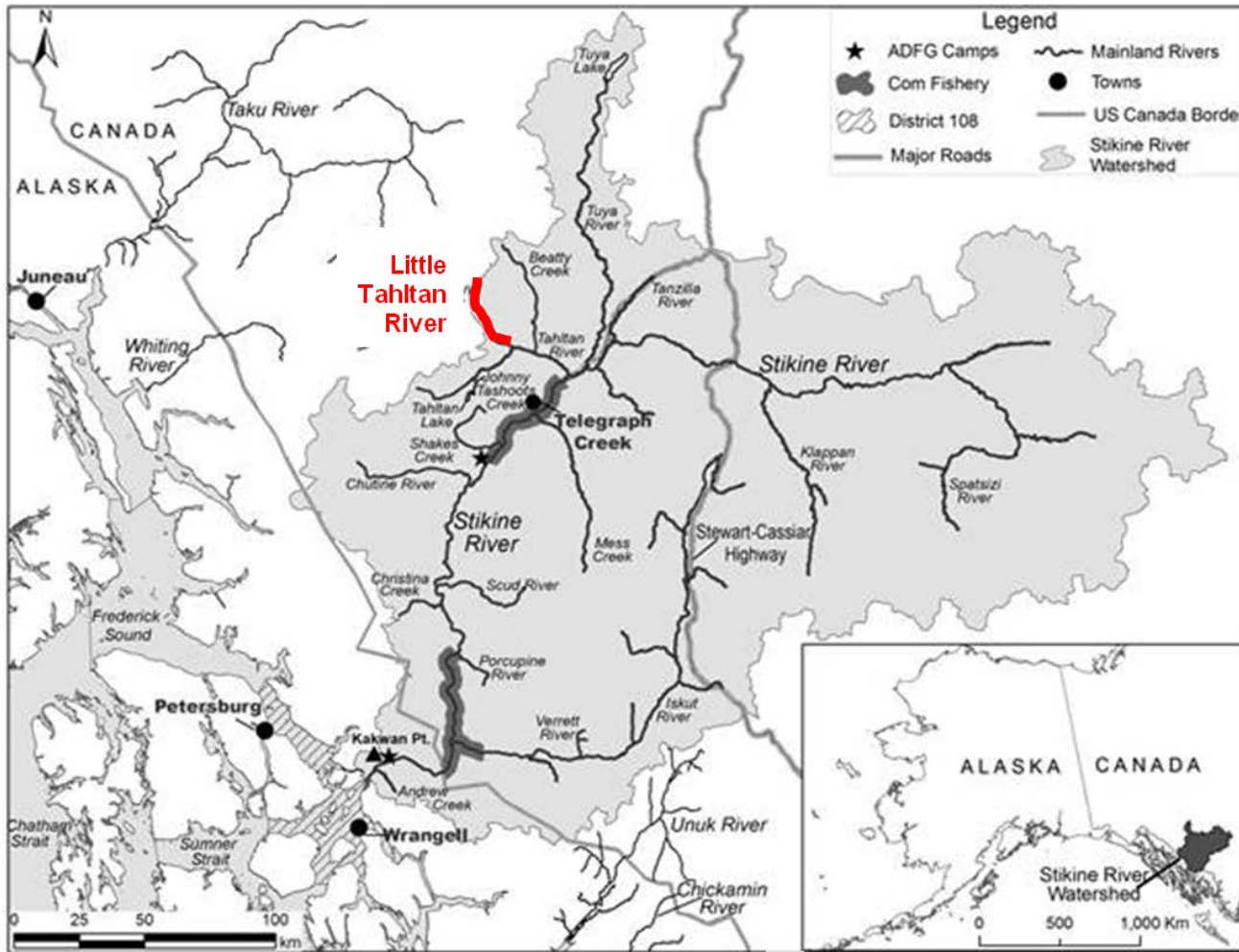
Table 18: Comparison of retrospective ranges in percentile-based and SR-based reference points. SEG values are from Figure 9 using the ADFG algorithm and the base case spawner time series. SEG definition as per Section 2.2. SMSY50 and LBM 90 values are from Figure 20 using the Ricker AR1 model. Definitions of SEG, SMSY50 and LBM90 definitions as per Section 2.5. Pattern in annual estimates shown in Figure 23. Range in estimates for retrospective test with end years ranging from 1998 to 2007

	ADFG SEG		Ricker AR1	
	Low	High	SMSY50	LBM90
Min	3,495	6,625	2,901	1,309
Max	4,400	7,830	4,732	3,097
Diff	905	1,205	1,831	1,788
Diff/Min	26%	18%	63%	137%

Table 19: Sensitivity of Yield-based Reference Ranges to Alternative Definitions. PGY ranges are numerical values corresponding to yield profiles based on overall median S_{MSY} . To create these profiles compare **yield** for different spawner levels to x% of **MSY for overall median S_{MSY}** , then check the % that is larger (i.e. PGY-70-70 is the optimum yield range based on 70% probability of 70% of MSY). OY ranges are numerical values corresponding to ADFG-type yield profiles. To create these profiles compare **yield** for different spawner levels to x% of **MSY for that parameter sample**, then check the % that is larger (i.e. OY-90-70 is the optimum yield range based on 90% probability of 70% of MSY). All values in 1,000s and rounded to the nearest 100 Spn. Figure 12 to Figure 14 show the underlying yield profiles. Blank cells indicate that the yield profile doesn't reach the probability cut-off at any spawner abundance. Note that comparisons are based on bias-corrected S_{MSY} estimates.

Criteria	SR Model	PGY	ADFG OY
%Prob of % MSY			
70-70	Ricker	1.7 – 3.6	1.1 – 4.2
70-70	Ricker AR1	1.9 – 3.5	1.2 – 4.3
70-70	Beverton-Holt	1.1 – 2.9	0.8 – 3.5
90-70	Ricker	--	1.3 – 3.9
90-70	Ricker AR1	--	1.3 – 3.8
90-70	Beverton-Holt	--	0.9 – 2.9
90-90	Ricker	--	1.9 - 3.2
90-90	Ricker AR1	--	2.0 – 3.2
90-90	Beverton-Holt	--	1.6 – 2.2
60-70	Ricker	1.3 - 4.2	1.1 – 4.3
60-70	Ricker AR1	1.4 - 4.2	1.1 – 4.4
60-70	Beverton-Holt	0.8 – 3.5	0.7 – 3.7
60-80	Ricker	1.6 – 3.7	1.3 – 4.0
60-80	Ricker AR1	1.8 – 3.7	1.4 – 4.1
60-80	Beverton-Holt	1.1 – 2.9	0.9 – 3.2
60-90	Ricker	--	1.7 – 3.6
60-90	Ricker AR1	--	1.7 – 3.6
60-90	Beverton-Holt	1.6 – 2.2	1.2 – 2.7

8 FIGURES



(Image provided by ADFG)

Figure 1: Map of Stikine drainage highlighting the Little Tahltan River.

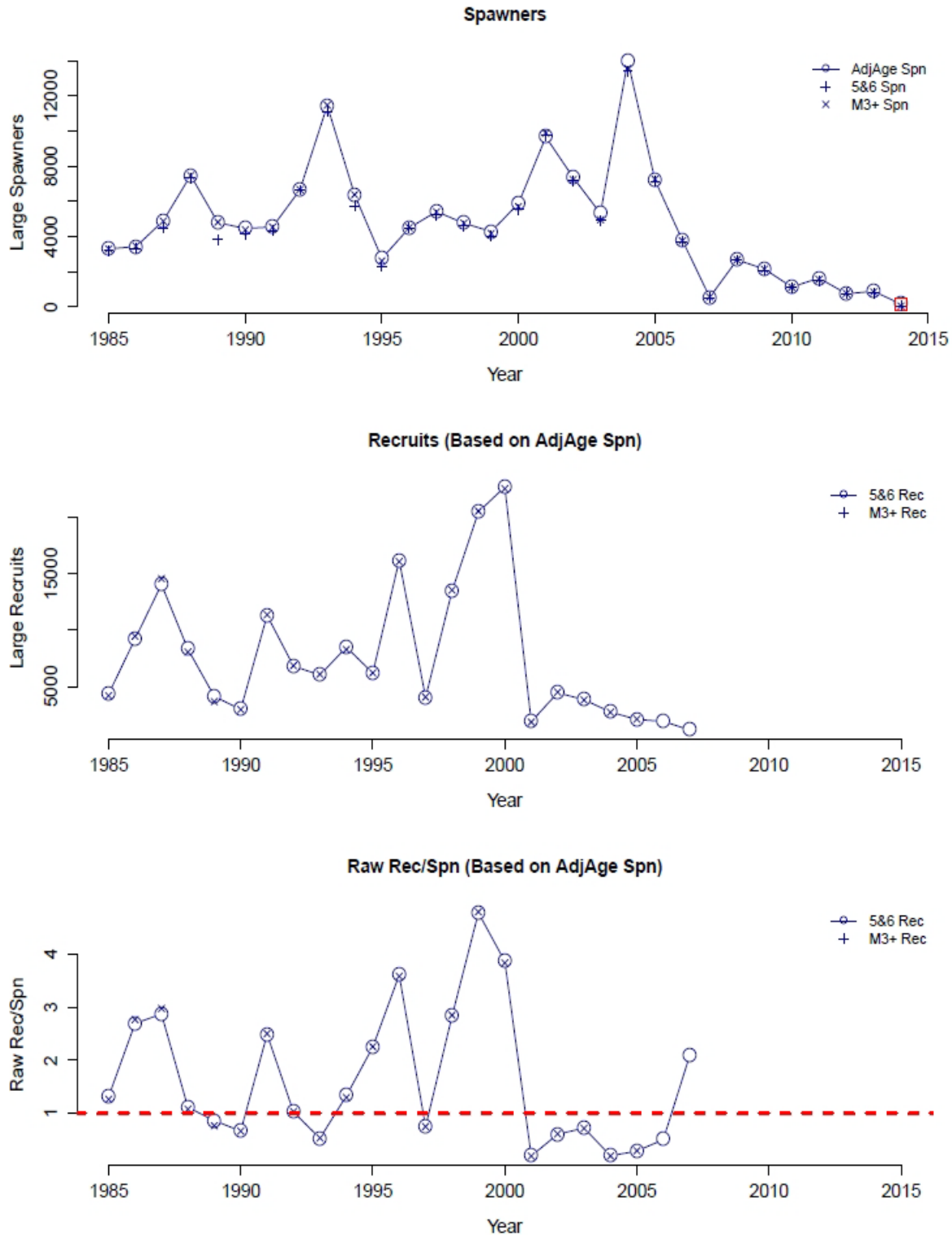


Figure 2: Abundance time series of spawners, recruits, and raw productivity (R/S) by brood year for Little Tahltan Chinook. Consistent estimates of spawner abundance are available from 1985 to 2014, based on weir counts. Adult recruit estimates are available for brood years 1985 to 2007, derived from annual estimates of spawner abundance and catch based on age composition. Data sources are summarized in Section 2.1.1.

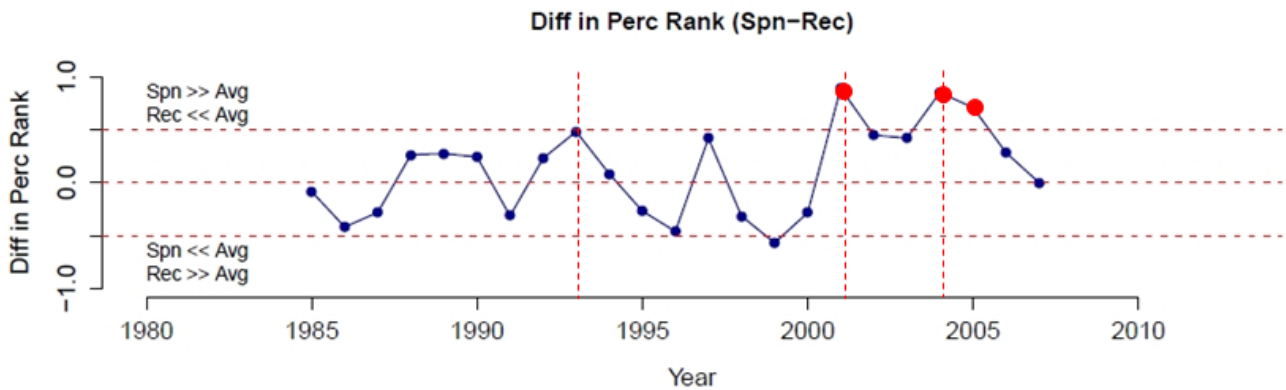
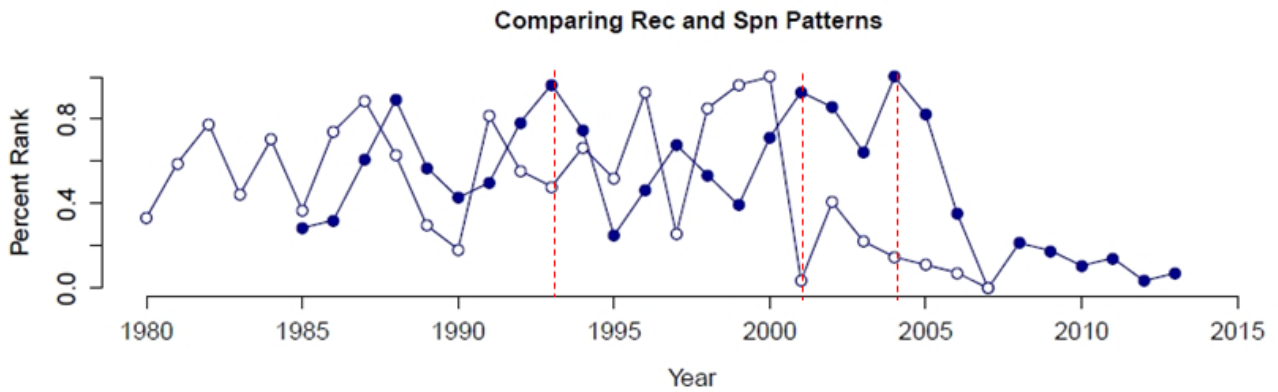
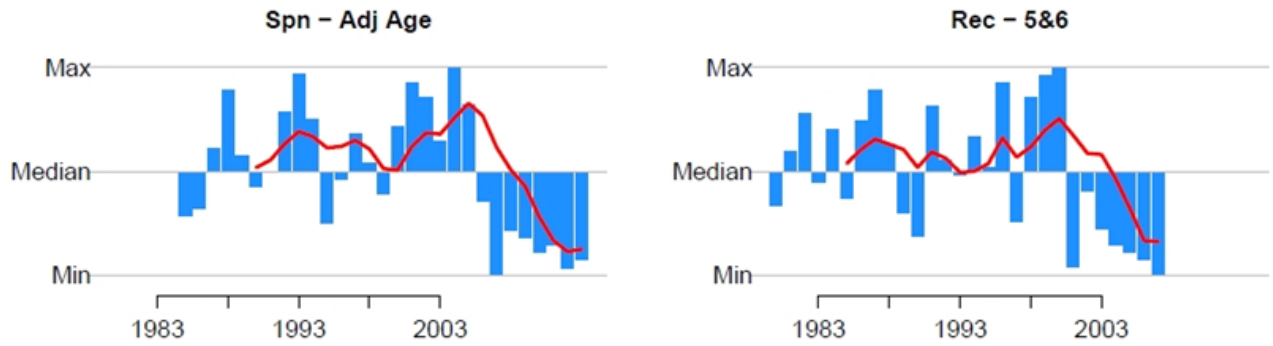


Figure 3: Rescaled patterns in spawners and recruits – Base Case. All panels show time series rescaled as percent ranks. In the top 2 panels, these ranks are converted to deviations from the median with the 6-yr moving average shown as a red line. The bottom panel shows the difference in percent ranks (Spn-Rec), such that a value of 1 would mean that the largest observed spawner abundance happened in the same brood year as the lowest observed recruitment. Brood years 2001, 2004, and 2005 are flagged as having spawner abundances near the upper end of the observed range associated with recruitment near the lower end of the observed range (i.e. biggest difference in percent ranks; red points in bottom panel). Vertical red lines in middle and bottom panel indicate years with 3 largest spawner abundances (1993, 2001, 2004). Percent rank calculations are documented in Section 13.2.

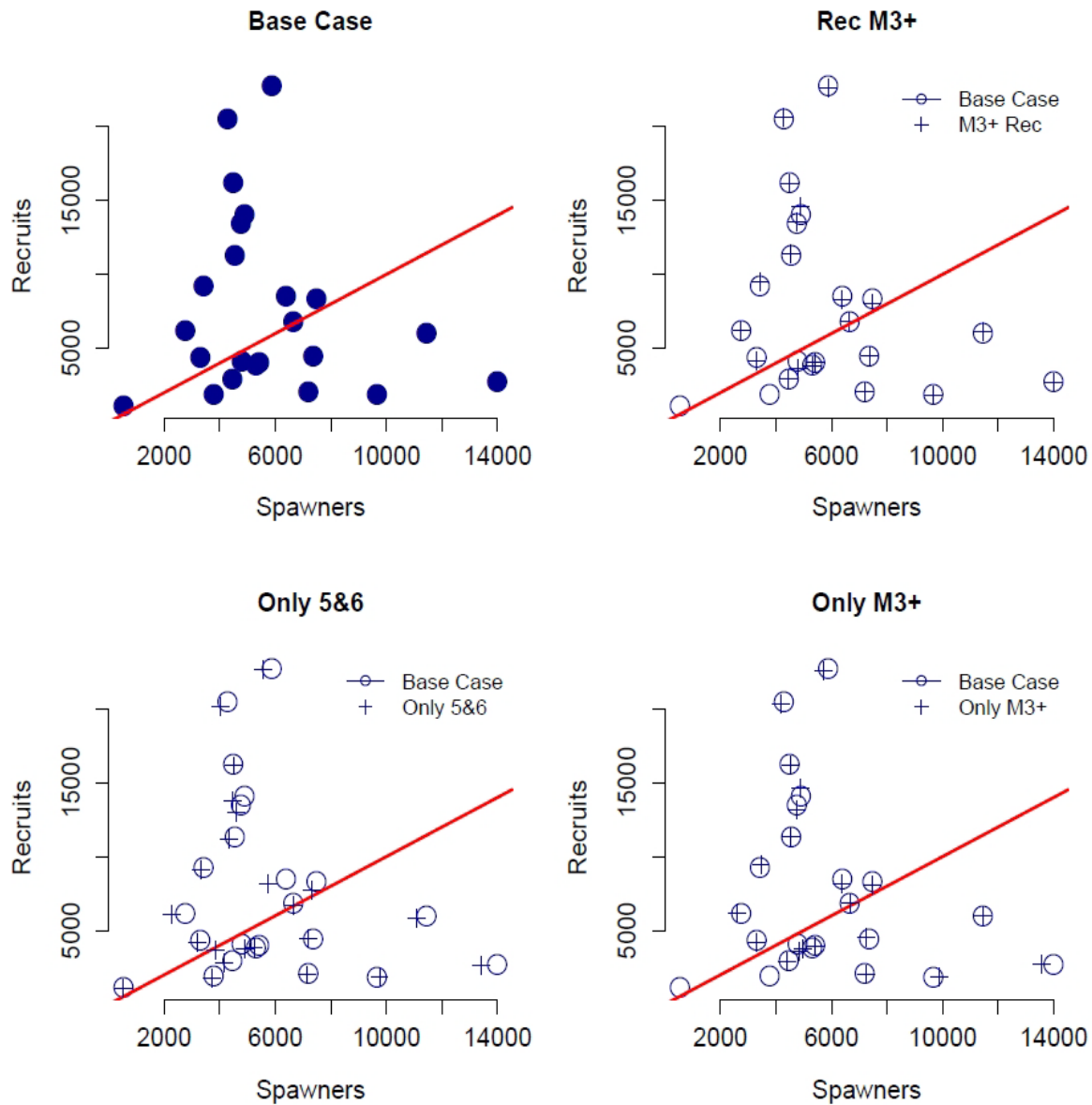


Figure 4: Pairwise plots of spawners and recruits by brood year for Little Tahltan Chinook. The panels show the effect of alternative assumptions about size (% small adults) and age composition on the Recruit vs. Spawner scatter plot, as per Section Table 5 Diagonal lines show replacement (i.e. recruits = spawners).

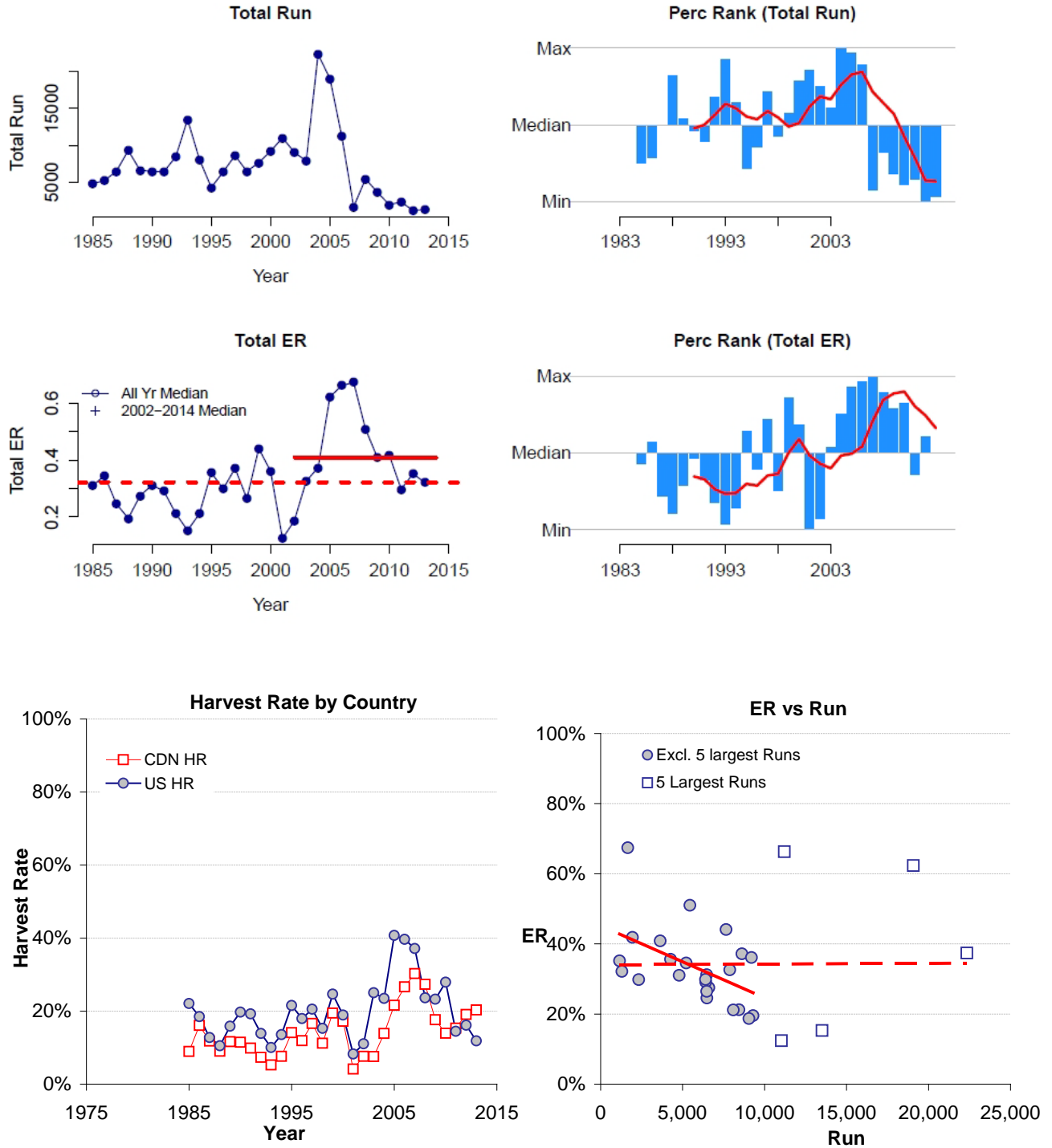


Figure 5: Overview of Little Tahltan Chinook harvest patterns since 1985. The top 2 panels show the pattern in total run size over time. The left panel shows the estimates and the panel on the right show the matching time series rescaled as ranked deviations from the median as a bar plot with 6-yr running average as a red line. The middle panels show total ER in the same format. The bottom panel shows how ER has changed with abundance in including all data or dropping 5 largest runs from the sample. Trend lines are simple linear regressions. Data sources are summarized in Section 2.1.1, with details documented in Appendix B. Percent rank calculations are documented in Section 13.2.

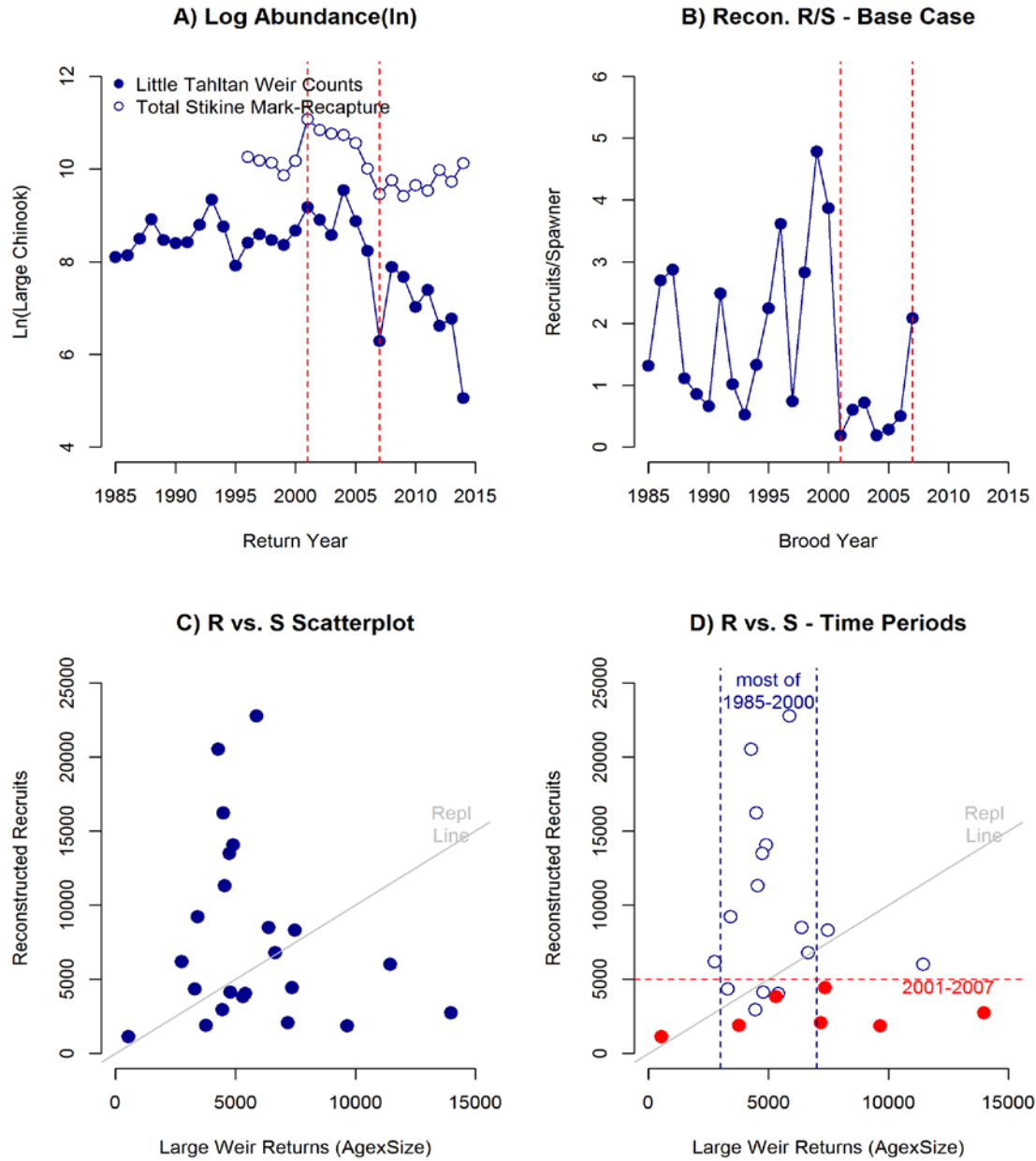


Figure 6: Illustration of Patterns in SR Estimates for Little Tahltan Chinook. Little Tahltan weir counts and lower-river Mark-Recapture estimates for the total Stikine initially followed a similar pattern but diverged starting in the 2007 return year (Panel A). Estimated productivity dropped precipitously in the 2001 brood year and stayed below replacement until the 2007 brood year, which had the lowest spawner abundance in the time series (Panel B). Panels C and D both show a scatter plot of estimated recruits and spawners, but Panel D separates the data points into 2 time periods (1985-2000 with stable spawner abundances and highly variable recruitment; 2001-2007 with highly variable spawner abundances and very poor recruitment). Three alternative explanations for these patterns were discussed at the CSAS review (DFO 2016a): (1) Inaccuracies in recent weir counts, (2) changing productivity regimes, and (3) stock collapse. Section 4.1 summarizes the arguments and discusses their implications.

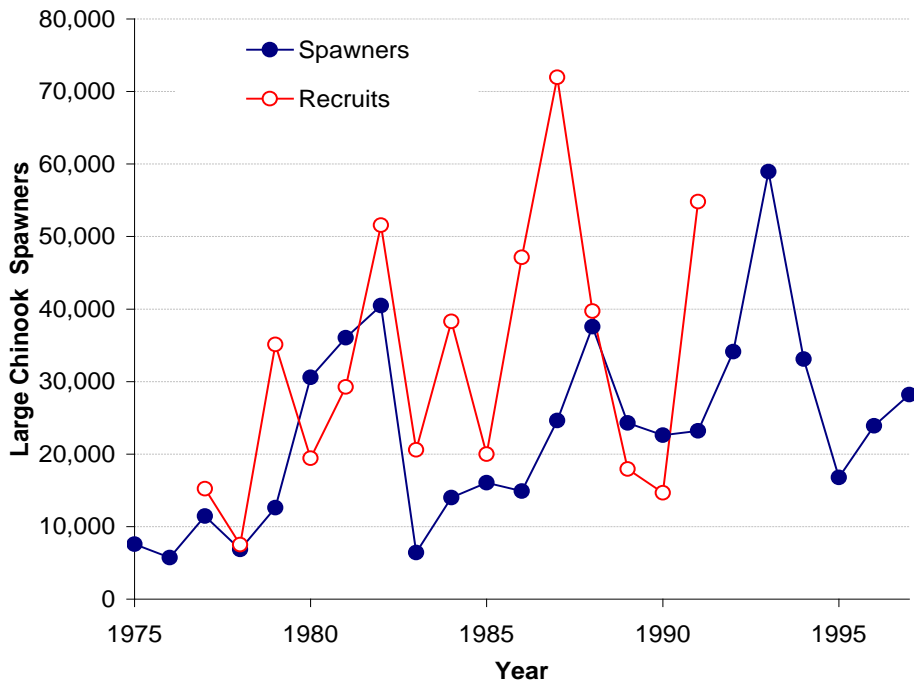
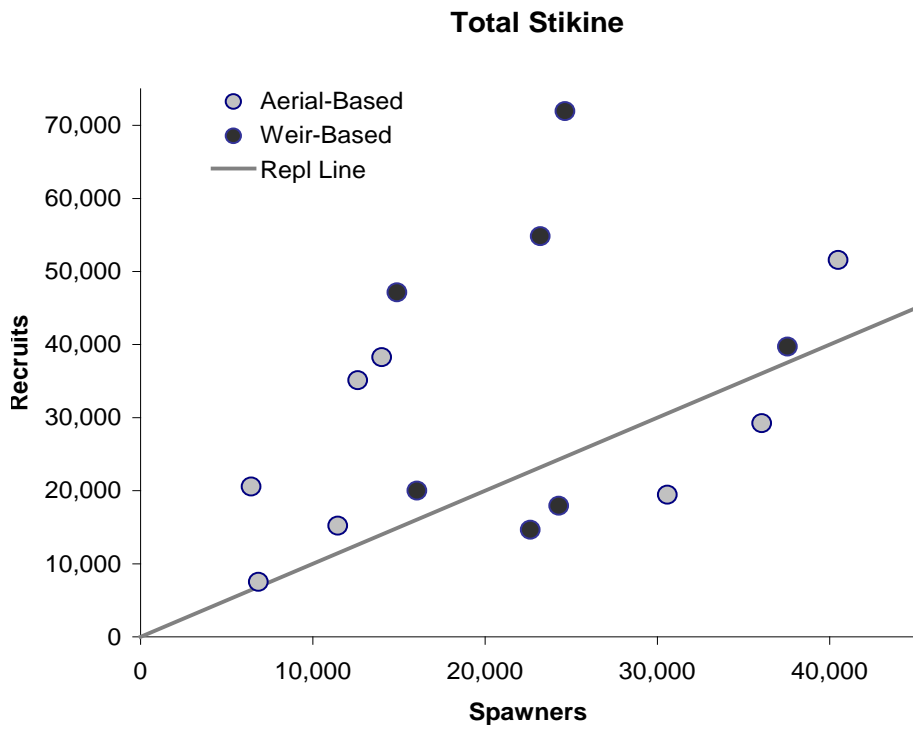


Figure 7: Patterns in SR estimates used by Bernard et al. (2000). Table B 5 lists their estimates.

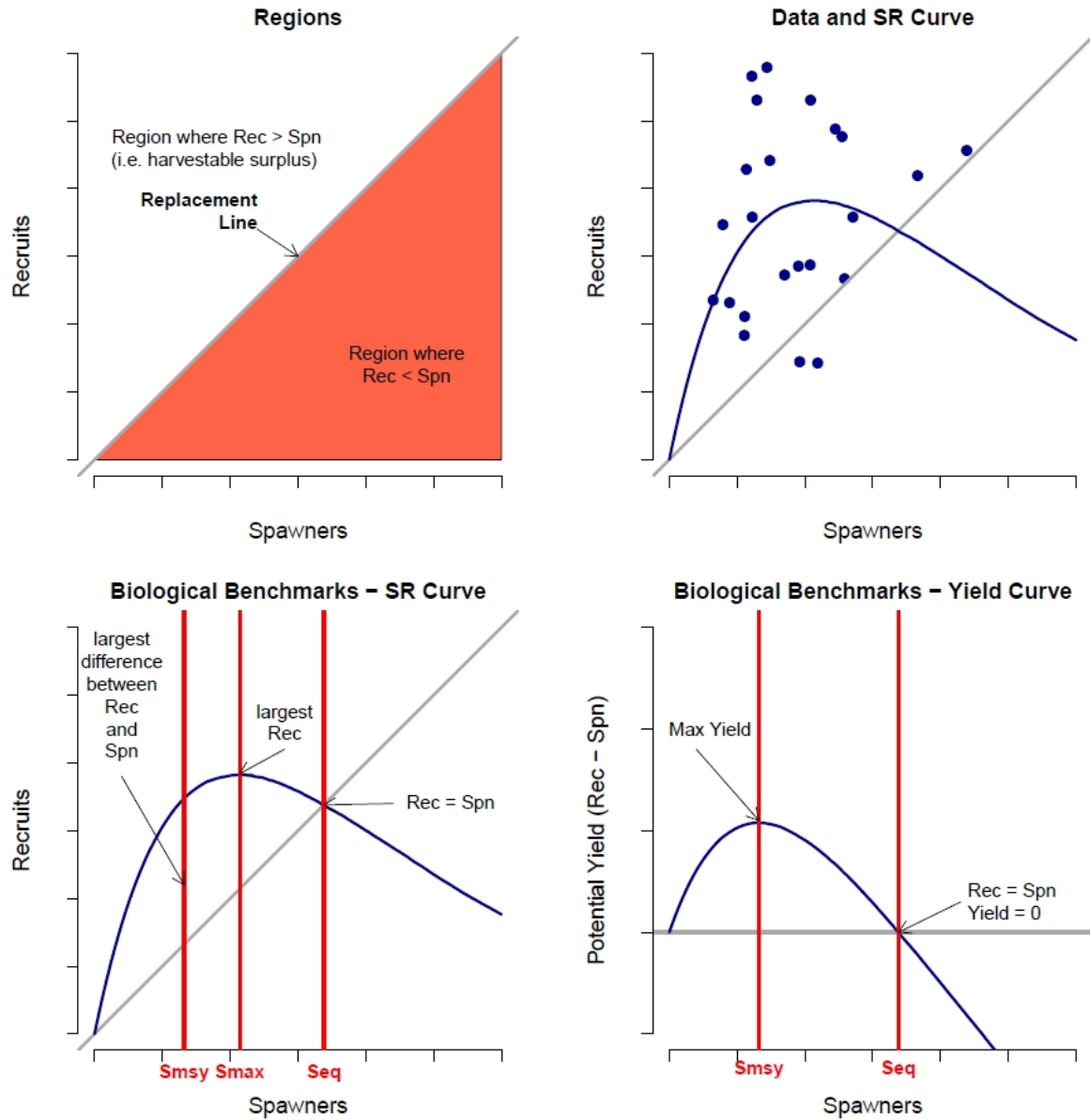


Figure 8: Graphical Illustration of Biological Benchmark Definitions. Biological benchmarks describe the estimated long-term average properties of the population, independent of the management approach. Figure taken from Pestal and Johnston (2015).

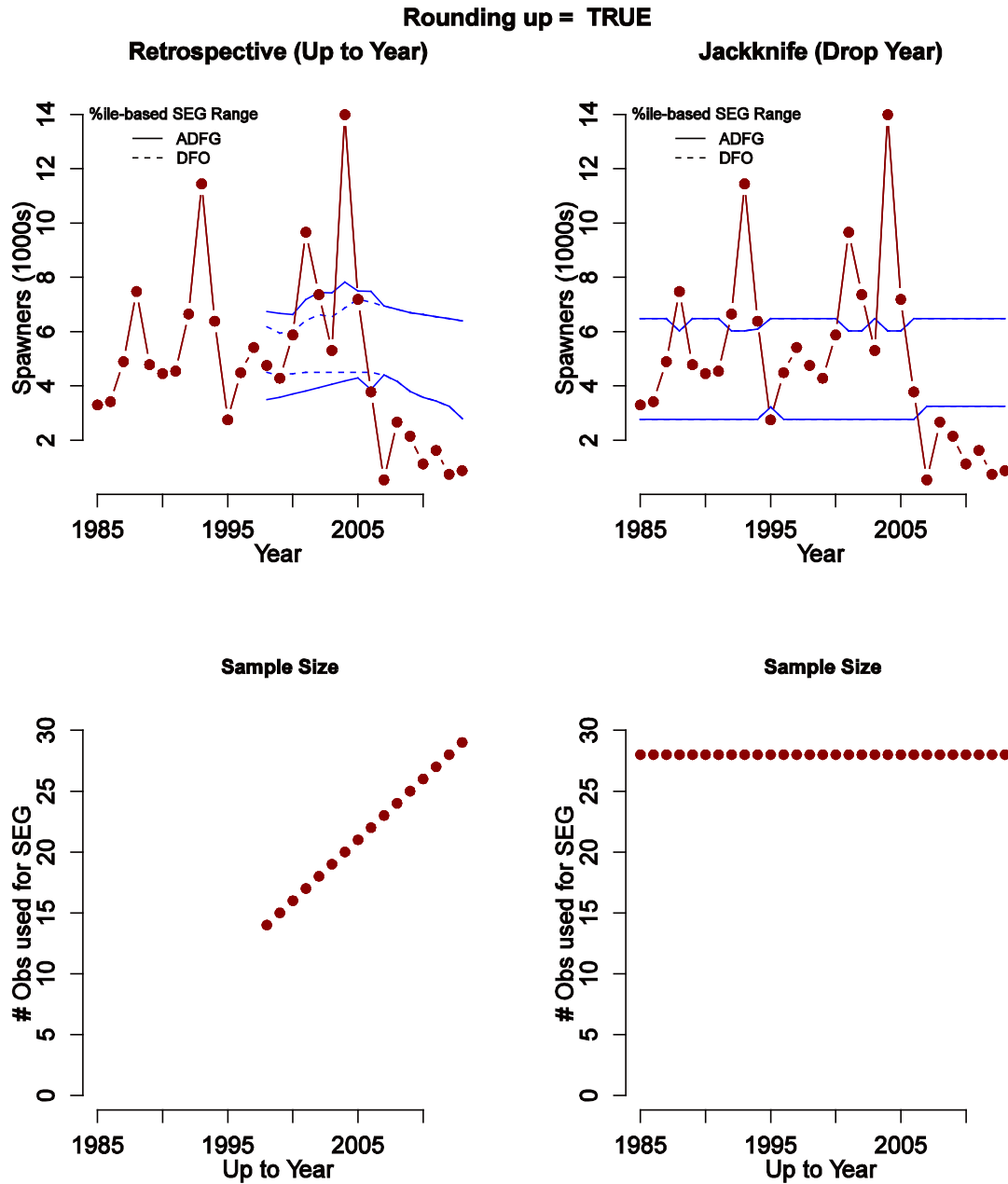


Figure 9: Sensitivity test of percentile-based reference ranges. Both top panels show the base-case time series of large Chinook and the estimated range for the Sustainable Escapement Goal (SEG) based on observed percentiles (2.2). Left panel shows the change in SEG over time as additional observations are added. Right panel shows effect of dropping individual observations. The SEG range is wide, but stable over time and insensitive to individual observations.

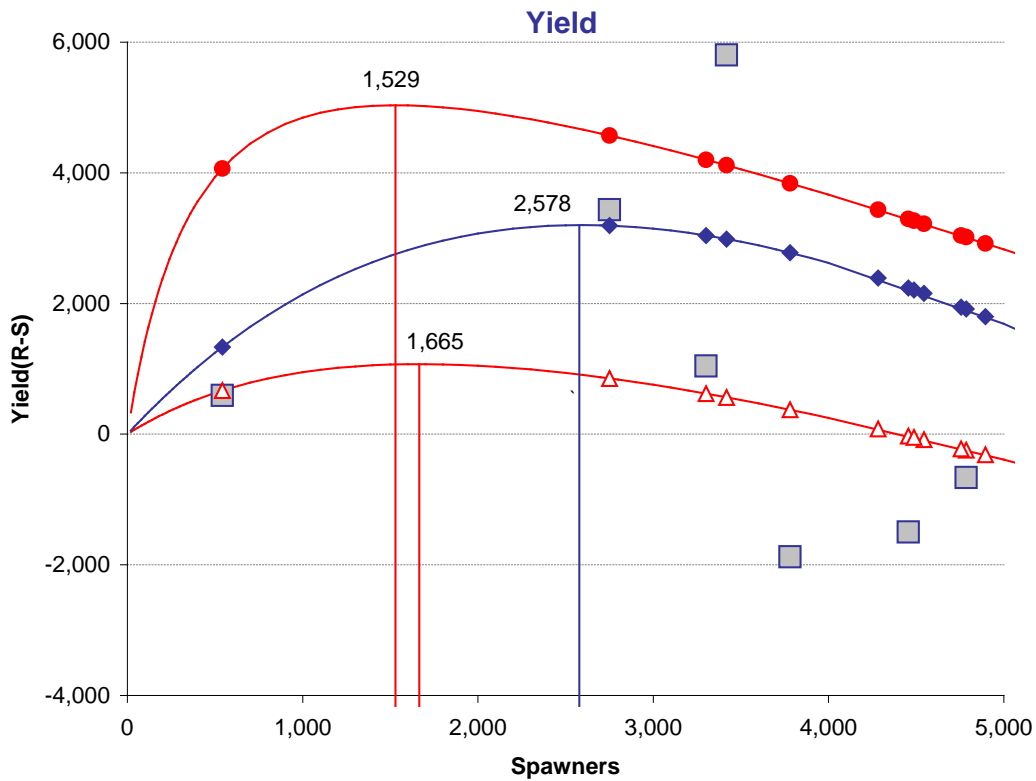
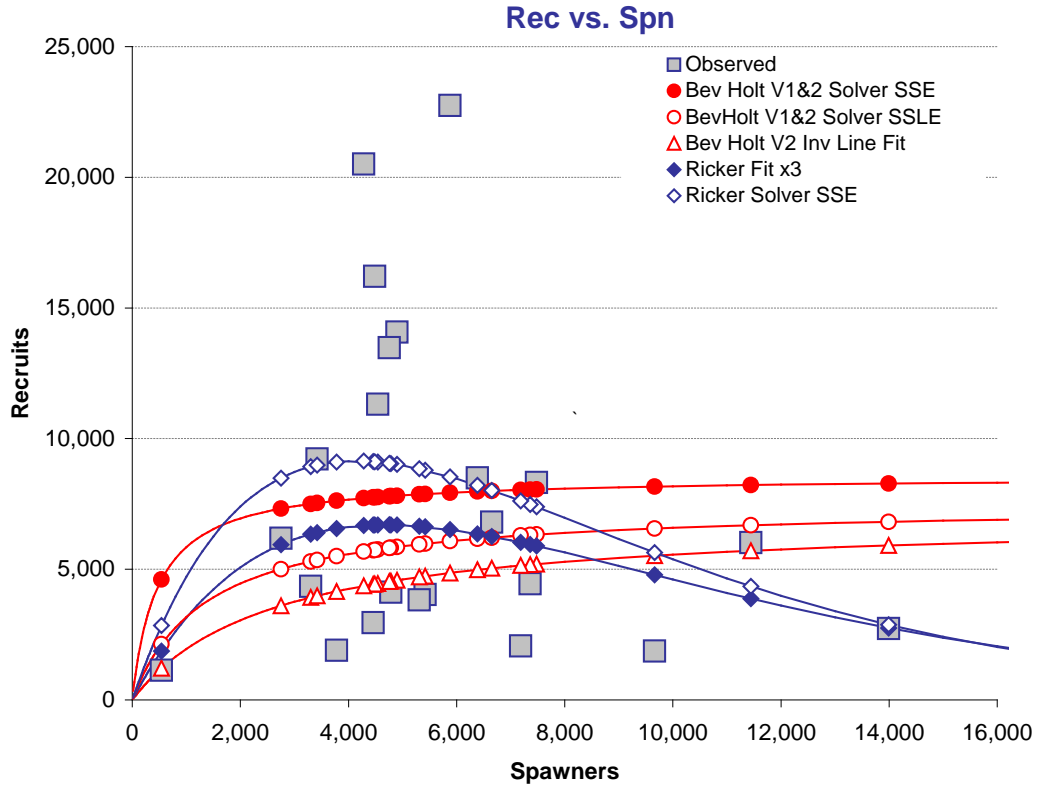


Figure 10: Plots of SR estimation cross-check using simple methods. The different SR curves correspond to the parameter estimates in Table 14. Note that these estimates are intended solely as a quick diagnostic check and should not be used.

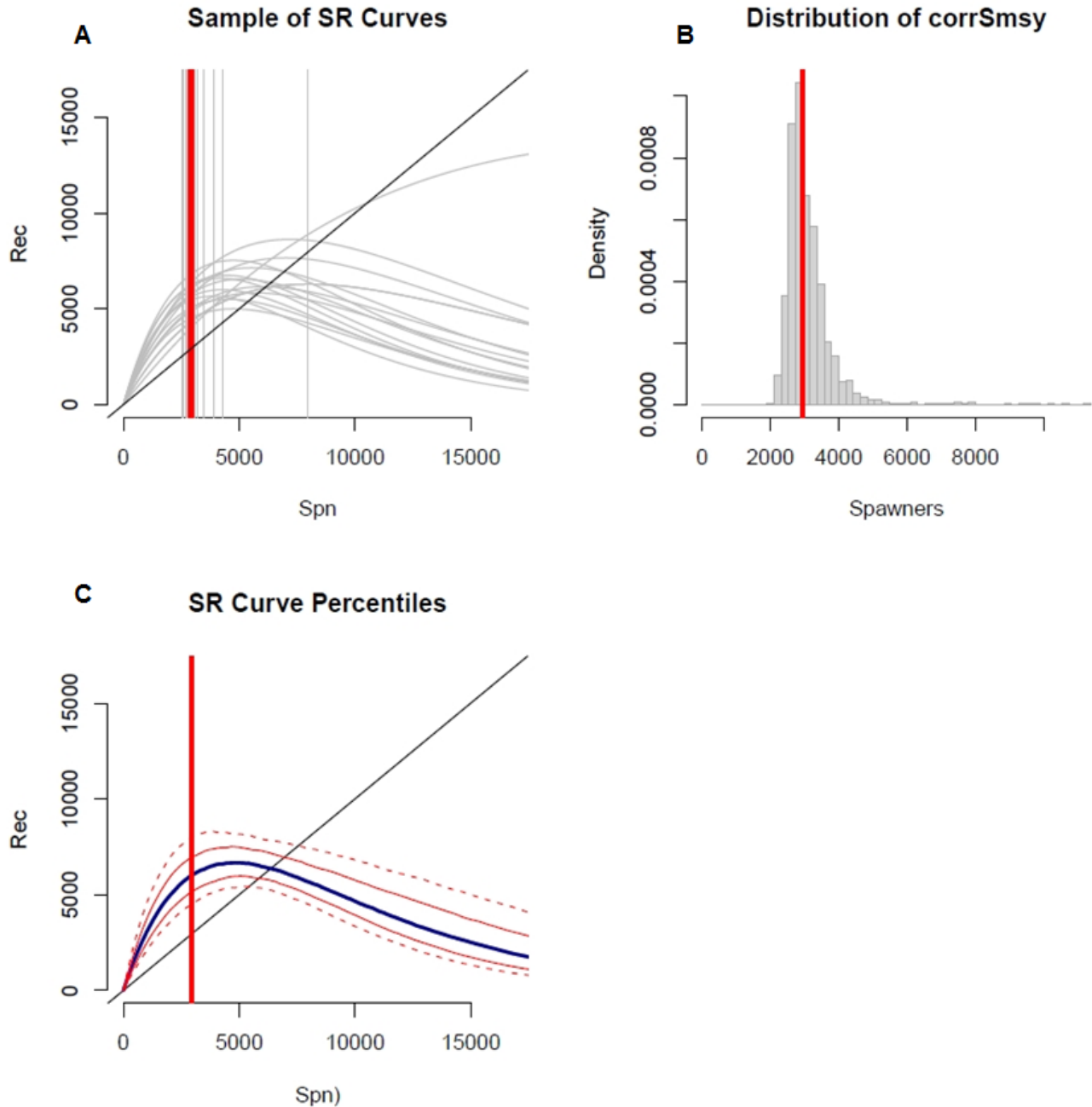


Figure 11: Illustration of uncertainty in spawner-recruit parameters and resulting uncertainty in estimates of S_{MSY} . All 3 panels show results for the Ricker AR1 model fitted to the Spn2Ad dataset. The vertical red line in all 3 panels marks the overall median estimate of S_{MSY} , labelled SMSY50 throughout the document. The diagonal line in Panels A and C is the replacement line with 1 recruit/spawner. Panel A shows a random subsample of 15 Ricker curves from the 2000 parameter sets sampled from the posterior distribution with vertical lines marking the corresponding S_{MSY} estimates for each curve. Panel B shows the distribution of all 2000 S_{MSY} estimates sampled from the posterior distribution. Panel C shows the median Ricker curve and percentile envelopes capturing 50% and 80% of the 2000 Ricker curves (i.e. 25th to 75th percentile, 10th to 90th percentile). Subsequent calculations can be based on either one of these 3 variations. For example, the alternative yield profiles in Figure 12 to Figure 15 are based either on comparisons to the median Ricker curve in Panel C or comparisons to each of the individual curves illustrated in Panel A.

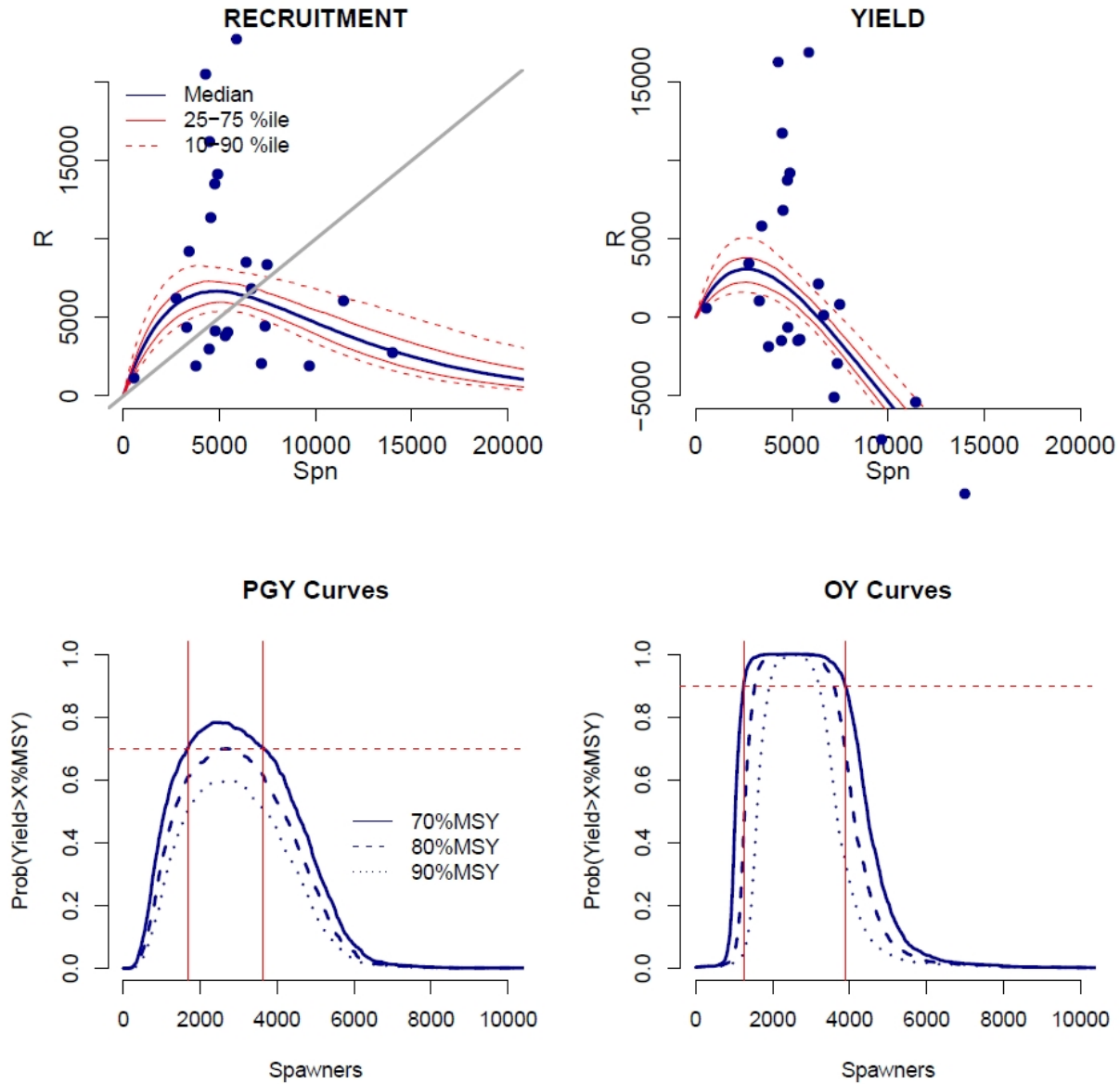


Figure 12: Ricker SR Fits – MCMC / Base Case Data Set. The Recruitment panel shows observed recruits (R) and spawners (S) for and base-case data set ($Spn=AdjAge$, $Rec=5\&6$ only), and the distribution of fitted values for basic Ricker model. Curves show the distribution of fitted values (i.e. distribution of recruitments calculated for each MCMC parameter sample). The diagonal line shows replacement (i.e. recruits = spawners). The Yield panel shows the same model fit, except that the vertical axis is yield, calculated as recruits – spawners ($R-S$). Horizontal lines show replacement (i.e. recruits = spawners; yield = 0). The PGY panel shows the same yield curves, except that the distribution of yields at each spawner level is expressed as the proportion of samples where yield exceeds 70%, 80%, or 90% of MSY (i.e. median yield at median SMSY). PGY70 is the range where more than 70% of the parameter samples produce yields larger than 70% MSY. The OY panel is similar to the PGY panel, except that yields are compared to MSY for each parameter set.

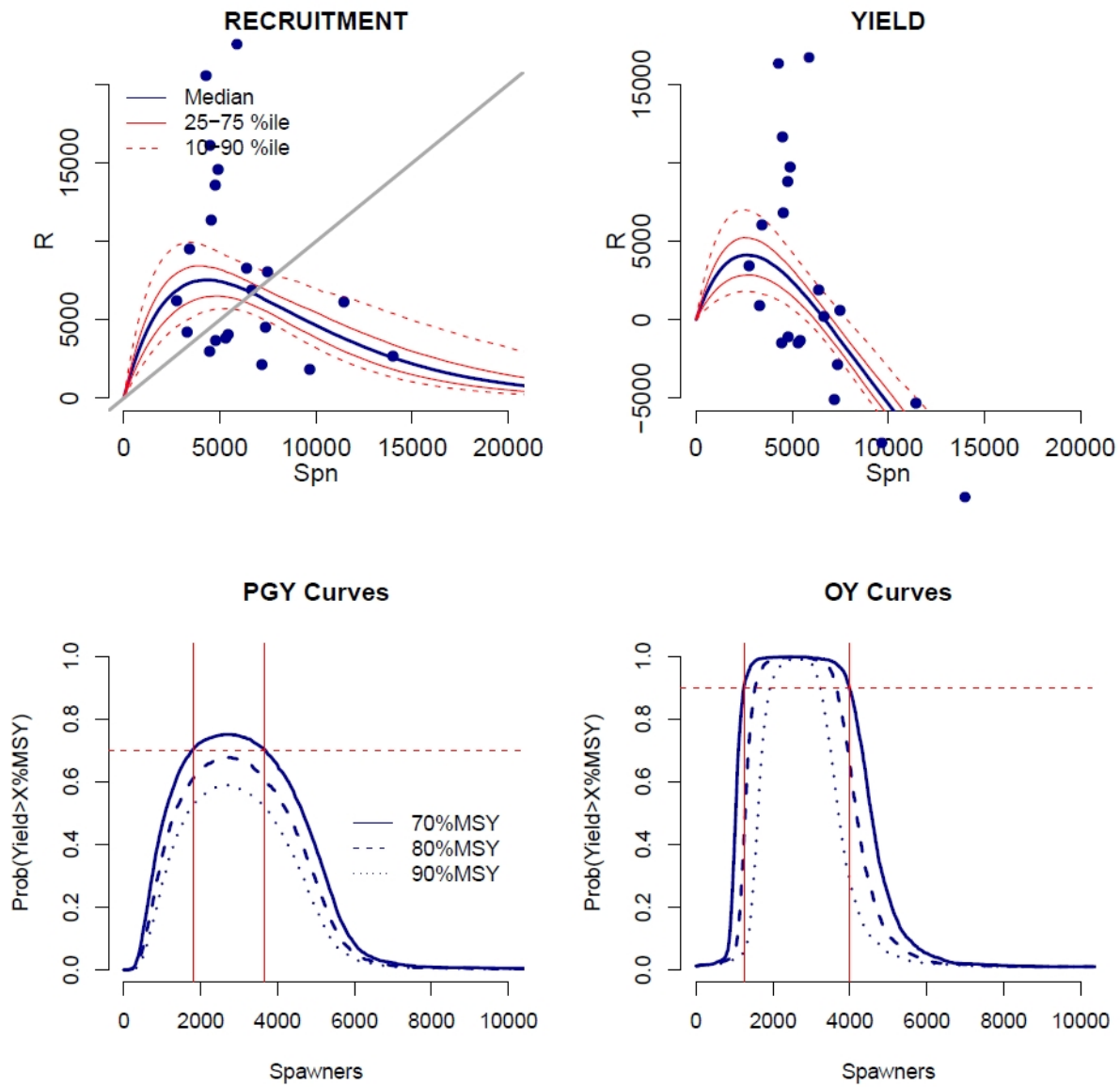


Figure 13: Ricker AR1 SR Fits – MCMC / Base Case Data Set. Same panels as in Figure 12.

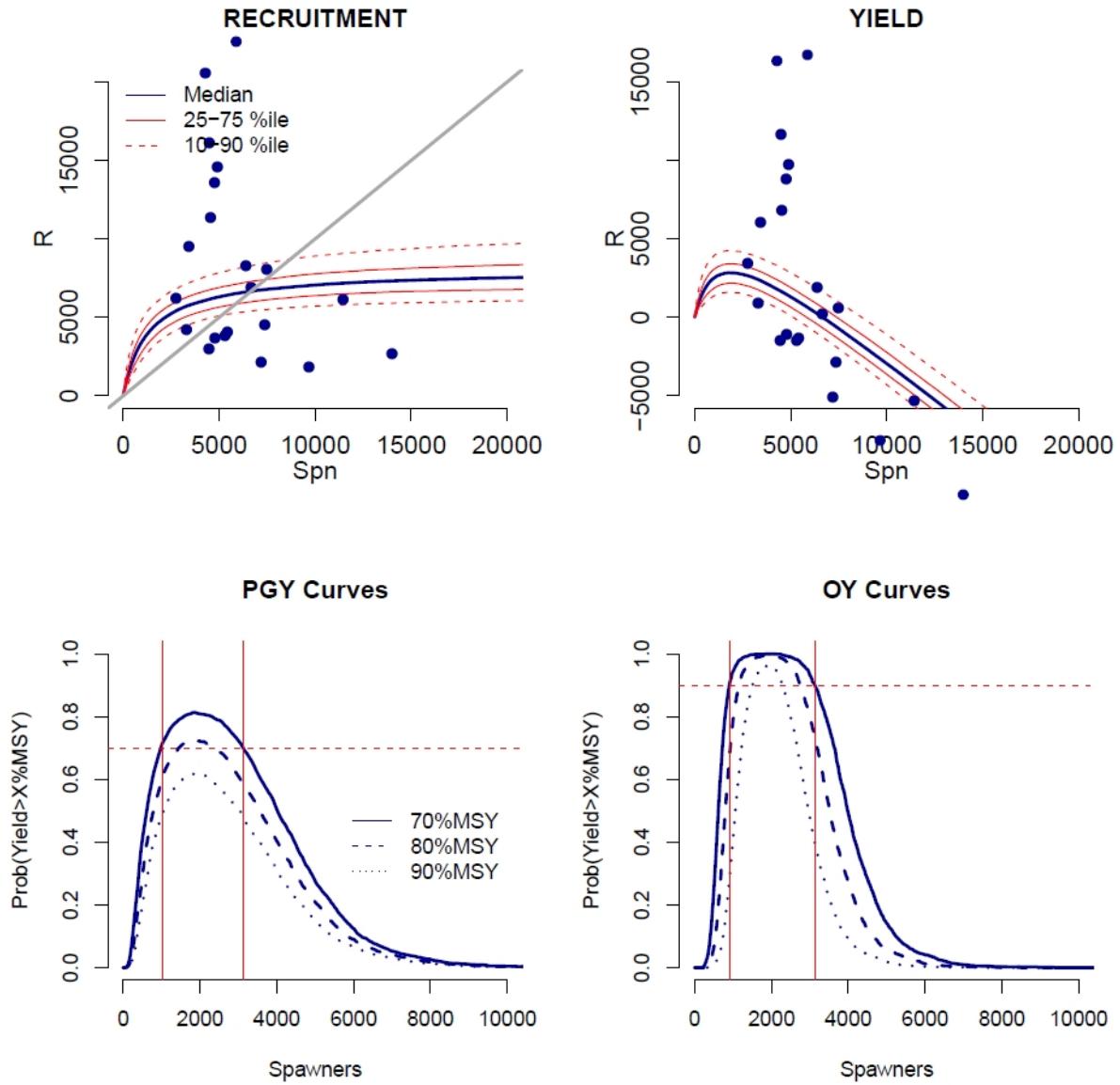


Figure 14: Beverton-Holt SR Fits – MCMC / Base Case Data Set. Same panels as in Figure 12.

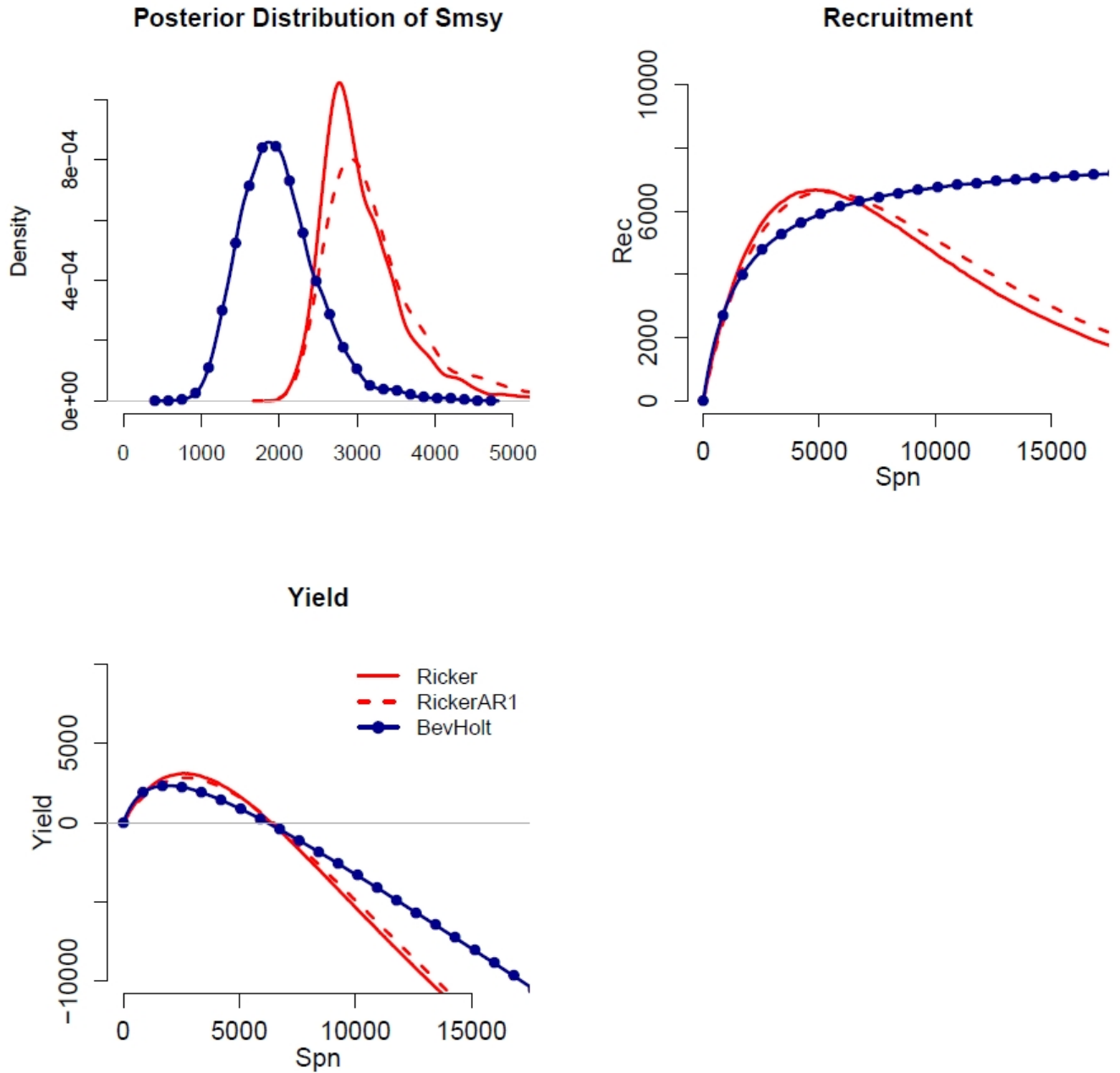


Figure 15: SR Fits comparison for 3 alternative models Base Case Data Set. Panels correspond to Figure 12, but show only the median curve in the top row and only the 70% MSY curves in the bottom row.

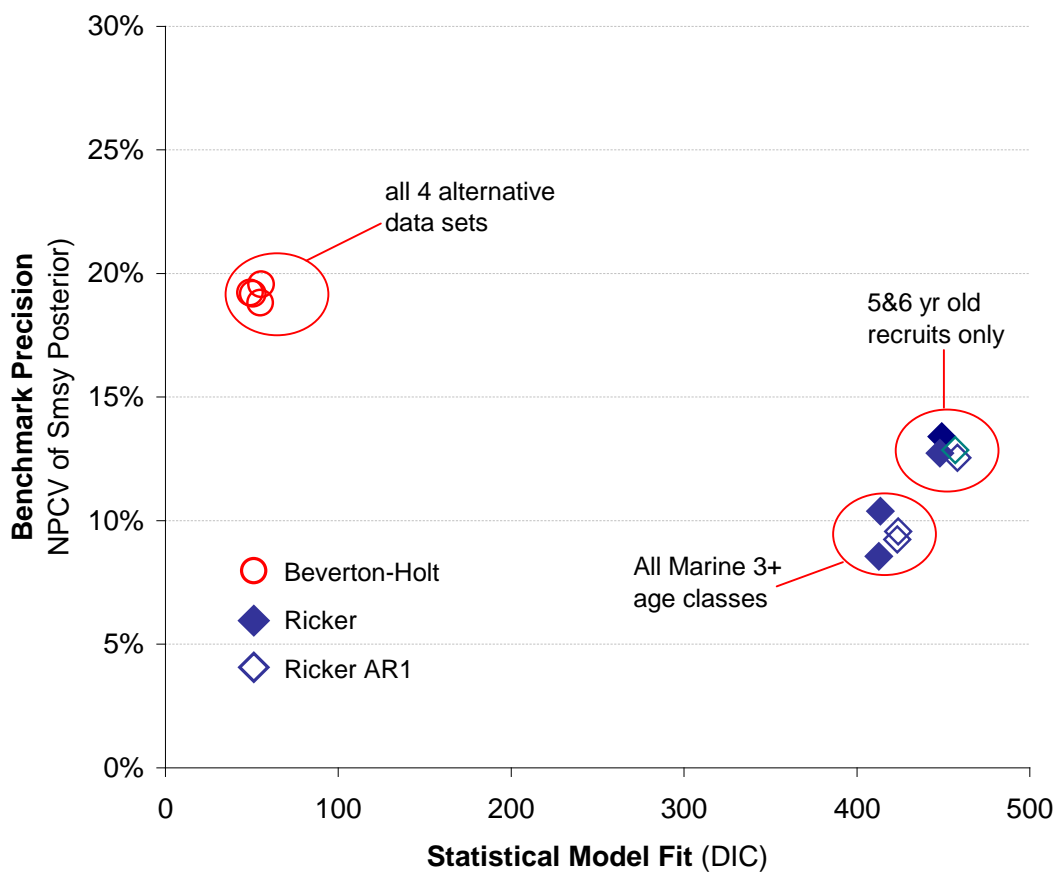


Figure 16: Model Fit vs. Benchmark Precision (DIC vs. NPCV). Each point in the figure corresponds to one of the 12 sensitivity analyses listed in Table 16 (4 data sets, 3 alternative SR models each). Model fits are expressed as the Deviance Information Criterion (DIC), which is the standard measure of fit for MCMC. Lower DIC values indicate better fit. Benchmark precision is expressed as the Non-Parametric Coefficient of Variation (NPCV) for the resulting SMSY estimate, following the approach by Clark et al. (2009). Lower NPCV values indicate higher precision (i.e. narrower range).

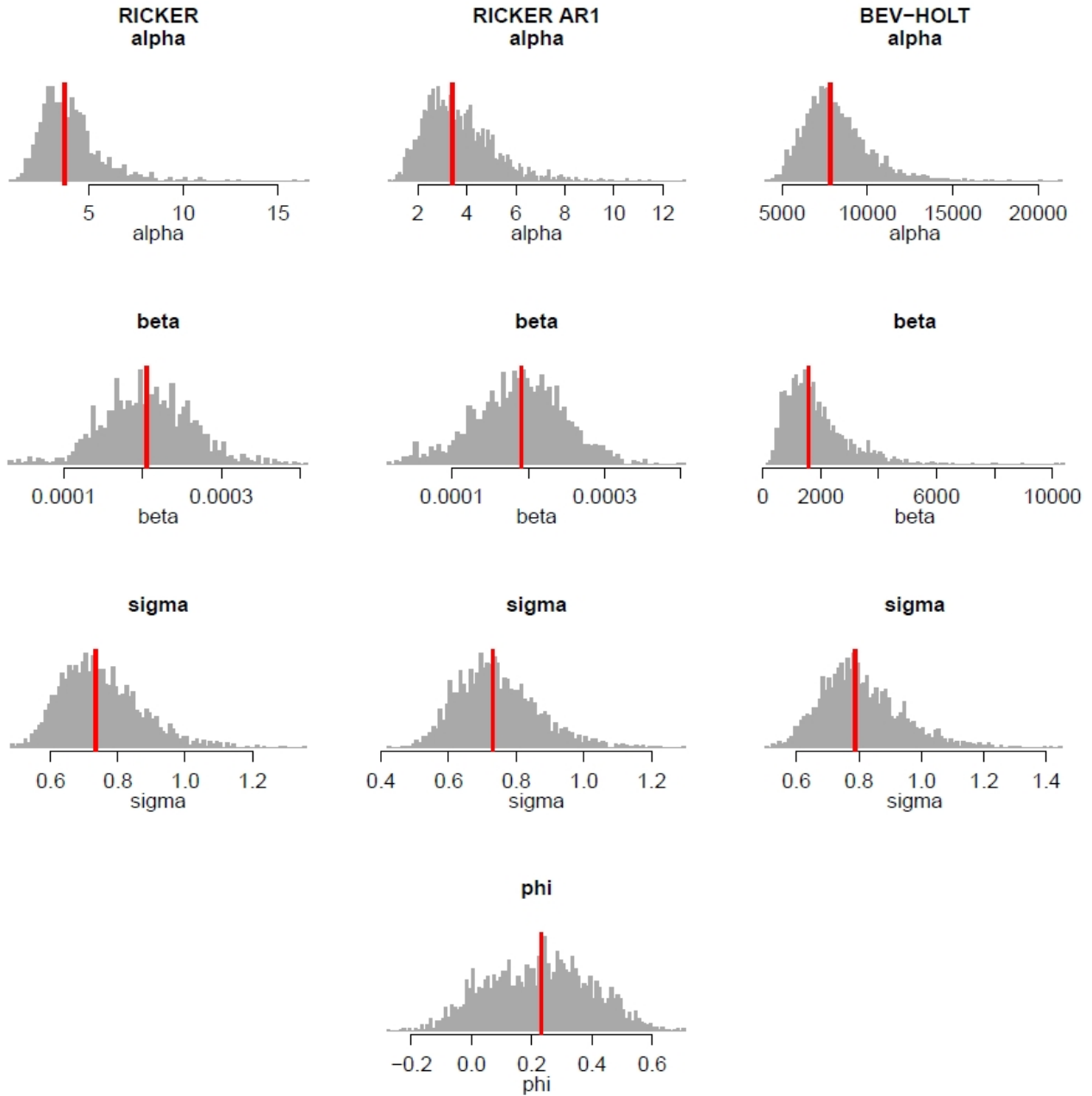


Figure 17: Posterior parameter distributions for 3 alternative SR Fits – Base Case Data Set. Each panel shows a histogram of 2,000 parameter samples, thinned from 2 chains of 40,000 MCMC samples each. Vertical lines show the median for each parameter sample. Table 7 lists parameter definitions.

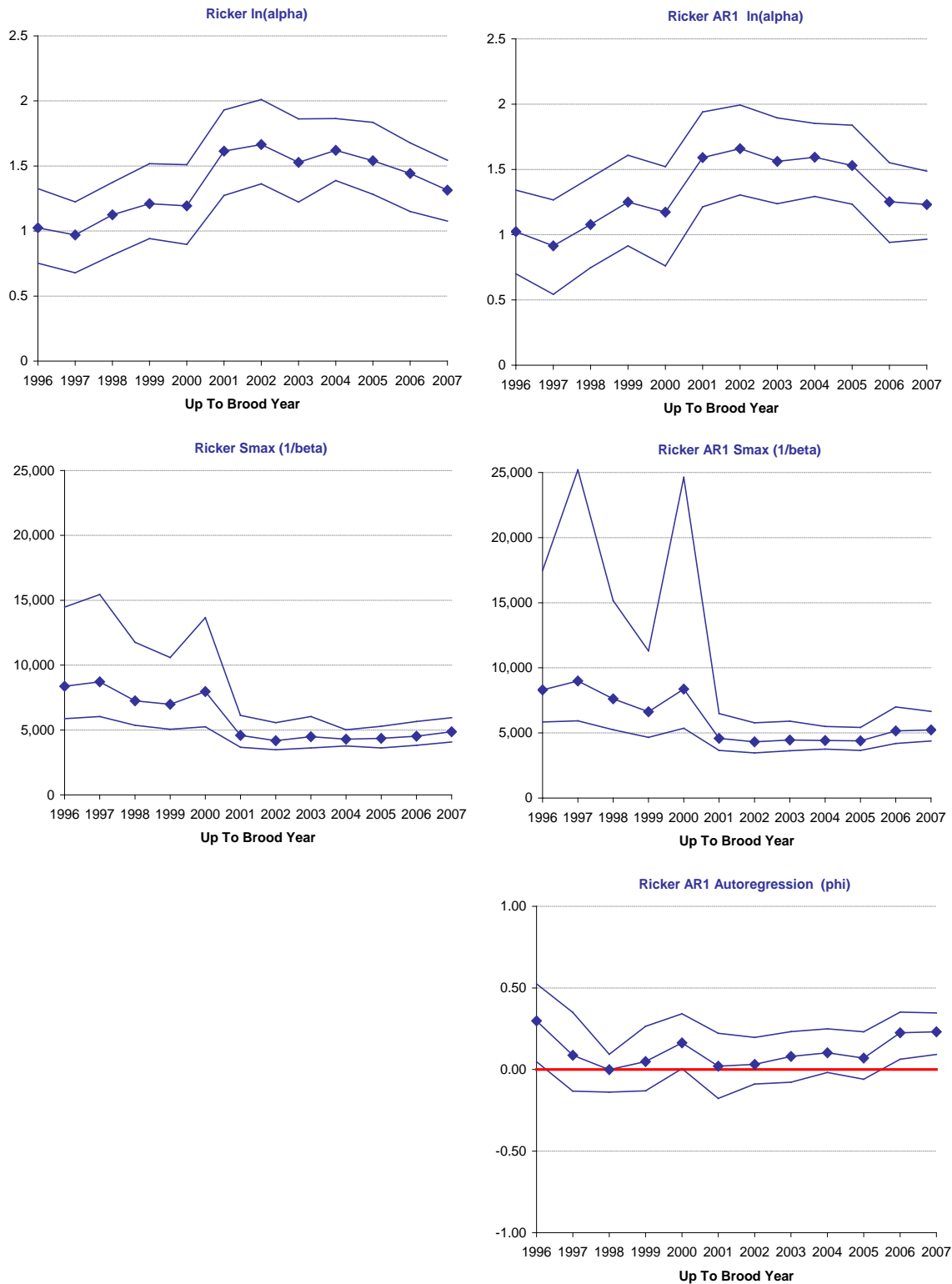


Figure 18: Retrospective test of Ricker and Ricker AR1 parameter estimates. All figures show the change in estimates as additional data are added, from model fits for the 1985-1996 brood years up to model fits for the 1985-2007 brood years. Each panel shows median and 25th/75th percentiles of the posterior distribution. The horizontal axes identify the last brood year used in the data set.

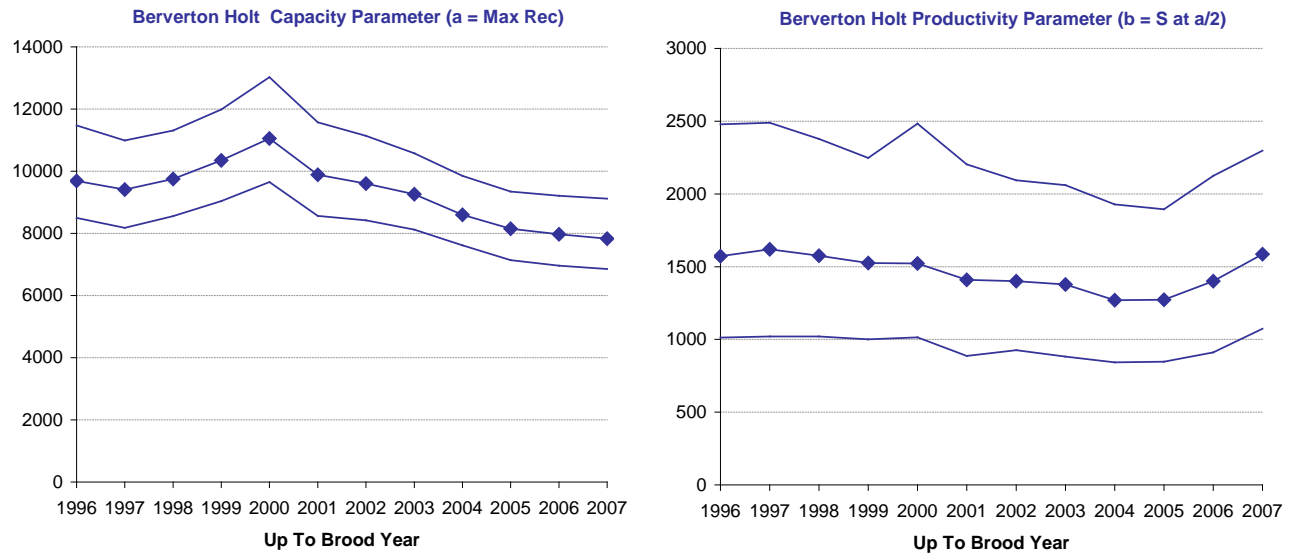


Figure 19: Retrospective test of Beverton-Holt parameter estimates. All figures show the change in estimates as additional data are added, starting with model fits for the 1985-1996 brood years up to model fits for the 1985-2007 brood years. Each panel shows median and 25th/75th percentiles of the posterior distribution. The horizontal axes identify the last brood year used in the data set.

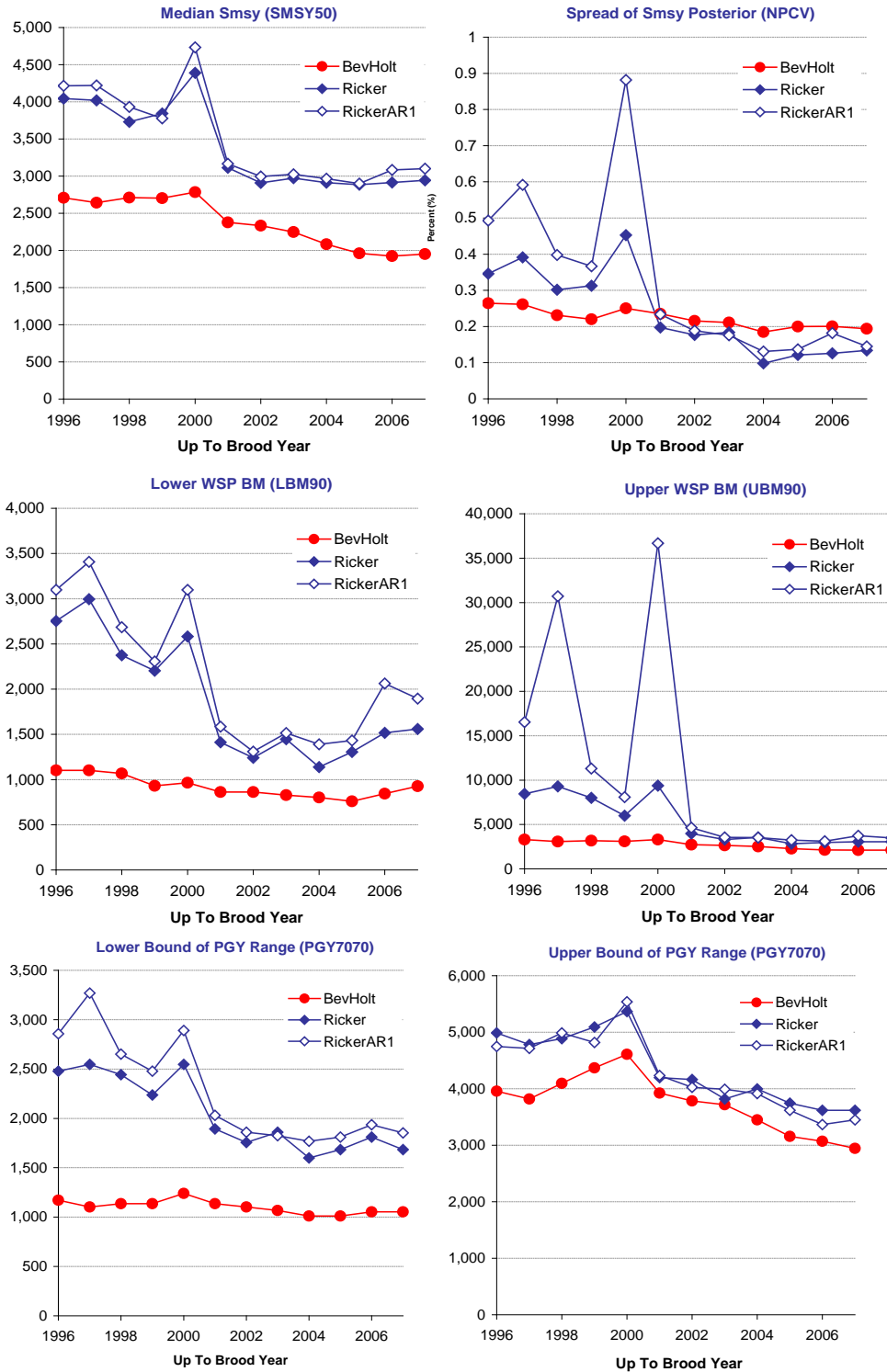


Figure 20: Retrospective test of Summary Reference Points (SRP) for 3 alternative spawner-recruit models. All figures show the change in estimates as additional data are added, starting with model fits for the 1985-1996 brood years up to model fits for the 1985-2007 brood years. SRP definitions as per Section 2.5. The horizontal axes identify the last brood year used in the data set.

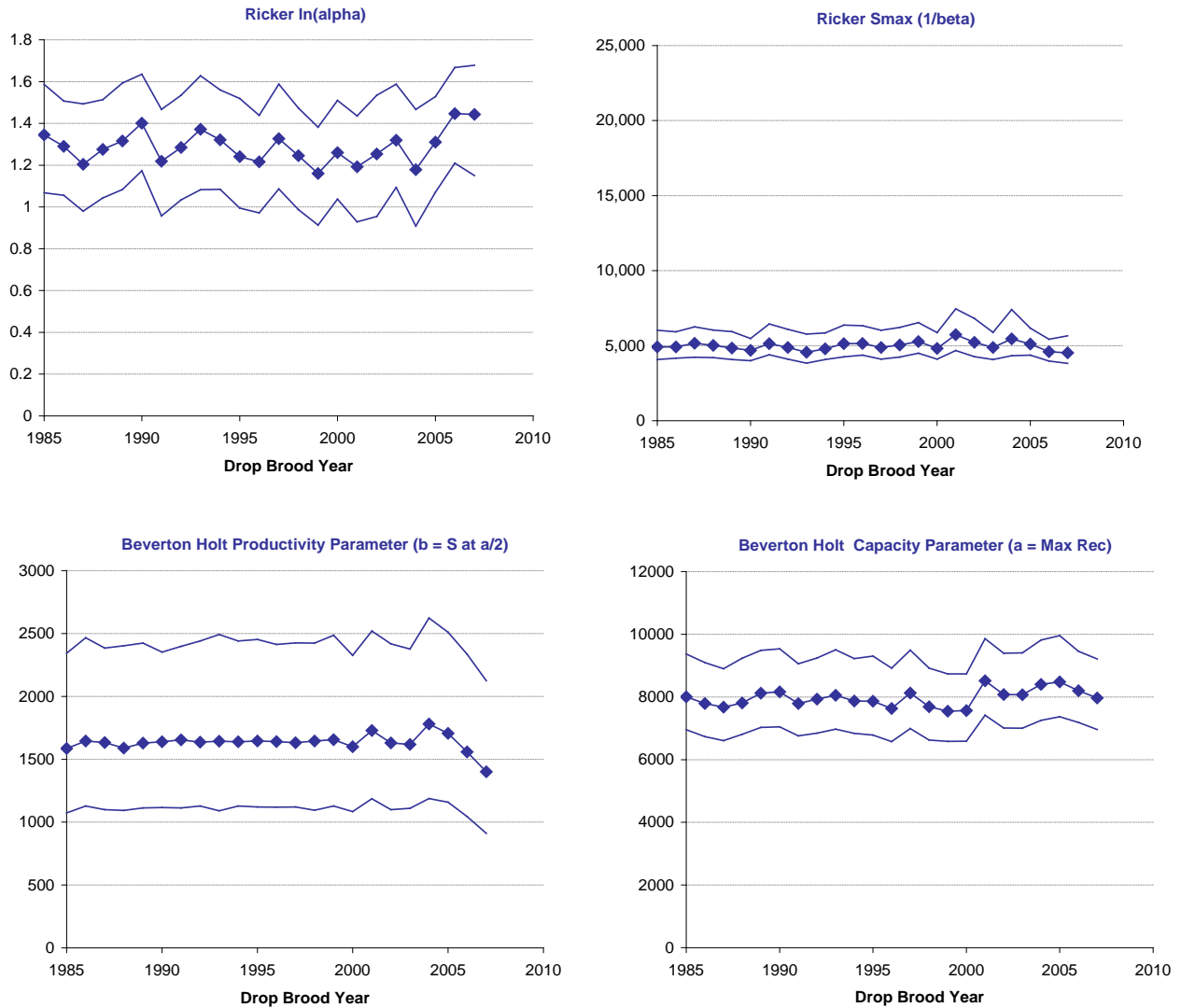


Figure 21: Jackknife test of Ricker and Beverton-Holt parameter estimates. All figures show the change in estimates as one of the observations is dropped. Each panel shows median and 25th/75th percentiles of the posterior distribution. The horizontal axes identify the brood year that was dropped from the data set. The Ricker AR1 model requires a continuous sequence of observations, and the jackknife test is therefore not applicable.

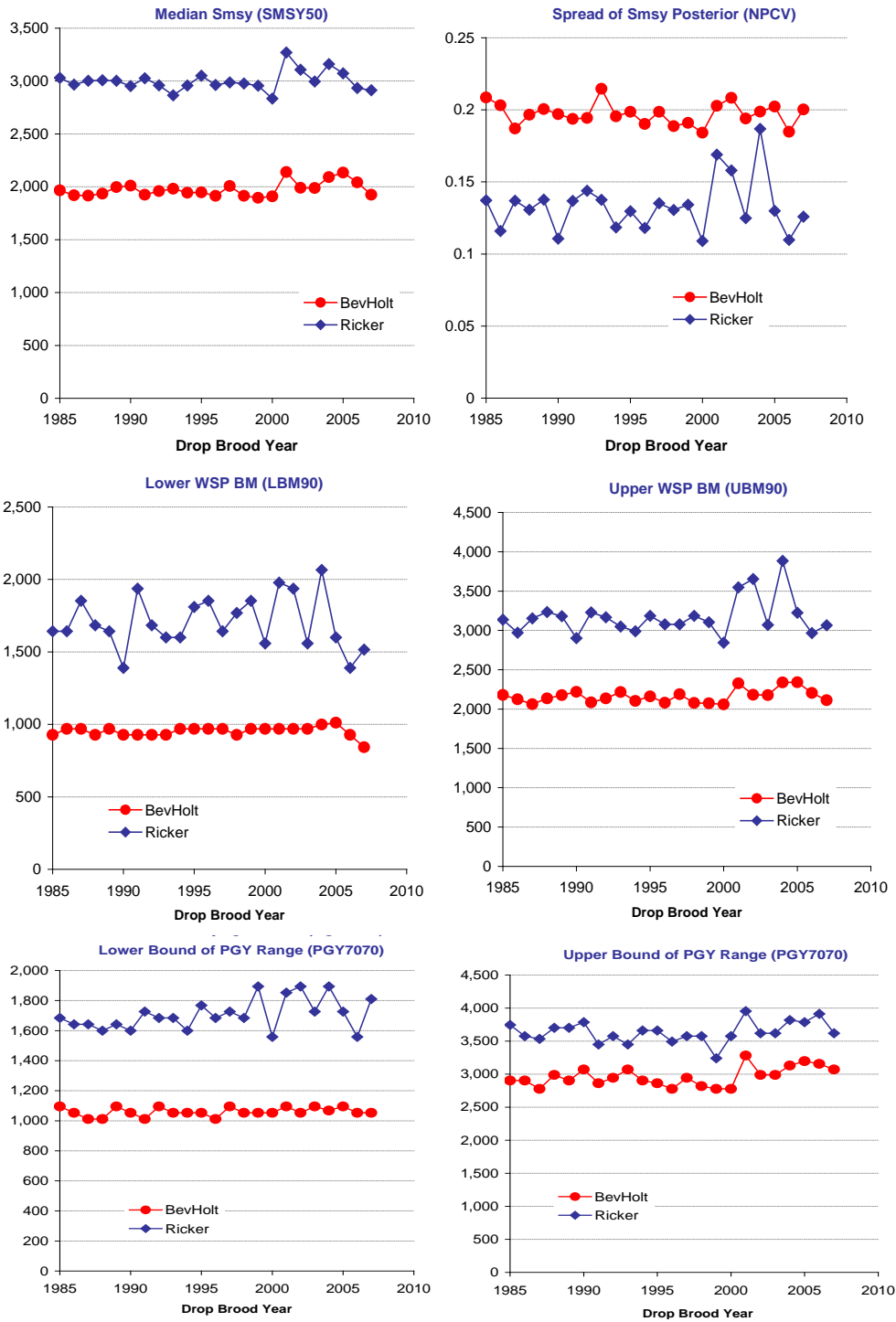


Figure 22: Jackknife test of Summary Reference Points (SRP) for Ricker and Beverton-Holt models. All figures show the change in estimates as one of the observations is dropped. The horizontal axes identify the brood year that was dropped from the data set. The Ricker AR1 model requires a continuous sequence of observations, and the jackknife test is therefore not applicable. SRP definitions as per Section 2.5. The horizontal axes identify the last brood year used in the data set.

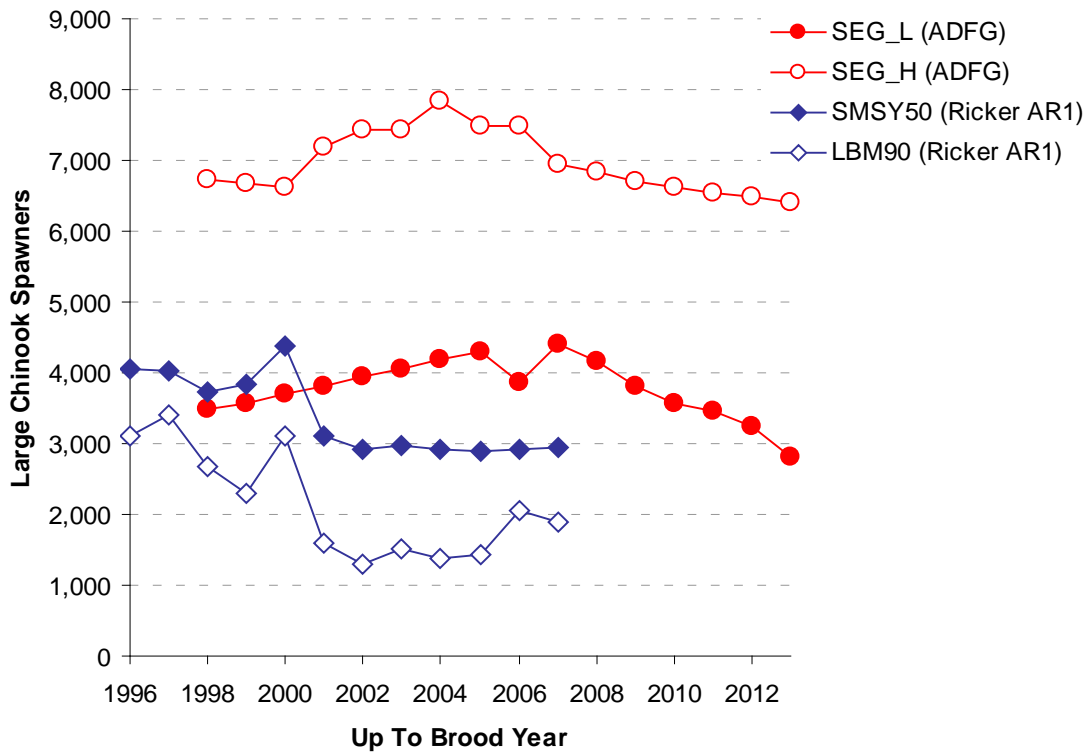


Figure 23: Retrospective pattern of percentile-based and SR-based reference values. SEG values are from Figure 9 using the ADFG algorithm and the base case spawner time series. SEG definition as per Section 2.2. SMSY50 and LBM 90 values are from Figure 20 using the Ricker AR1 model. Definitions of SEG, SMSY50 and LBM90 definitions as per Section 2.5. Ranges are summarized in Table 18.

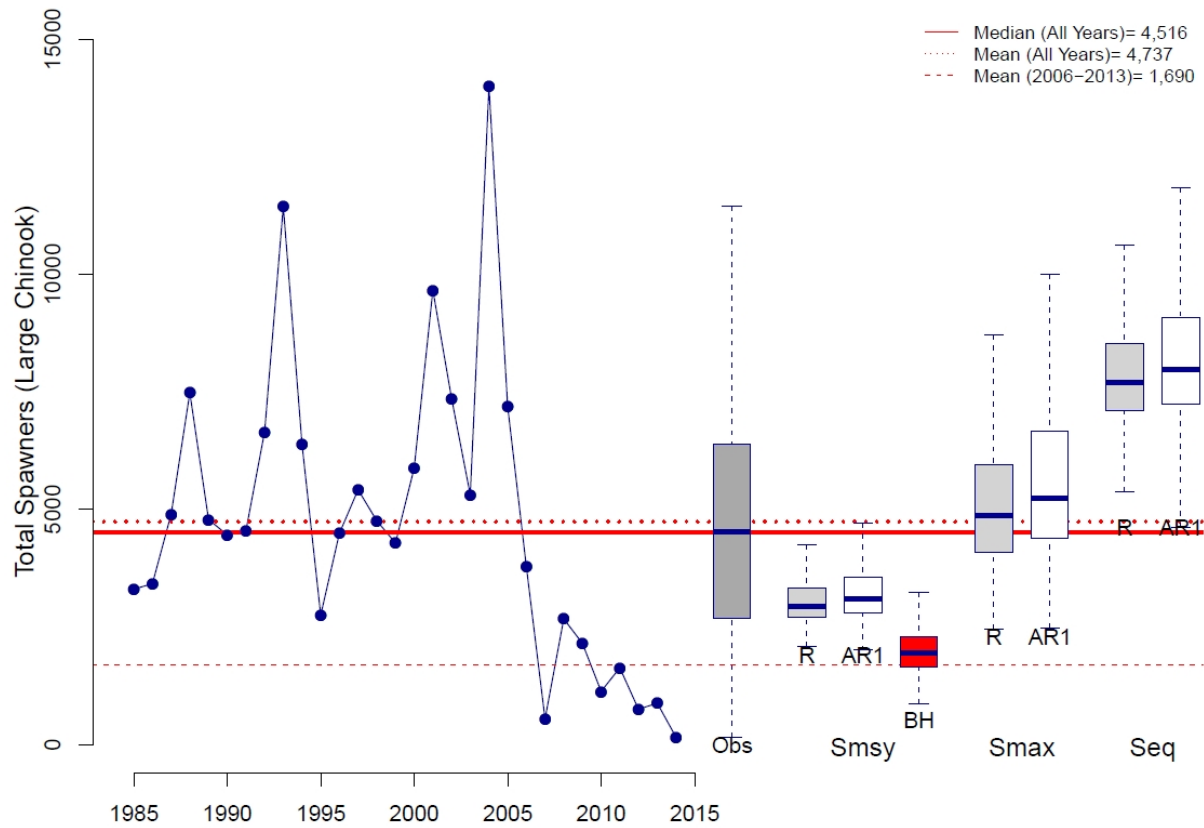


Figure 24: Observed Spn compared to biological benchmarks for 3 alternative forms of the SR models. Observed time series of spawners is the same data as plotted in Figure 2. Box plots show the range of observed values and posterior distributions of benchmark estimates (p10, p25, median, p75, p90). Table 6 defines the benchmarks and Table 8 lists the equations used to calculate them. Figure 8 illustrates the benchmark definitions. The two Ricker model forms have the same general properties, but the Ricker AR1 form corrects for observed patterns in residuals. The Beverton-Holt model has approaches a maximum recruitment, rather than the density-dependent reduction in recruitment characteristic for the Ricker models.

9 APPENDIX A: SURVEY OF CHINOOK COUNTING WEIRS

This Appendix has three parts. Table A 1 to Table A 3 summarize the results of an informal e-mail survey of Chinook stock assessment experts conducted between November 2015 and March 2016. All contributors are identified in the tables. Table A 4 summarizes weir-related information in stock assessment reports published by DFO and ADFG. Table A 5 summarizes weir-related information from the most recent annual CTC report on catch and escapement data.

The intent of this survey was to follow up on anecdotal evidence mentioned during the CSAS review (DFO 2016a) and start the process of documenting lessons learned related to the role of counting weirs in Chinook stock assessment. Note that this is not a formal peer-reviewed synthesis of counting weir operations (e.g. differences in fish handling procedures, site characteristics), but such a synthesis would be very useful and we include it in our recommendations (Section 5.3).

Table A 1: Overview of Chinook weirs – Transboundary Rivers.

Major River	System	Weir Characteristics					Co-migrating Species	Weir Effects	Source pers. comm.
		Active Years	Distinct Pop'n	Dist. from Ocean	Dist. to Spn. Gr.				
Stikine	Little Tahltan	1985 to Current	Inconclusive		<1km	None	UNKNOWN. Potential shift in spawning distribution and increased bear predation, but no direct evidence. Indirect clues include 1. recent disconnect between weir counts and MR survey in the lower Stikine, 2. unexpected age composition estimates.	Sections 2.1.1.1 and 2.1.2	
Taku	Nahlin River		Yes			Sockeye	YES. Weir removed due to fish refusing to pass the weir and fish spawning below the weir, where spawning had not been observed before (poor habitat).	Phil Richards ADFG, Douglas, Alaska	
Alsek	Klukshu weir	1976 to Current	Yes	190km	5km	Sockeye	MINOR. Chinook do not appear to be held up significantly by weir. Minor delays may result from weir not being open overnight. No observed effect on spawning distribution.	Bill Waugh, DFO, Whitehorse, Yukon	

Table A 2: Overview of Chinook weirs – Northern BC.

Major River	System	Active Years	Weir Effects	Source pers. comm.
Skeena	Kitwanga River		YES. Fence calibration projects (same methods & people as before fence) produced unreliable expansion factors. The fence did hold back Chinook and continues to do so. They spawn in the riffles below the fence. Local Fishery Officer noted that they never used to spawn there.	Winther (2008)
Skeena	Babine		YES. Chinook pass the fence but it does hold them up. Unknown whether there are any effects on spawning distribution	Ivan Winther, DFO, Prince Rupert, BC
Nass - Coastal	Kincolith River	1995, 1996, 2001, 2002 & 2005 to 2007	YES. No observed effect on spawning distribution, but may have affected migration time, and possibly increased harvest due to delayed migration. (Notes: weir well below spawning sites. Some handling occurred, tidal influence, two passage areas in some years).	Richard Alexander LGL, Vancouver, Alexander and Stewart (2008)
Nass - Middle	Seaskinnish Creek	2007, 2008 & 2010	YES. No observed effect on spawning distribution detected in three years of study; but some passage delays were noted and thought to be predator (otter/bear) associated. (Notes: no handling; all video recorded; one passage chamber)	Richard Alexander LGL, Vancouver, BC
Nass – Upper	Kwinageese River	2002, 2005, 2006, 2009 to Current	NO. Have checked with radio telemetry and carcass vs. weir comparisons, and showed no effect. Also similar prop of total Upper Nass CU in years with or without weir (Notes: weir well below spawning sites, no handling at weir, all video; one passage chamber; 2007/2008 slide).	Richard Alexander LGL, Vancouver, BC

Table A 3: Overview of Chinook weirs – Fraser River and Vancouver Island.

Area	System	Active Years	Weir Effects	Source pers. comm.
Fraser	Eagle River		YES. Redistribution of spawners to locations downstream of the Eagle River fence. Once fence operations were discontinued in the late 90's, Chinook returned to their previous spawning distribution (i.e. fence does not go for Coho until after Chinook have passed)	Richard Bailey, DFO, Kamloops, BC
Fraser	Bowron River		YES. Weirs discontinued due to observed downstream redistributions and refusal to pass. The likely issue is the falling hydrograph and the lack of freshet to stimulate passage.	Richard Bailey, DFO, Kamloops, BC
Fraser	Chilako River	Up to 2000		
Fraser	Kuzkwa River			
Fraser	Stellako River			
Fraser	Salmon River (near Prince George)	Up to 1998		
Fraser	Salmon River (at Salmon Arm)	Active	YES. Often have passage issues although there is virtually no good quality spawning habitat between the fence and Shuswap Lake. Only remaining fence where Chinook enumeration happens in the Fraser (mainly for brood stock).	Richard Bailey, DFO, Kamloops, BC
Van Isl.	Mesachie		NO. None Observed.	Steve Baillie, DFO, Nanaimo, BC
Van Isl.	Lachmach		NO. None Observed.	Steve Baillie, DFO, Nanaimo, BC
Van Isl.	Black		NO. None Observed.	Steve Baillie, DFO, Nanaimo, BC
Van Isl.	Colquitz		NO. None Observed.	Steve Baillie, DFO, Nanaimo, BC
Van Isl.	Heydon		NO. None Observed.	Steve Baillie, DFO, Nanaimo
Van Isl.	Myrtle		NO. None Observed.	Steve Baillie, DFO, Nanaimo
Van Isl.	Sakinaw		NO. None Observed.	Steve Baillie, DFO, Nanaimo, BC
Van Isl.	Cowichan	1988 to Current	YES. No effects on spawning distribution observed, because weir is located in the lower mainstem. However, have modified weir site and design over time to reduce Chinook holding below weir and passing at night.	Steve Baillie, DFO, Nanaimo; Gayle Brown, DFO, Nanaimo, BC

Table A 4: Overview of Chinook weir commentary in reports published by DFO and ADFG. This overview is based on searching online report inventories for “Chinook”, then searching the reports for any occurrence of “weir” or “fence”.

Region	Stocks/CUs	Weir comments	Report Reference
Stikine	Total Stikine, expanded from Little Tahltan weir counts	Found that age composition estimates from carcass surveys (1981-1988) were similar to weir samples (1985-1988). Recommended continuation of the weir as part of the Stikine stock assessment program, which also included mark-recapture. Found high correlation between Little Tahltan weir counts and Beatty Creek aerial-based index, but poor correlation with Tahltan River aerial-based index (frequent poor water clarity due to glacial source). Considered weir counts as sufficient quality as basis for Stikine-wide spawning goal estimate. Recommended that both the weir and the MR program in the lower river should continue. No comment regarding weir effects on Chinook spawning.	Bernard et al. (1999) DFO, Also ADFG FMS 00-01
Various	Many stocks throughout BC and Alaska	Their Appendix A summarizes the quality of escapement estimates for many Chinook stocks. Weir counts used in both Alaska and BC: Andrew Creek (expand visual estimates based on 4 yrs of weir counts used to develop an expansion factors for visual survey, and resulting estimates were classified as very good). King Salmon River (10yrs of weir counts, excellent quality), Klukshu River (16 years of weir counts, rated as excellent), Stikine River (18yrs of Little Tahltan weir counts expanded based on MR estimates, rated as excellent) , Nelson River (13 yrs of weir counts, but focused on sockeye timing, so rated as poor quality), Situk River (excellent quality estimates based on weir counts), Kincolith (NC) weir counts used to calibrate visual surveys on Ishkeenickh River. Cowichan (5 years with weir counts, 4 yrs with partial fence counts, and 1 year with MR used to expand visual estimates, rated as fair quality). No comment on weir effects.	Parken et al. (2006) DFO
Southern BC	35 Cons. Units	Southern BC Chinook have gone through an intensive process of data review in preparation for a COSEWIC assessment and status assessment under Canada's <i>Wild Salmon Policy</i> . Spawner time series for each CU were developed through a detailed assessment of available observations (various sites, years), which included a data quality filtering step and in-filling of site estimates. Concerns of quality of weir counts or weir effects on spawning behaviour are not explicitly documented in the resulting reports, but may have been indirectly address in the initial quality filtering of records for the BC interior CUs where weirs have been almost entirely discontinued (see Table A 3)	Brown et al. ³
Fraser River	61 stocks (spawning streams, tributaries)	Mention that 2 fences were active at the time (Dome Creek – Upper Fraser, Salmon River in Salmon Arm) and 2 fences had been discontinued (Chilako, Salmon River – Upper Fraser), but do not discuss the reason for discontinuing or any observed weir effects. Salmon River at Salmon Arm was classified as a high-quality fence count. (see Table A 3)	English et al. (2007) DFO
Strait of	Cowichan	Describe how weir counts are used as part of a comprehensive assessment program that	Tompkins et al.

Region	Stocks/CUs	Weir comments	Report Reference
Georgia	River	also includes swim surveys, aerial surveys, and mark-recapture estimates. Their Appendix 2 includes detailed commentary for each annual estimate from the different surveys, and a clearly documented rationale for constructing a best available spawner time series. No comments regarding weir effects. The main sources of uncertainty they identify are flooding and expansion factors to account for migration after the weir is removed.	(2005) DFO
Strait of Juan de Fuca	San Juan River	Fence and snorkel assessment classified as highly reliable for 2001 (4 out of 5). No mention of effects on Ck spawning.	Riddell et al. (2002) DFO
Skeena	Kitsumkalum River Summers	Uses Babine fence counts. No mention of weir effects.	McNicol (1999) DFO
Taku	Nahlin, Kowatua, Tatsamenie	Used a combination of carcass surveys, carcass weirs, and live weirs to estimate age-sex composition of spawners (1989, 1990, 1995-1997), and confirmed representativeness of samples with mark-recapture experiments. No mention of weir effects. 2010 update uses same combination of data and also does not mention any weir effects.	McPherson et al. (1999). DFO. Also ADFG FMS 00-02. McPherson et al. (2010) ADFG
Alsek	Klukshu	Considered Klukshu weir counts as a full census leading to a very precise estimate of total Chinook run into the Klukshu River system (their p. 34, 42) and focused SR analysis on Klukshu rather than total Alsek expansion, based on reviewers' feedback on earlier draft (their p28). Used Klukshu weir counts for 1988-1992 to argue that SEAK troll was not a major source of mortality, as had been previously assumed (their p. 28). Considered Klukshu weir as the primary management tool for Alsek River Chinook for the long-term.	McPherson et al. (1998) ADFG
Alsek	Klukshu	Update of McPherson et al. (1998). Age composition at weir and in Cdn. Sport fishery similar in years with both samples, but commercial catch was consistently younger, and carcass samples were biased older. For SR fits, used Klukshu weir counts expanded to total Alsek based on mark-recapture surveys. No mention of weir effects.	Bernard and Jones (2010) ADFG.
Upper Cook Inlet	Various	For Chinook, have Deshka River weir since 1995 and Crooked Creek weir since 1976. Little Susitna River weir operated in 4 years to get expansion factor for aerial counts. No mention of weir effects. 2010 paper includes a general statement, not specific to Chinook: <i>"Weir data tends to be the most reliable assessment tool, providing a count of the total number of fish in the escapement. Depending on its location, mark-recapture and sonar projects typically provide the next most reliable abundance estimates."</i>	Fair et al. (2007), Fair et al. (2010) ADFG
Lower Cook Inlet, Bristol Bay	Anchor River	Anchor River assessed with sonar and floating weir since 2003, Ninilchik River with weir during part of run, but still considered more reliable index than aerial surveys. Both used as basis for spawning goal recommendation. For Anchor River, used 31 yrs of aerial surveys and 5 yrs of weir/sonar estimates. No mention of weir effects.	Otis et al. (2010), Otis et al. (2013), ADFG

Region	Stocks/CUs	Weir comments	Report Reference
Bristol Bay	Anchor River, Ninilchik River	Anchor River assessed with sonar and floating weir since 2003, Ninilchik River with weir during part of run. Both used as basis for spawning goal recommendation. No mention of weir effects.	Otis and Szarzi (2007). Szarzi et al. (2007). ADFG
Bristol Bay	Naknek River	Big Creek weir. Data sufficient to track status against SEG. No mention of weir effects.	Baker et al. (2009) ADFG
Bristol Bay	Naknek River	Combination of Big Creek weir and aerial survey classified as fair quality data. No mention of weir effects.	Fair et al. (2012), Erickson et al. (2015) ADFG
Unuk		Spawning ground weirs (1983, 1988, and 1989) and live weir on Cripple Creek (1986, 1991, and 1992) considered to yield unbiased estimates of age-sex composition. No mention of weir effects.	Hendrich et al. (2008) ADFG
Yakutat	Situk	Small watershed close to coast. Situk weir operated about 20km upstream from 1976-1987, then moved close to estuary. Weir counts of large Chinook (>440 MEF) are considered a census without sampling error, but counts of small fish incomplete and therefore excluded from enumerating total returns. The weir was moved due to timing of in-season information. Counts of Chinook migration overlap with large sockeye population. Their Appendix B1 summarizes weir operations. No mention of weir effects.	McPherson et al. (2005) ADFG
Alaska	All	Their Table 18-21 list all managed systems and identifies the methods used to enumerate spawners and develop spawning goals. In Southeast, 2-3 of 11 systems use goals based on weir counts and SR fits (Klukshu/Alsek, and Situk). <i>Note that separate goals for Klukshu and total Alsek are identified.</i> In Central region, 4 of 30 systems use weirs counts; in two the goals are based on SR fits (Deshka and Anchor Rivers) and for the other 2 based on percentile method (Crooked Creek and Ninilchik River). Of the 25 systems in the Arctic-Yukon-Kuskokwim region, 5-6 are enumerated with weirs, and 1 of those (Middle Fork – Goodnews River) has a spawning goal based on SR fits while the other 4-5 are based on the percentile method (Tuluksak River weir not listed after 2012 report). In the Westward region, all 4 systems are enumerated with weir counts and have goals based on SR fits. In 2011, recommended switch from aerial to weir-based percentile goal for 2 systems (East Fork Andreafsky River, Gisasa River). No mention of weir effects.	Munro and Volk (2011, 2012, 2013, 2014, 2015) ADFG
Kuskokwim	Various tributaries	6 tributaries with weir counts. Use weir counts for Kwethluk, George, and Kogrukluks Rivers to get spawning goals as a proportion of the drainage-wide goal, which is based on the percentile method. Kogrukluks River has longest time series, with weir counts back to 1976. No mention of weir effects.	Hamazaki et al. (2012) ADFG
Kenai	Various	Tributary weirs on Funny, Russian, and Killey rivers, and Slikok Creek. Their pg. 4 has a description of weir operations (location, setup, co-migrating sockeye). No mention of weir	McKinley and Fleishman (2013)

Region	Stocks/CUs	Weir comments	Report Reference
		effects.	
Southeast Alaska	Various	Enumeration for Stikine (Little Tahltan), Klukshu/Alesek, and Situk Rivers based on weir counts or weir expansions, and biological spawning goals have been developed for all 3 systems. Note that Stikine enumeration also includes a MR program. King River, Andrew Creek, estimates based on weir expansion. No mention of weir effects.	Heinl et al. (2014) ADFG

Table A 5: Overview of Chinook weir commentary in the CTC Annual Report (PSC 2015).

Region	Stocks/CUs	Weir comments
Trans-boundary Rivers	Stikine	No explicit comment on quality of Little Tahltan weir data or weir effects, but states that total Stikine Chinook “escapement assessments have met US CTC data standards since 1996”, which is when the lower-river MR program started, and reference a highly stable weir/MR ratio of 17%-20% from Pahlke and Etherton (1999) without commenting on the recent disconnect between the 2 time series (e.g. Panel A in Figure 6).
SEAK	Situk River	Assessments based solely on weir counts. “ADFG assessments of the Situk River escapements of Chinook salmon meet US and Bilateral CTC data standards and have continuously done so since 1976.” No mention of weir effects.
Trans-boundary Rivers	Alesek River	Klukshu weir since 1976, and expansion factor for weir counts based on MR program from 1998 to 2004 (Total Alesek escapement = 4* Klukshu count). “The Alesek Chinook salmon escapement assessments meet US CTC data standards; however, they fail to meet Bilateral CTC data standards due to the CVs ranging from 24% to 61%.” No explicit comment on quality of weir data or weir effects.
NBC	Nass	Kwinageese River weir is part of the Nass River assessment program, which also includes MR in the lower Nass, the Meziadin River fishway, and deadpitch surveys (e.g. Damdochax). Kincolith fence counts in 2001, 2002, 2005, and 2007. No comment on quality of weir data or weir effects.
NBC	Skeena	40 surveys, mostly visual observations (aerial or stream walk). Weirs on Babine, Sustut, and Kitwanga Rivers. No comment on quality of weir data or weir effects.
Lower Strait of Georgia	Cowichan	Weir counts since 1988 and carcass MR program from 1995 to 2004. High level of enhancement. Reference Tompkins et al. (2005), which is summarized in Table A 4 above. No comment on quality of weir data or weir effects.

10 APPENDIX B: ABUNDANCE DATA

Table B 1: Spawner abundance for Little Tahltan River Chinook Salmon 1985-2014. Descriptions in Section 2.1.1.1. 2014 excluded from analyses because of rock slide. The base case time series for subsequent analyses is marked with yellow shading and bold font. Annual age composition estimates listed in Table B 2, and size distribution by age class listed in Table B.3.

Year	Weir Counts and visual size classification				Based on age classes				Based on size samples		Based on size sample by age class	
	Large	Jack	% Jack	Total	Prop Not M3+	Count -M3+	Prop not 5.2 or 6.2	Count 5.2&6.2	% Small*	Count Large	Prop Jack	Count - Adj Age
1985	3,114	316	9.2%	3,430	4.1%	3,289	6.6%	3,204	-	-	3.8%	3,301
1986	2,891	572	16.5%	3,463	0.3%	3,453	4.3%	3,314	-	-	1.3%	3,419
1987	4,783	365	7.1%	5,148	5.3%	4,875	13.1%	4,474	-	-	4.9%	4,895
1988	7,292	327	4.3%	7,619	2.0%	7,467	4.0%	7,314	-	-	1.8%	7,478
1989	4,715	199	4.0%	4,914	2.0%	4,816	22.0%	3,833	-	-	2.6%	4,785
1990	4,392	417	8.7%	4,809	9.0%	4,376	14.0%	4,136	-	-	7.4%	4,456
1991	4,506	313	6.5%	4,819	6.0%	4,530	10.0%	4,337	-	-	5.7%	4,544
1992	6,627	131	1.9%	6,758	1.3%	6,670	1.6%	6,650	-	-	1.6%	6,649
1993	11,449	60	0.5%	11,509	0.3%	11,474	3.6%	11,095	-	-	0.6%	11,443
1994	6,387	121	1.9%	6,508	2.0%	6,378	12.0%	5,727	-	-	1.9%	6,384
1995	3,072	135	4.2%	3,207	18.5%	2,614	28.9%	2,280	-	-	14.2%	2,751
1996	4,821	22	0.5%	4,843	6.9%	4,509	7.3%	4,489	-	-	7.3%	4,487
1997	5,557	54	1.0%	5,611	3.7%	5,403	6.8%	5,229	-	-	3.5%	5,417
1998	4,879	37	0.8%	4,916	3.2%	4,759	6.3%	4,606	-	-	3.3%	4,756
1999	4,738	202	4.1%	4,940	15.6%	4,169	18.5%	4,026	-	-	13.3%	4,283
2000	6,640	108	1.6%	6,748	15.6%	5,695	17.9%	5,540	13.16%	5,860	12.9%	5,878
2001	9,738	269	2.7%	10,007	1.2%	9,887	2.6%	9,747	3.26%	9,681	3.5%	9,661
2002	7,490	618	7.6%	8,108	10.8%	7,232	11.4%	7,184	13.18%	7,039	9.2%	7,361
2003	6,492	334	4.9%	6,826	27.4%	4,956	28.2%	4,901	17.10%	5,659	22.2%	5,309
2004	16,381	250	1.5%	16,631	18.5%	13,554	19.3%	13,421	14.93%	14,148	15.9%	13,991
2005	7,387	231	3.0%	7,618	4.8%	7,252	6.1%	7,153	6.31%	7,137	5.6%	7,188

Year	Weir Counts and visual size classification				Based on age classes				Based on size samples	Based on size sample by age class		
	Large	Jack	% Jack	Total	Prop Not M3+	Count -M3+	Prop not 5.2 or 6.2	Count 5.2&6.2	% Small*	Count Large	Prop Jack	Count - Adj Age
2006	3,860	93	2.4%	3,953	5.1%	3,751	5.8%	3,724	7.16%	3,670	4.4%	3,780
2007	562	12	2.1%	574	4.8%	546	9.4%	520	18.25%	469	5.6%	542
2008	2,663	139	5.0%	2,802	4.3%	2,682	4.5%	2,676	5.63%	2,644	4.7%	2,670
2009	2,245	99	4.2%	2,344	8.9%	2,135	12.3%	2,056	9.51%	2,121	8.3%	2,149
2010	1,057	221	17.3%	1,278	12.8%	1,114	13.6%	1,104	19.88%	1,024	11.8%	1,128
2011	1,753	194	10.0%	1,947	20.1%	1,556	24.1%	1,478	22.26%	1,514	16.3%	1,629
2012	720	51	6.6%	771	1.7%	758	3.9%	741	5.23%	731	3.1%	747
2013	878	183	17.2%	1,061	20.5%	843	25.6%	789	29.44%	749	17.2%	879
*2014	169	40	19.1%	209	80.5%	41	81.5%	39	-	-	24.5%	158

Table B 2: Age distribution of Chinook Salmon sampled at Little Tahltan weir 2000-2014. Descriptions in Section 2.1.1.1.

EU GR	Age Classes													Total	% Not M3+	% Not 5.2 or 6.2
	1.1 3.2	0.3 4.1	1.2 4.2	2.1 4.3	0.4 5.1	1.3 5.2	2.2 5.3	1.4 6.2	2.3 6.3	1.5 7.2	2.4 7.3	1.6 8.2	2.5 8.3			
1985	2.1	0.0	1.5	0.0	0.0	15.4	0.5	80.0	0.0	2.0	0.5	0.0	0.0	102.0	4.1	6.6
1986	0.0	0.3	0.3	0.0	1.4	31.9	0.0	63.5	0.6	1.7	0.0	0.0	0.0	99.7	0.3	4.3
1987	1.2	0.8	4.1	0.0	2.1	17.8	0.0	68.3	0.0	4.8	0.1	0.0	0.0	99.2	5.3	13.1
1988	0.0	0.0	2.0	0.0	0.0	9.0	0.0	87.0	0.0	2.0	0.0	0.0	0.0	100.0	2.0	4.0
1989	0.0	0.0	2.0	0.0	0.0	35.0	0.0	43.0	0.0	19.0	1.0	0.0	0.0	100.0	2.0	22.0
1990	1.0	0.0	8.0	0.0	0.0	7.0	0.0	79.0	0.0	5.0	0.0	0.0	0.0	100.0	9.0	14.0
1991	0.0	0.0	6.0	0.0	0.0	36.0	0.0	53.0	0.0	3.0	1.0	0.0	0.0	99.0	6.0	10.0
1992	0.0	0.0	1.2	0.0	0.0	21.1	0.1	77.2	0.0	0.2	0.1	0.0	0.0	99.9	1.3	1.6
1993	0.0	0.0	0.3	0.0	0.0	8.9	0.0	87.5	0.5	2.6	0.2	0.0	0.0	100.0	0.3	3.6
1994	0.0	0.0	2.0	0.0	0.0	11.0	0.0	76.0	0.0	8.0	2.0	0.0	0.0	99.0	2.0	12.0
1995	0.4	0.0	17.3	0.3	0.0	19.6	0.5	51.6	0.2	9.0	0.8	0.2	0.2	100.1	18.5	28.9
1996	0.3	0.0	6.5	0.0	0.0	66.8	0.1	25.8	0.0	0.4	0.0	0.0	0.0	99.9	6.9	7.3
1997	0.5	0.0	2.9	0.0	0.0	20.7	0.3	72.5	1.4	0.6	1.1	0.0	0.0	100.0	3.7	6.8
1998	0.2	0.0	3.0	0.0	0.1	22.9	0.0	70.9	0.5	2.5	0.0	0.0	0.0	100.1	3.2	6.3
1999	2.6	0.0	12.6	0.2	0.0	34.3	0.2	47.4	0.3	2.4	0.2	0.0	0.0	100.2	15.6	18.5
2000	0.2	0.0	15.2	0.0	0.0	35.0	0.2	47.1	0.1	1.8	0.4	0.0	0.0	100.0	15.6	17.9
2001	0.3	0.0	0.9	0.0	0.0	77.4	0.0	20.0	1.1	0.3	0.0	0.0	0.0	100.0	1.2	2.6
2002	1.9	0.0	8.9	0.0	0.0	15.7	0.0	72.8	0.2	0.0	0.4	0.0	0.0	99.9	10.8	11.4
2003	1.9	0.0	24.6	0.4	0.0	49.8	0.5	22.1	0.4	0.1	0.3	0.0	0.0	100.1	27.4	28.2
2004	0.8	0.0	17.6	0.0	0.0	51.8	0.1	29.0	0.7	0.1	0.0	0.0	0.0	100.1	18.5	19.3
2005	0.1	0.0	4.6	0.0	0.0	63.4	0.1	30.4	1.1	0.1	0.1	0.0	0.0	99.9	4.8	6.1
2006	0.4	0.0	4.7	0.0	0.0	11.4	0.0	82.8	0.0	0.4	0.3	0.0	0.0	100.0	5.1	5.8
2007	0.0	0.0	4.8	0.0	0.0	62.7	0.0	27.9	0.0	4.6	0.0	0.0	0.0	100.0	4.8	9.4
2008	1.0	0.0	3.3	0.0	0.0	37.7	0.0	57.7	0.2	0.0	0.0	0.0	0.0	99.9	4.3	4.5
2009	0.0	0.0	8.9	0.0	0.0	47.3	0.0	40.3	0.9	2.5	0.0	0.0	0.0	99.9	8.9	12.3
2010	1.4	0.0	11.4	0.0	0.0	52.1	0.0	34.3	0.8	0.0	0.0	0.0	0.0	100.0	12.8	13.6
2011	0.0	0.0	19.3	0.0	0.0	46.8	0.8	29.2	2.8	1.2	0.0	0.0	0.0	100.1	20.1	24.1
2012	0.0	0.0	1.7	0.0	0.0	56.7	0.0	39.4	1.3	0.3	0.6	0.0	0.0	100.0	1.7	3.9

	Age Classes														Total	% Not M3+	% Not 5.2 or 6.2
	EU	1.1	0.3	1.2	2.1	0.4	1.3	2.2	1.4	2.3	1.5	2.4	1.6	2.5			
GR	3.2	4.1	4.2	4.3	5.1	5.2	5.3	6.2	6.3	7.2	7.3	8.2	8.3				
2013	0.2	0.0	20.3	0.0	0.0	48.4	0.0	26.0	0.3	3.5	1.3	0.0	0.0	100.0	20.5	25.6	
2014*	0.0	0.0	32.1	47.4	0.0	0.0	1.0	18.7	1.0	0.0	0.0	0.0	0.0	100.2	80.5	81.5	
Min (excl 2014)	0.0	0.0	0.3	0.0	0.0	7.0	0.0	20.0	0.0	0.0	0.0	0.0	0.0	99.0	0.3	1.6	
Median(excl 2014)	0.2	0.0	4.7	0.0	0.0	35.0	0.0	51.6	0.2	1.8	0.1	0.0	0.0	100.0	5.1	10.0	
Max(excl 2014)	2.6	0.8	24.6	0.4	2.1	77.4	0.8	87.5	2.8	19.0	2.0	0.2	0.2	102.0	27.4	28.9	

Table B 3: Size distribution by age class of Chinook Salmon sampled at Little Tahltan weir 2000-2013. Descriptions in Section 2.1.1.1. % small adults (<660mm FL).

	Age Classes														Sample Sizes														
	EU	1.1	0.3	1.2	2.1	0.4	1.3	2.2	1.4	2.3	1.5	2.4	1.6	2.5	GR	3.2	4.1	4.2	4.3	5.1	5.2	5.3	6.2	6.3	7.2	7.3	8.2	8.3	Large
2000	100	0	73	0	0	3	0	0	0	0	0	0	0	0	706	98													
2001	100	0	88	0	0	2	0	0	0	0	0	0	0	0	559	15													
2002	100	0	94	0	0	9	0	0	0	0	0	0	0	0	648	107													
2003	100	0	62	0	0	1	0	0	0	0	0	0	0	0	694	145													
2004	100	0	76	0	0	2	0	0	0	0	0	0	0	0	548	106													
2005	100	0	77	0	0	4	100	0	0	0	0	0	0	0	748	33													
2006	100	0	89	0	0	0	0	0	0	0	0	0	0	0	171	9													
2007	0	0	100	0	0	4	0	0	0	0	0	0	0	0	67	8													
2008	100	0	83	0	0	5	0	0	0	0	0	0	0	0	253	18													
2009	0	0	78	0	0	4	0	0	100	0	0	0	0	0	99	10													
2010	100	0	90	0	0	1	0	0	100	0	0	0	0	0	138	25													
2011	0	0	100	0	0	2	0	0	0	0	0	0	0	0	279	8													
2012	0	0	100	0	0	2	0	0	0	0	0	0	0	0	279	8													
2013	100	0	91	0	0	13	2	0	0	0	0	0	0	0	158	65													
Range of annual % Small Adults																													
Min	100	0	62	0	0	0	0	0	0	0	0	0	0	0															
Med	100	0	88	0	0	2	0	0	0	0	0	0	0	0															
Max	100	0	100	0	0	13	100	0	100	0	0	0	0	0															
Sample sizes by age class															<u>Total</u>														
N Large	0	0	160	0	0	2,744	289	2,079	35	31	9	0	0		5,347														
N Small	50	0	512	0	0	88	2	1	2	0	0	0	0		655														
Overall % Small Adults																													
Overall	100	0	76	0	0	3	1	0	5	0	0	0	0																

Table B 4: Sample Size for Age and Size Distributions for 1985 to 2013. Descriptions in Section 2.1.1.1.

Year	Count	Sample Size	
		Aged and unaged fish	Aged fish only
1985	3,430	195	195
1986	3,463	288	288
1987	5,148	237	237
1988	7,619	359	359
1989	4,914	340	340
1990	4,809	527	527
1991	4,819	518	518
1992	6,758	666	674
1993	11,509	634	634
1994	6,508	648	648
1995	3,207	524	524
1996	4,843	517	517
1997	5,611	528	528
1998	4,916	598	598
1999	4,940	1,175	681
2000	6,748	1,368	804
2001	10,007	1,413	573
2002	8,108	1,268	755
2003	6,826	1,306	839
2004	16,631	1,396	654
2005	7,618	1,148	781
2006	3,953	359	180
2007	574	149	75
2008	2,802	375	271
2009	2,344	284	108
2010	1,057	674	163
2011	1,753	548	172
2012	771	604	287
2013	1,061	411	223

Table B 5: SR estimates from Bernard et al. (2000). Base case spawner estimates from our Table B 1.

Year	Base Case (Weir Ret Adj)	From Bernard et al. (2000) Tables 2 and 8			
		Little Tahltan Counts		Total Stikine	
		Aerial	Weir	Spn	Rec
1975	-	700	-	7,571	-
1976	-	400	-	5,723	-
1977	-	800	-	11,445	15,223
1978	-	632	-	6,835	7,520
1979	-	1,166	-	12,610	35,107
1980	-	2,137	-	30,573	19,438
1981	-	3,334	-	36,057	29,245

From Bernard et al. (2000) Tables 2 and 8

Year	Base Case (Weir Ret Adj)	Little Tahltan Counts		Total Stikine	
		Aerial	Weir	Spn	Rec
1982	-	2,830	-	40,488	51,568
1983	-	594	-	6,424	20,575
1984	-	1,294	-	13,995	38,284
1985	3,301	1,598	3,114	16,037	20,000
1986	3,419	1,201	2,891	14,889	47,132
1987	4,895	2,706	4,783	24,632	71,951
1988	7,478	3,796	7,292	37,554	39,733
1989	4,785	2,527	4,715	24,282	17,947
1990	4,456	1,755	4,392	22,619	14,659
1991	4,544	1,768	4,506	23,206	54,824
1992	6,649	3,607	6,627	34,129	-
1993	11,443	4,010	11,449	58,962	-
1994	6,384	2,422	6,426	33,094	-
1995	2,751	1,117	3,259	16,784	-
1996	4,487	1,920	4,840	23,886	-
1997	5,417	1,907	5,613	28,185	-
1998	4,756	-	-	-	-
1999	4,283	-	-	-	-
2000	5,878	-	-	-	-
2001	9,661	-	-	-	-
2002	7,361	-	-	-	-
2003	5,309	-	-	-	-
2004	13,991	-	-	-	-
2005	7,188	-	-	-	-
2006	3,780	-	-	-	-
2007	542	-	-	-	-
2008	2,670	-	-	-	-
2009	2,149	-	-	-	-
2010	1,128	-	-	-	-
2011	1,629	-	-	-	-
2012	747	-	-	-	-
2013	879	-	-	-	-

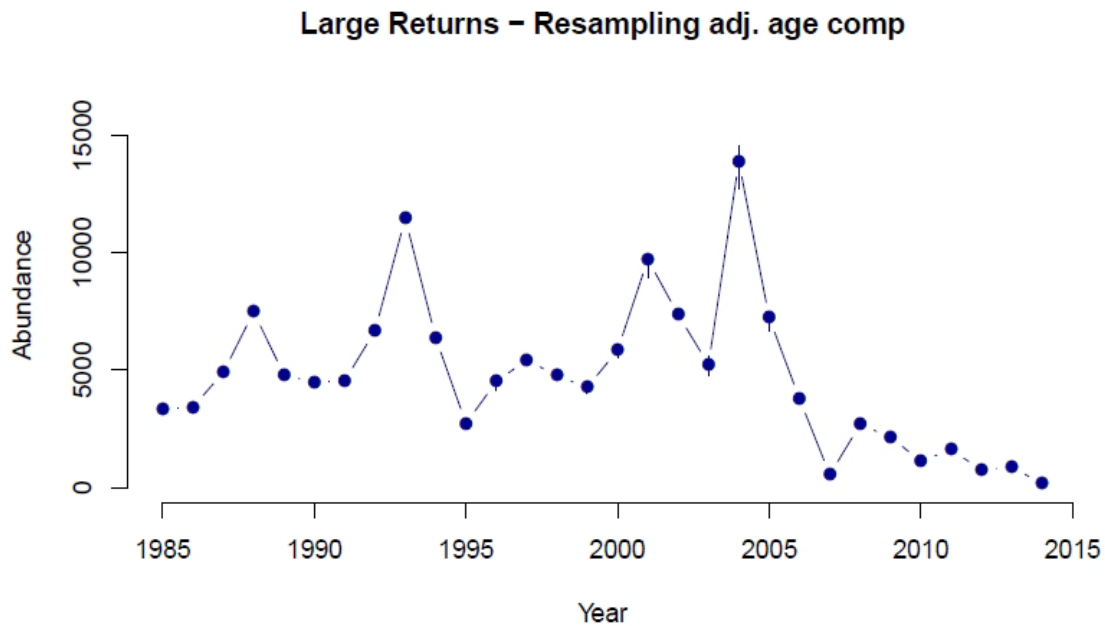
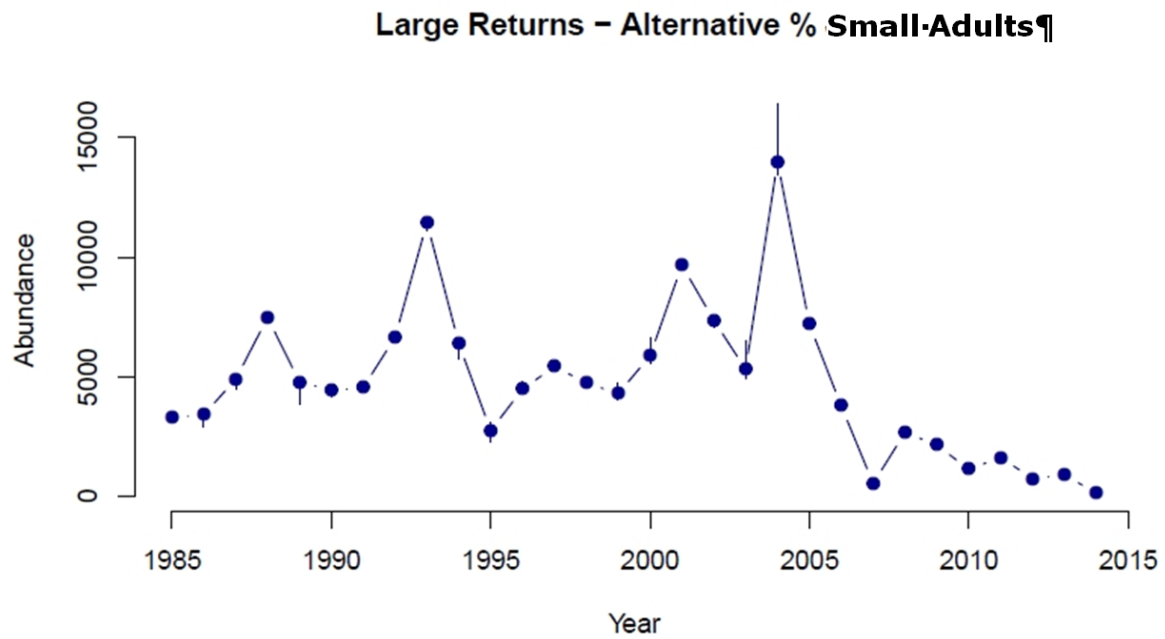


Figure B 1: Alternative spawner time series for large Chinook Salmon. The base case time series for subsequent analyses uses adjusted age classifications to remove small adults, shown as the main line. The top panel shows alternative estimates for % small adults as vertical bars, which in many cases are smaller than the point. The bottom panel shows sensitivity to resampling from annual adjusted age classifications, weighted by annual sample size. The 2014 return year is excluded from subsequent analyses because of the rock slide. The 4 alternative time series and the resampled estimates are very similar to the base case in most years. Figure B 1 shows the % differences.

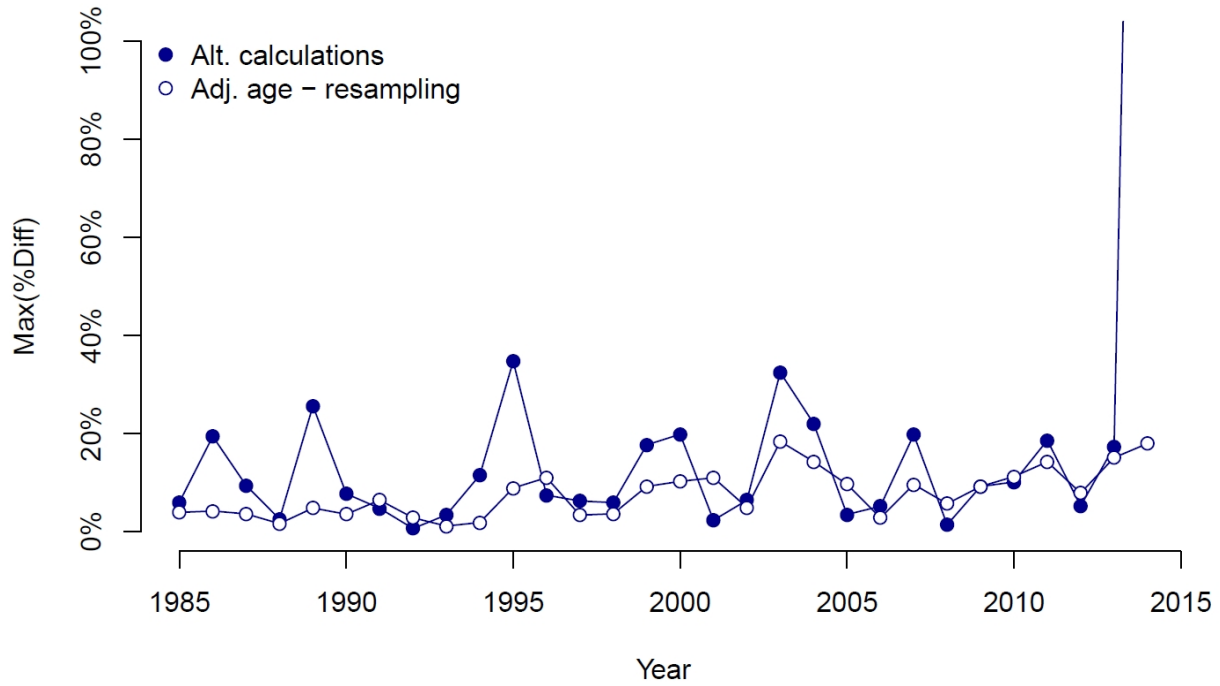


Figure B 2: Differences between alternative spawner time series. The 2014 return year is excluded from subsequent analyses because of the rock slide. The resulting age composition is so unusual that the range of estimates is off the chart (largest estimate is more than triple the smallest estimate, but actual values range from 39 fish to 169 fish, and this range is so small the whiskers in the top panel of Figure B 1 are not visible).

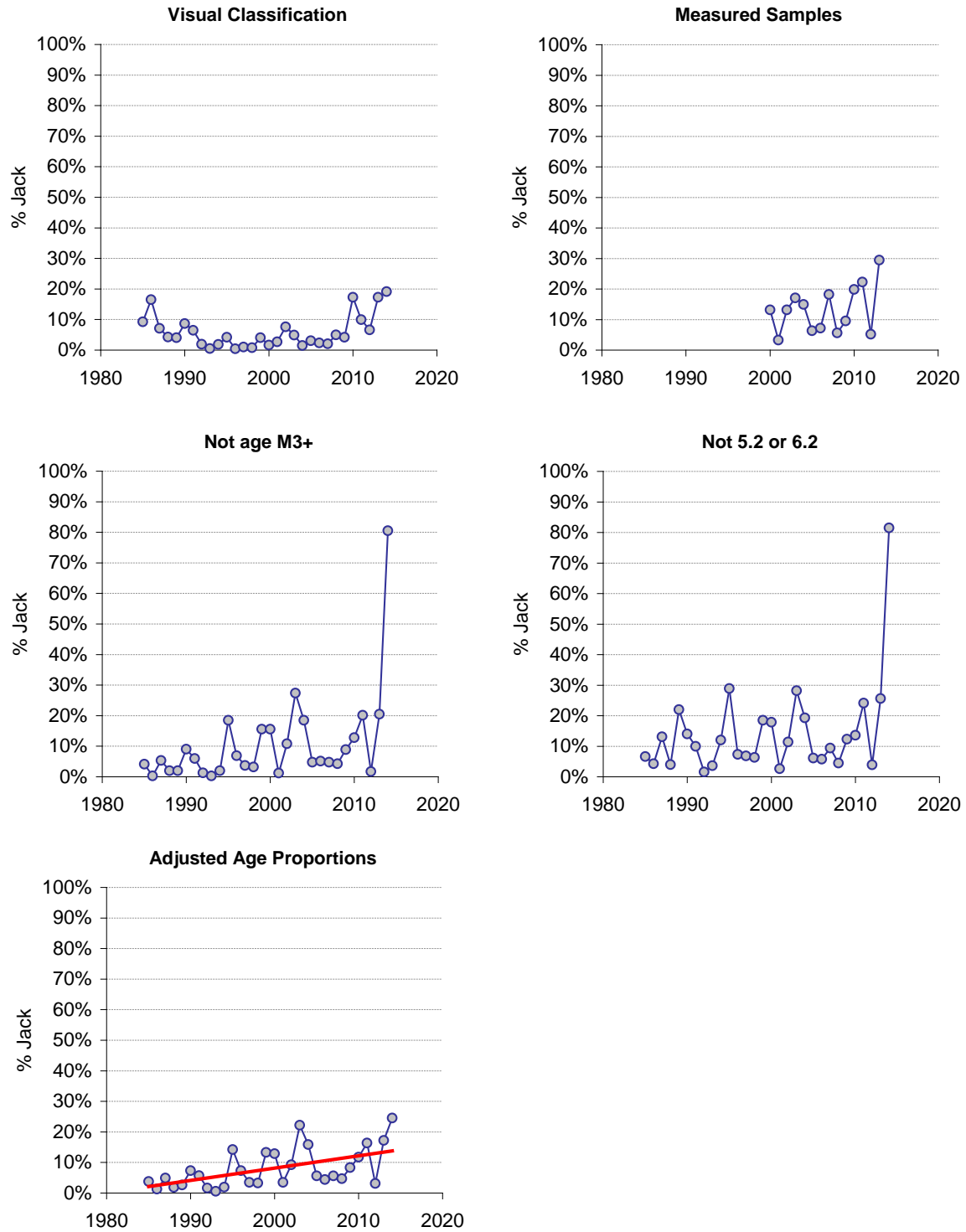
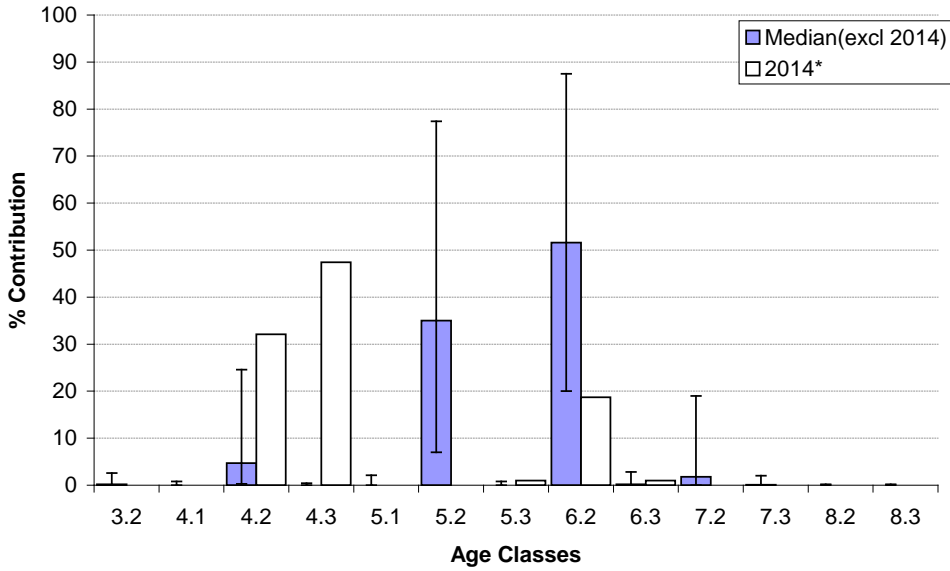


Figure B 3: Pattern in proportion of small adults estimated using 5 alternative approaches.



Patterns in Main Age Classes

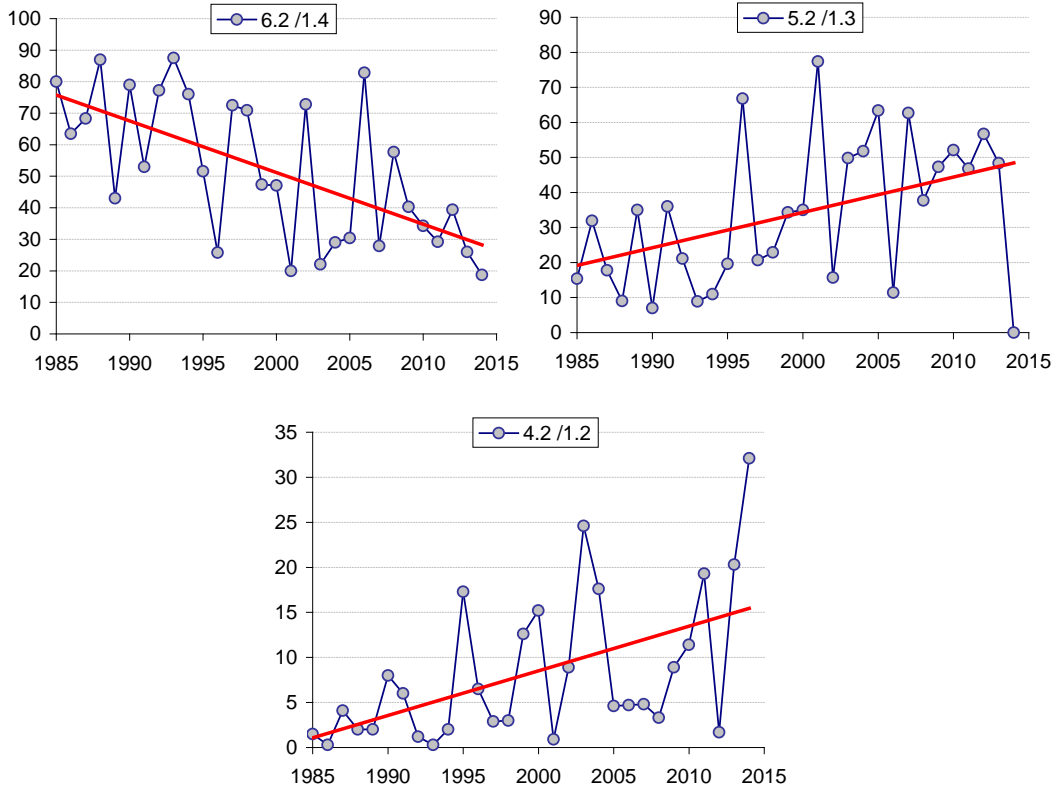


Figure B 4: Chinook age composition at Little Tahltan weir. Median age composition of Chinook Salmon sampled at Little Tahltan weir for 1985 to 2013 compared to observations from 2014 return year affected by the rock slide. Bars show median and observed range. Annual proportions and sample sizes are listed in Table B 2. The smaller panels show changes over time.

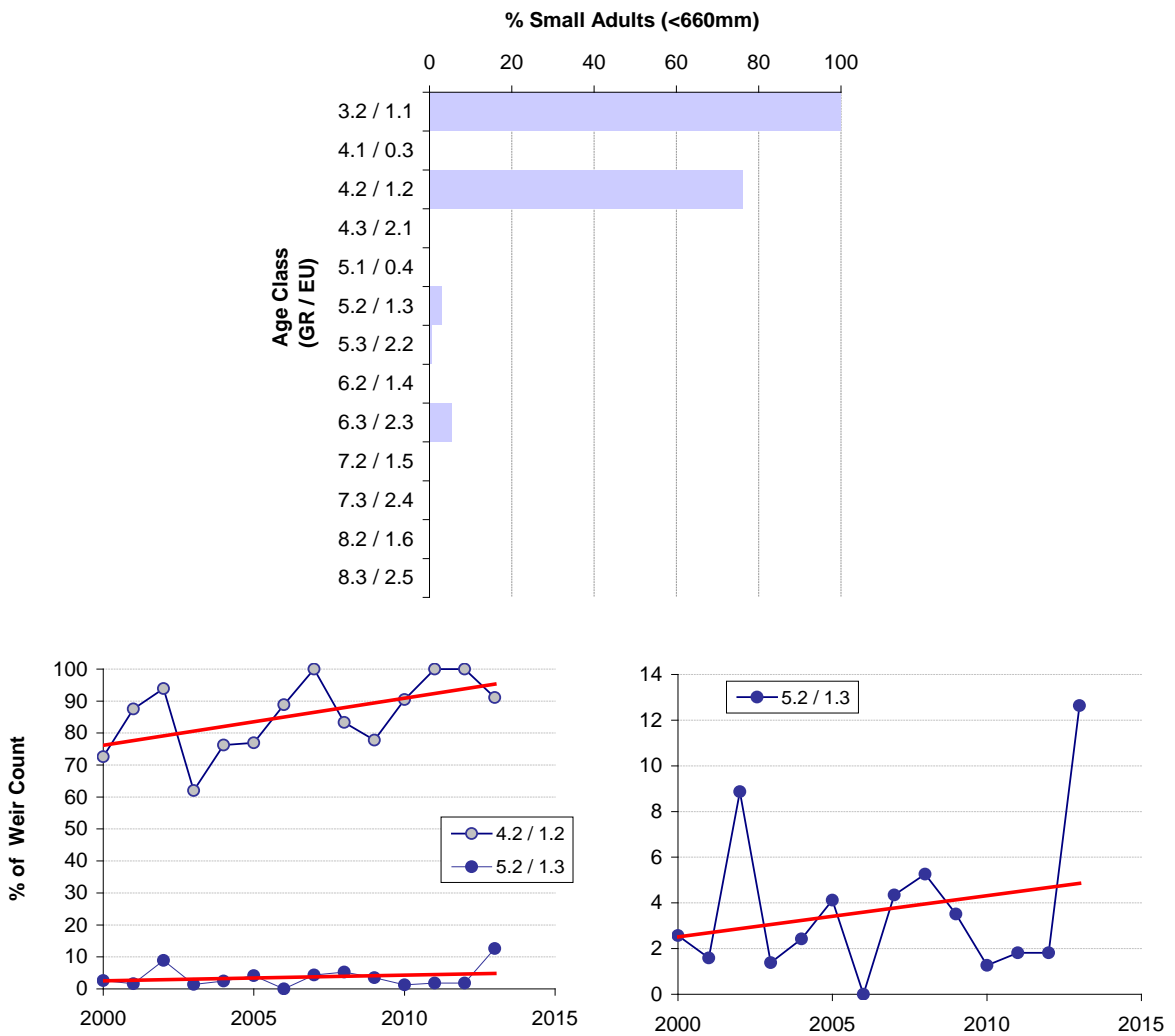


Figure B 5: Size composition by age class sampled at Little Tahltan weir. Overall proportion of small adults (<660mm) in measured samples at Little Tahltan weir from 2000 to 2013. Annual proportions and sample sizes are listed in Table B.3.

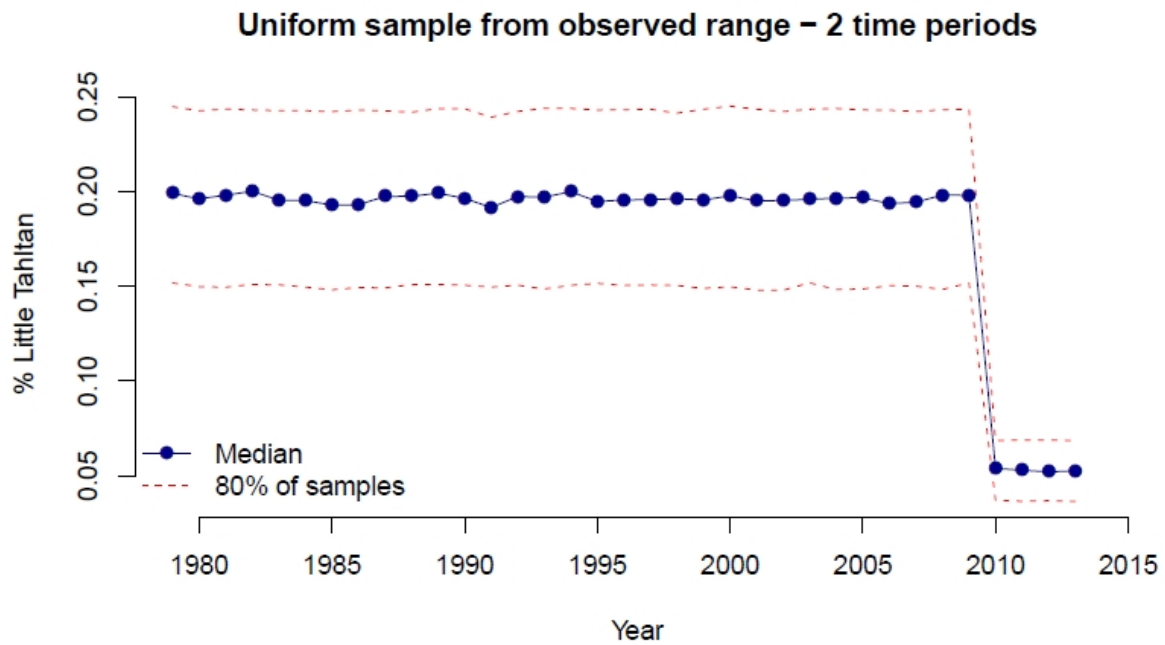
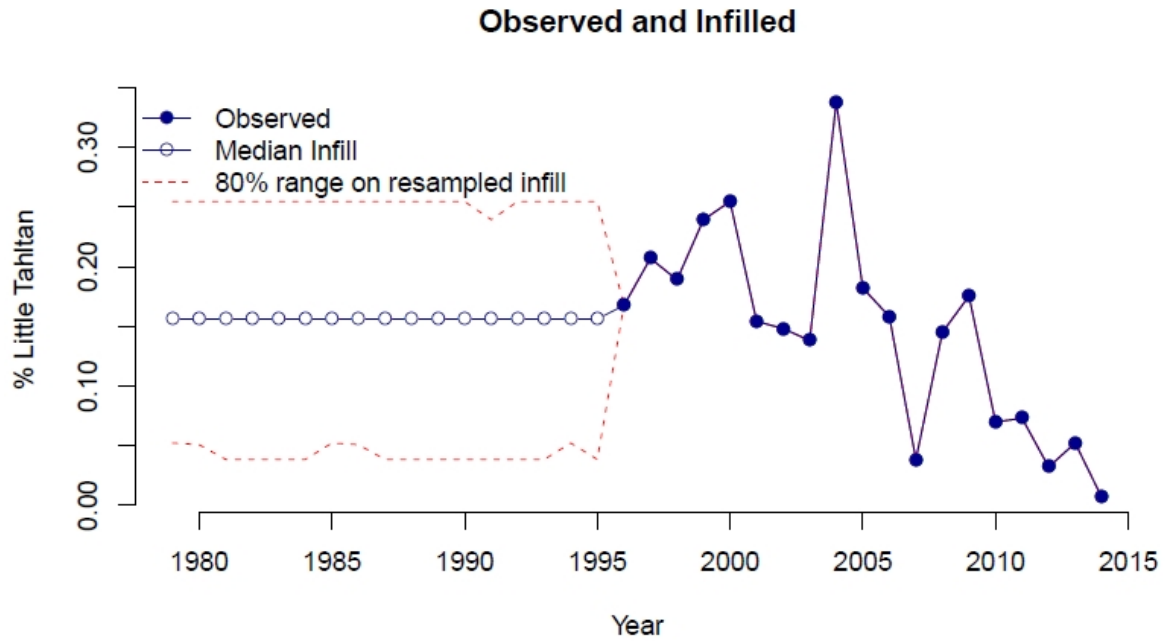


Figure B 6: Proportion of Little Tahltan Chinook in Marine and Lower River Catches.

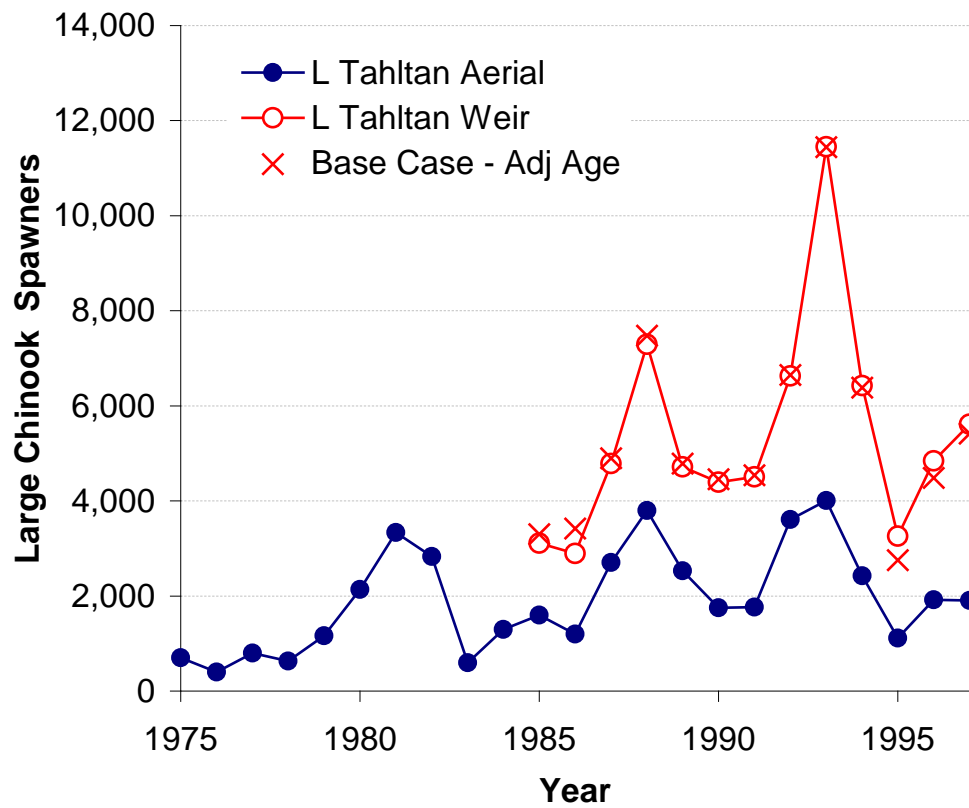


Figure B 7: Comparison of aerial survey estimates and weir-based estimates. Aerial and weir counts from Table 2 in Bernard et al. (2000). Base Case spawner time series from Table B 2. Aerial counts were highly correlation with weir counts, so overflights were discontinued.

11 APPENDIX C: PRODUCTION ESTIMATES

Table C 1: Harvest of large Stikine Chinook in Canadian Fisheries. Sources and assumptions described in Section 2.1.1.5. Figure C 1 shows patterns in total catch and the estimated contribution of Little Tahltan Chinook to the total Stikine catch. Shaded column with bold font marks values used in run reconstruction.

YEAR	Total Stikine Catches				
	Lower River	Upper River			UR Total
	Comm	FSC	Sport	Comm	
1979	775	850	84	0	934
1980	1,488	587	154	156	897
1981	664	586	241	154	981
1982	1,693	618	205	76	899
1983	922	1,066	43	75	1,184
1984	0	702	94	0	796
1985	347	887	104	62	1,053
1986	1,171	1,595	105	145	1,845
1987	1,151	1,366	156	128	1,650
1988	1,208	1,375	231	221	1,827
1989	1,694	1,193	150	71	1,414
1990	2,249	892	146	68	1,106
1991	959	1,063	146	149	1,358
1992	962	1,042	205	75	1,322
1993	994	1,071	438	46	1,555
1994	1,174	889	247	77	1,213
1995	1,666	814	121	26	961
1996	1,929	878	184	85	1,147
1997	3,469	1,249	213	51	1,513
1998	1,942	633	187	12	832
1999	2,916	1,228	188	36	1,452
2000	2,210	1,495	256	9	1,760
2001	885	709	202	0	911
2002	642	1,293	466	5	1,764
2003	1,367	1,055	213	31	1,299
2004	4,551	1,922	109	1	2,032
2005	20,251	894	118	29	1,041
2006	17,053	737	40	23	800
2007	11,600	597	0	35	632
2008	7,959	919	46	49	1,014
2009	2,085	632	20	37	689
2010	1,907	744	50	64	858
2011	2,997	733	76	16	825
2012	5,097	683	64	6	753
2013	1,901	1,317	50	8	1,375
2014	1,407	1,123	50	0	1,173

Table C 2: Harvest of large Stikine Chinook in US Troll Fisheries. Sources and assumptions described in Section 2.1.1.6. Italics mark infilled values. Figure C 2 shows patterns in total catch and the estimated contribution of Little Tahltan Chinook to the total Stikine-bound catch. Shaded column with bold font marks values used in run reconstruction.

EU/GR YEAR	CWT-based Estimates				GSI-based Estimates				
	1.3/5.2 Catch	SE	1.4/6.2 Catch	SE	Total Catch	SE	Total Catch	10p	90p
1981	1,371	-	1,419	-	2,790	-	-	-	-
1982	1,371	-	1,419	-	2,790	-	-	-	-
1983	1,371	-	1,419	-	2,790	-	-	-	-
1984	1,371	-	1,419	-	2,790	-	-	-	-
1985	1,371	-	1,419	-	2,790	-	-	-	-
1986	1,371	-	1,419	-	2,790	-	-	-	-
1987	1,371	-	1,419	-	2,790	-	-	-	-
1988	1,371	-	1,419	-	2,790	-	-	-	-
1989	1,371	-	1,419	-	2,790	-	-	-	-
1990	1,371	-	1,419	-	2,790	-	-	-	-
1991	1,371	-	1,419	-	2,790	-	-	-	-
1992	1,371	-	1,419	-	2,790	-	-	-	-
1993	1,371	-	1,419	-	2,790	-	-	-	-
1994	1,371	-	1,419	-	2,790	-	-	-	-
1995	1,371	-	1,419	-	2,790	-	-	-	-
1996	1,371	-	1,419	-	2,790	-	-	-	-
1997	1,371	-	1,419	-	2,790	-	-	-	-
1998	1,371	-	1,419	-	2,790	-	-	-	-
1999	1,371	-	1,419	-	2,790	-	-	-	-
2000	1,371	-	1,419	-	2,790	-	-	-	-
2001	1,371	-	1,419	-	2,790	-	-	-	-
2002	1,371	-	1,419	-	2,790	-	-	-	-
2003	9,232	4,906	1,419	-	10,651	-	-	-	-
2004	2,488	2,252	5,590	2,140	8,078	4,392	8,202	5,842	11,144
2005	8,228	2,054	5,662	4,252	13,890	6,306	10,417	8,123	13,080
2006	566	566	6,517	1,818	7,083	2,384	3,985	1,786	8,227
2007	2,531	755	3,836	1,747	6,366	2,502	4,600	3,435	6,124
2008	574	410	1,835	630	2,409	1,041	4,628	2,798	6,658
2009	1,121	483	1,676	660	2,797	1,143	3,473	2,063	5,302

EU/GR YEAR	CWT-based Estimates				GSI-based Estimates				
	1.3/5.2 Catch	SE	1.4/6.2 Catch	SE	Total Catch	SE	Catch	10p	90p
2010	2,814	967	2,814	484	5,627	1,451	1,750	803	2,961
2011	1,291	482	556	555	1,847	1,038	2,574	1,573	3,627
2012	2,030	494	1,386	501	3,417	995	1,998	1,073	3,104
2013	396	322	786	343	1,182	665	1,980	977	3,154
2014	-	-	882	1,044	-	-	724	84	1,522

Table C 3: Harvest of Stikine Chinook in US Gillnet and Sport Fisheries outside District 108. Sources and assumptions described in Section 2.1.1.6. Italics mark infilled values. Figure C 3 shows patterns in total catch and the estimated contribution of Little Tahltan Chinook to the total Stikine-bound catch. Shaded column with bold font marks values used in run reconstruction.

EU GR YEAR	CWT-based Estimates					
	1.3 5.2 Catch	SE	1.4 6.2 Catch	SE	Total Catch	SE
1981	-	-	-	-	864	-
1982	-	-	-	-	864	-
1983	-	-	-	-	864	-
1984	-	-	-	-	864	-
1985	-	-	-	-	864	-
1986	-	-	-	-	864	-
1987	-	-	-	-	864	-
1988	-	-	-	-	864	-
1989	-	-	-	-	864	-
1990	-	-	-	-	864	-
1991	-	-	-	-	864	-
1992	-	-	-	-	864	-
1993	-	-	-	-	864	-
1994	-	-	-	-	864	-
1995	-	-	-	-	864	-
1996	-	-	-	-	864	-
1997	-	-	-	-	864	-
1998	-	-	-	-	864	-
1999	-	-	-	-	864	-
2000	-	-	-	-	864	-

CWT-based Estimates						
EU	1.3		1.4		Total	
GR	5.2		6.2		Total	
YEAR	Catch	SE	Catch	SE	Catch	SE
2001	-	-	-	-	864	-
2002	-	-	-	-	864	-
2003	295	294	0	0	295	294
2004	0	0	0	0	0	0
2005	1,595	1,129	2,253	2,253	3,848	3,382
2006	0	0	420	296	420	296
2007	101	101	245	244	346	345
2008	0	0	100	99	100	99
2009	741	303	149	148	890	451
2010	1,292	745	0	0	1,292	745
2011	926	511	202	202	1,128	713
2012	272	121	253	179	525	300
2013	283	212	375	173	658	385
2014	-	-	318	231	-	-

Table C 4: Harvest of Stikine Chinook in US Gillnet Fisheries Inside District 108. Sources and assumptions described in Section 2.1.1.6. Figure C 4 shows patterns in total catch and the estimated contribution of Little Tahltan Chinook to the total Stikine-bound catch.

CWT-based Estimates								
EU	1.3		1.4		1.5		Total	
GR	5.2		6.2		7.2		Total	
YEAR	Catch	SE	Catch	SE	Catch	SE	Catch	SE
1981	67	-	209	-	1	-	277	-
1982	176	-	815	-	11	-	1,002	-
1983	10	-	14	-	1	-	25	-
1984	4	-	5	-	1	-	10	-
1985	3	-	11	-	0	-	14	-
1986	22	-	47	-	1	-	70	-
1987	29	-	86	-	3	-	118	-
1988	16	-	153	-	3	-	172	-
1989	102	-	125	-	55	-	282	-
1990	18	-	200	-	13	-	231	-

CWT-based Estimates								
YEAR	EU	1.3	1.4	1.5	Total			
	GR	5.2	6.2	7.2	Catch	SE	Catch	SE
1991		230	345	20	595	-	-	-
1992		111	408	1	520	-	-	-
1993		76	708	22	806	-	-	-
1994		138	994	100	1,232	-	-	-
1995		154	384	66	604	-	-	-
1996		569	213	0	782	-	-	-
1997		399	1,318	9	1,726	-	-	-
1998		-	-	-	129	-	-	-
1999		-	-	-	564	-	-	-
2000		-	-	-	604	-	-	-
2001		-	-	-	6	-	-	-
2002		-	-	-	21	-	-	-
2003		-	-	-	84	-	-	-
2004		-	-	-	4,522	-	-	-
2005		-	-	-	21,233	-	-	-
2006		-	-	-	17,259	-	-	-
2007		-	-	-	7,057	-	-	-
2008		-	-	-	4,905	-	-	-
2009		-	-	-	244	-	-	-
2010		-	-	-	238	-	-	-
2011		-	-	-	970	-	-	-
2012		-	-	-	1,209	-	-	-
2013		-	-	-	455	-	-	-
2014		-	-	-	204	-	-	-

Table C 5: Harvest of Stikine Chinook in US Sport Fisheries Inside District 108. Sources and assumptions described in Section 2.1.1.6. Figure C 4 shows patterns in total catch and the estimated contribution of Little Tahltan Chinook to the total Stikine-bound catch.

		CWT-based Estimates							
YEAR	EU GR	1.3		1.4		1.5		Total	
		5.2		6.2		7.2		Catch	SE
		Catch	SE	Catch	SE	Catch	SE	Catch	SE
1981		576	79	1,804	220	12	7	2,392	306
1982		587	99	2,722	335	37	17	3,346	451
1983		1,016	188	1,523	230	127	58	2,666	476
1984		1,981	245	267	65	13	14	2,261	324
1985		628	101	2,451	301	25	3	3,104	405
1986		799	116	1,622	206	40	15	2,461	337
1987		336	58	1,147	145	56	17	1,539	220
1988		225	49	2,170	264	45	16	2,440	329
1989		992	136	1,242	164	542	89	2,776	389
1990		330	61	3,723	450	232	47	4,285	558
1991		1,412	187	2,126	267	120	36	3,658	490
1992		709	99	2,608	317	5	3	3,322	419
1993		401	67	3,719	449	107	28	4,227	544
1994		243	37	1,724	209	175	31	2,142	277
1995		399	59	1,052	133	188	33	1,639	225
1996		1,744	216	670	96	10	7	2,424	319
1997		731	106	2,426	298	19	10	3,176	414
1998		-	-	-	-	-	-	1,438	-
1999		-	-	-	-	-	-	3,668	-
2000		-	-	-	-	-	-	2,581	-
2001		-	-	-	-	-	-	2,263	-
2002		-	-	-	-	-	-	3,077	-
2003		-	-	-	-	-	-	3,252	-
2004		-	-	-	-	-	-	2,939	-
2005		-	-	-	-	-	-	3,665	-
2006		-	-	-	-	-	-	3,346	-
2007		-	-	-	-	-	-	2,218	-
2008		-	-	-	-	-	-	1,453	-
2009		-	-	-	-	-	-	887	-

		CWT-based Estimates							
		1.3		1.4		1.5			
		5.2		6.2		7.2		Total	
YEAR		Catch	SE	Catch	SE	Catch	SE	Catch	SE
2010	EU	-	-	-	-	-	-	586	-
2011	GR	-	-	-	-	-	-	650	-
2012		-	-	-	-	-	-	608	-
2013		-	-	-	-	-	-	636	-
2014		-	-	-	-	-	-	697	-

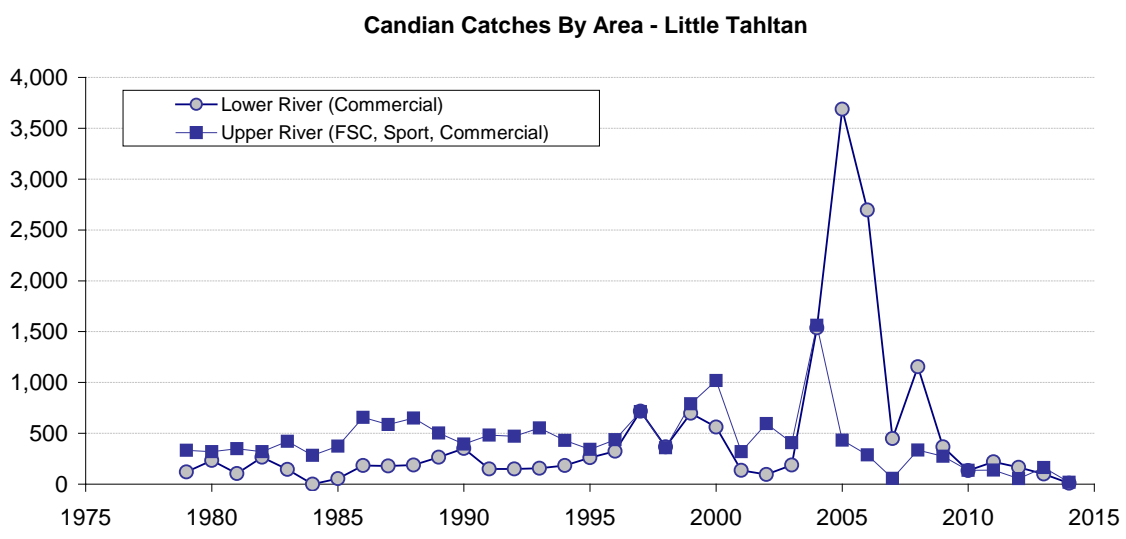
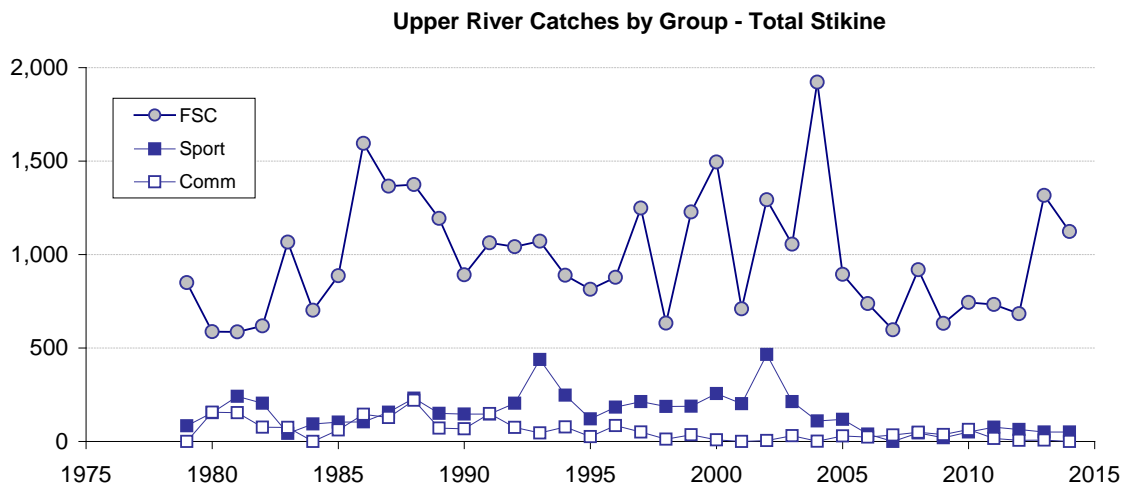
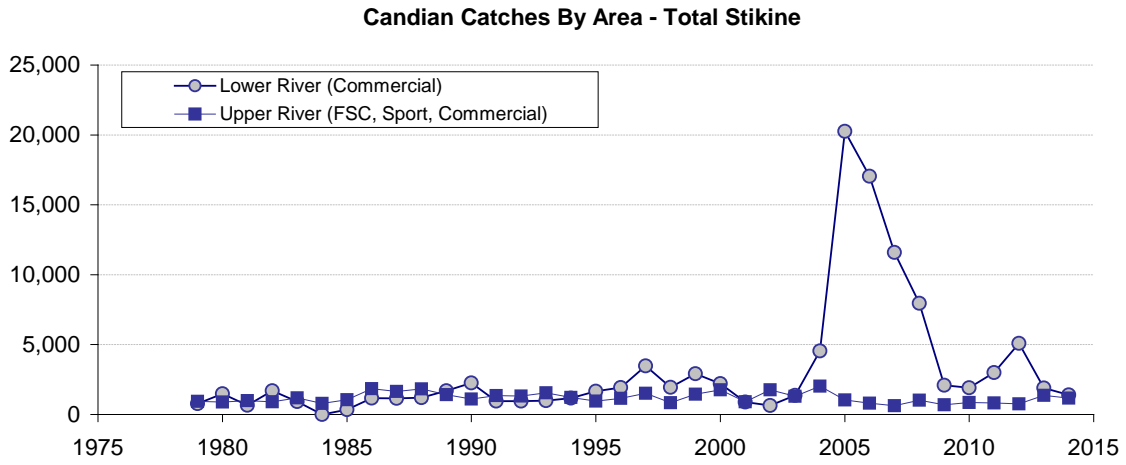


Figure C 1: Pattern in Canadian catches.

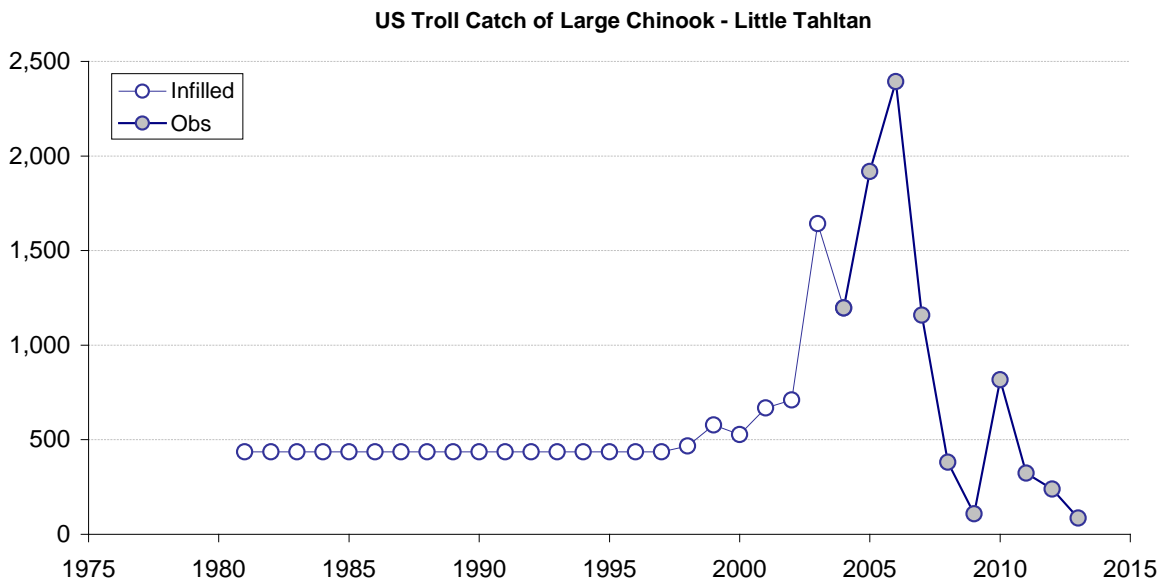
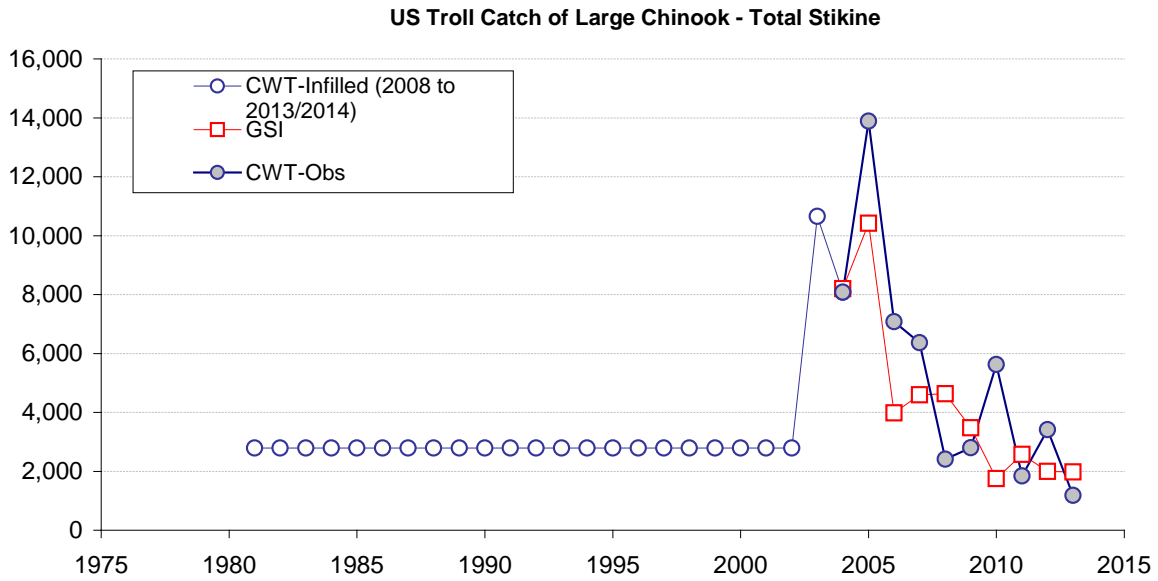
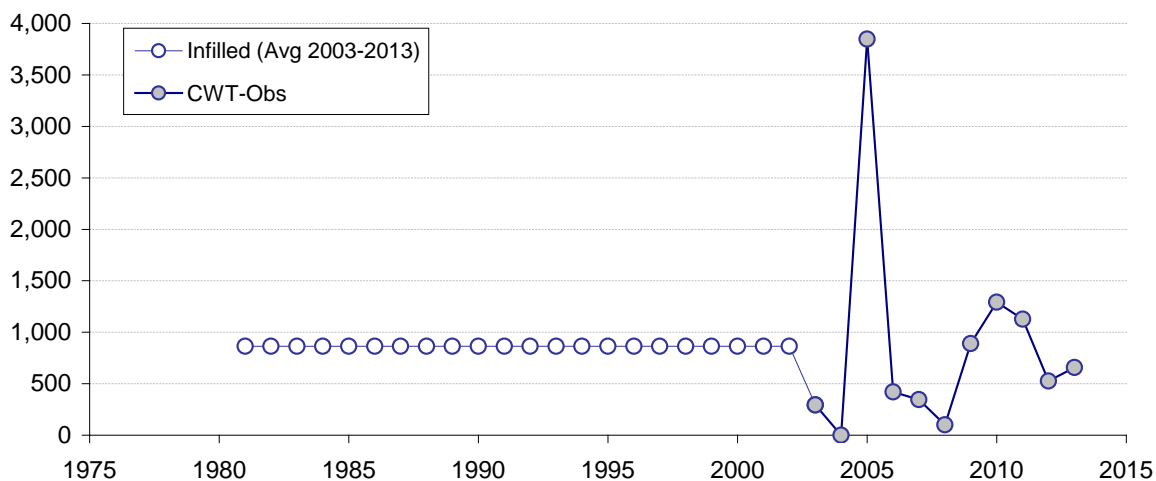


Figure C 2: Pattern in US troll catches. Infilled values have at least one infilled component (5yr-old catch, 6yr-old catch, or Little Tahltan proportion). Bottom panel uses median infilled proportion.

US GN & SportCatch outside of D108 of Large Chinook - Total Stikine



US GN & SportCatch outside of D108 of Large Chinook - Little Tahltan

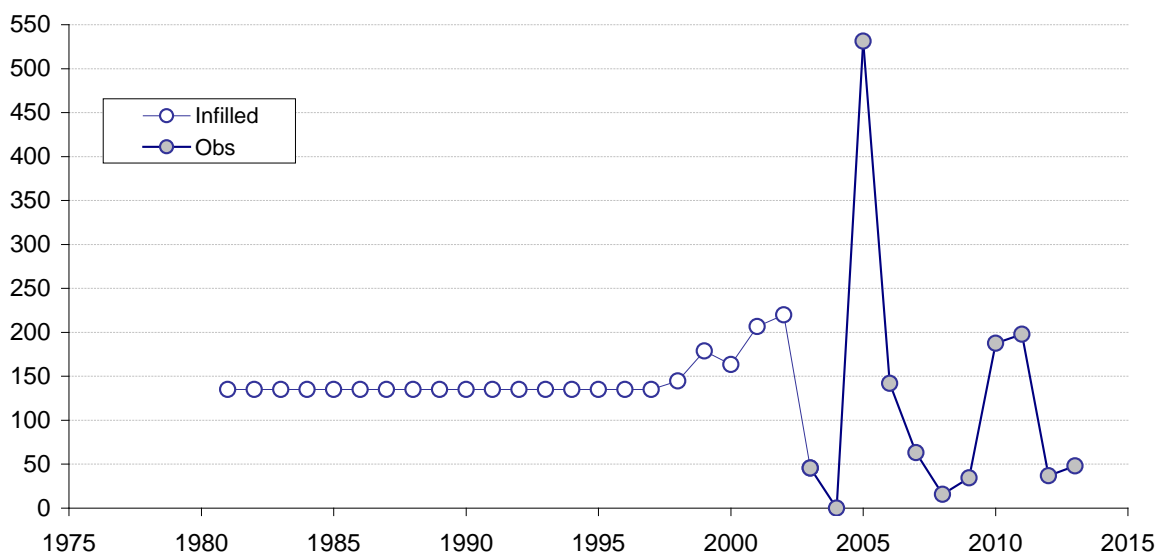
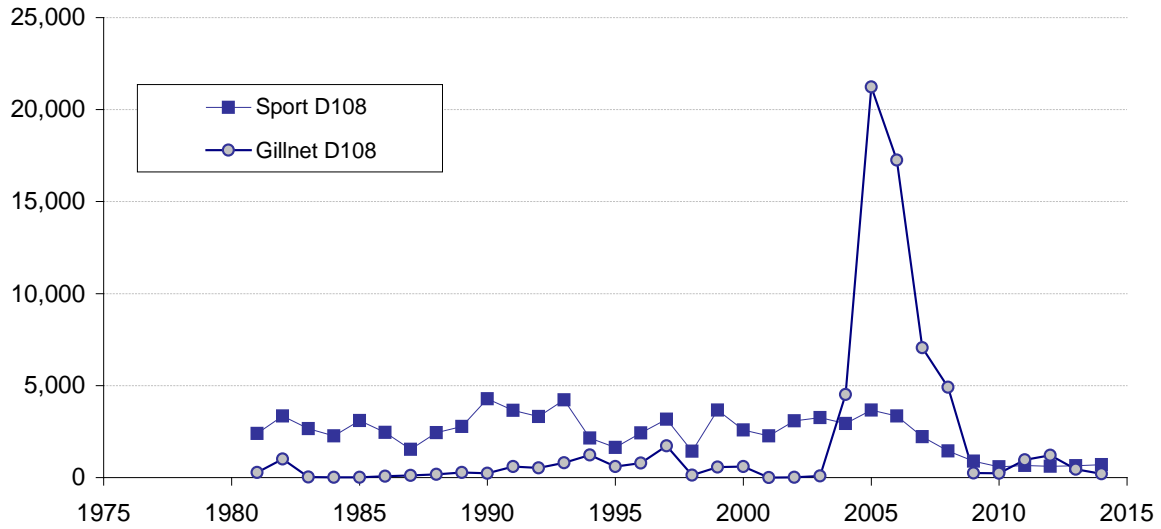


Figure C 3: Pattern in US Gillnet and Sport Catches outside District 108. Infilled values have at least one infilled component (5yr-old catch, 6yr-old catch, or Little Tahltan proportion). Bottom panel uses median infilled proportion. Values in Table C 3. Descriptions in Section 2.1.1.6.

US GN & Sport Catch inside of D108 of Large Chinook - Total Stikine



US GN & Sport Catch inside of D108 of Large Chinook - Little Tahltan

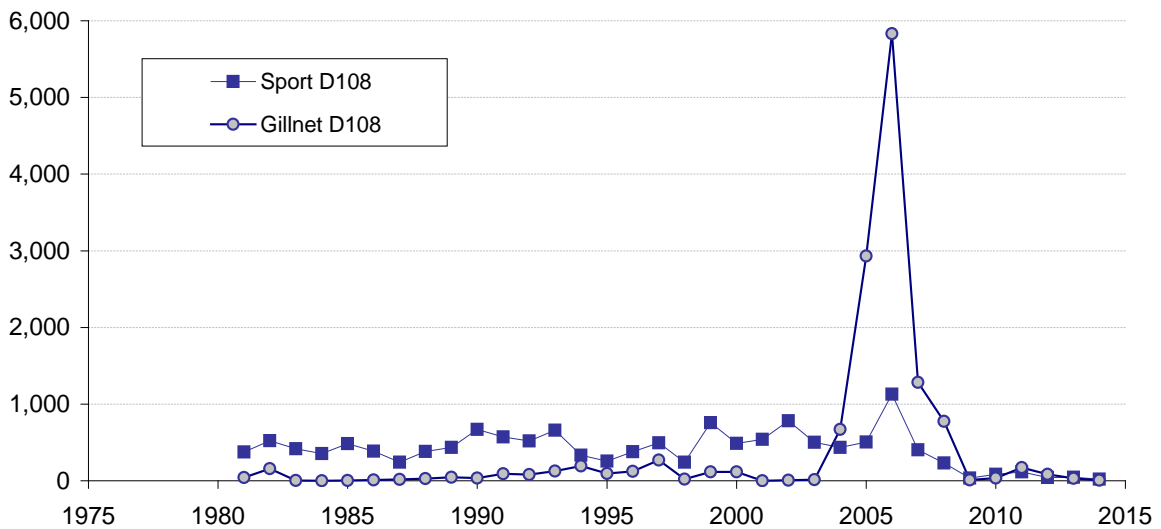


Figure C 4: Pattern in US Gillnet and Sport Catches inside District 108. Values in Table C 4 and Table C 5. Descriptions in Section 2.1.1.6.

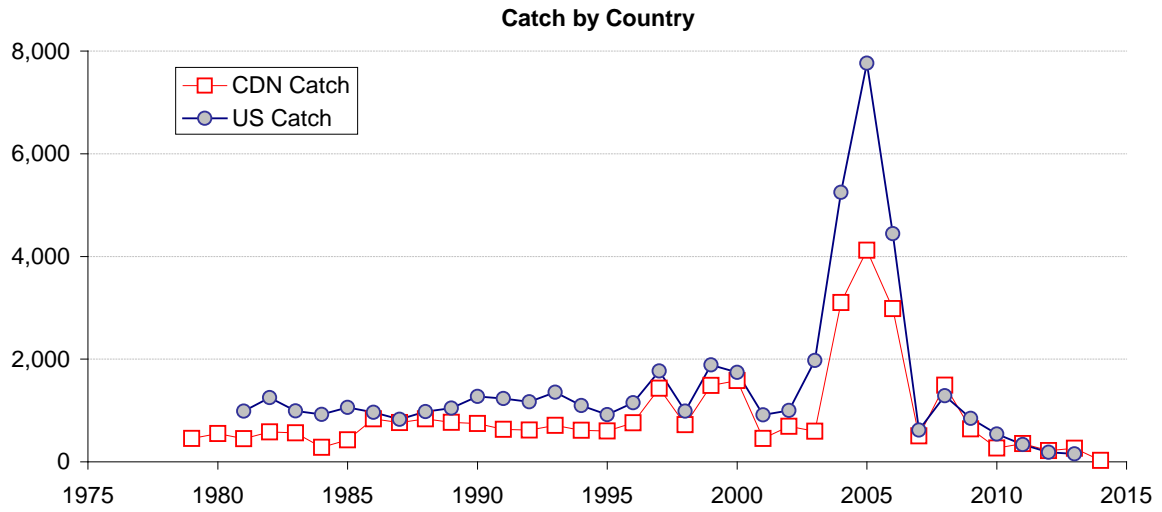
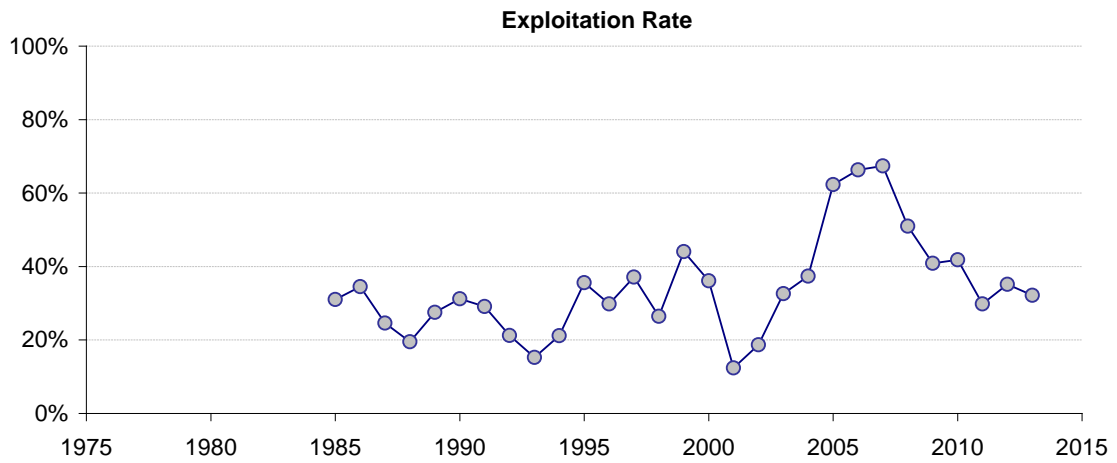
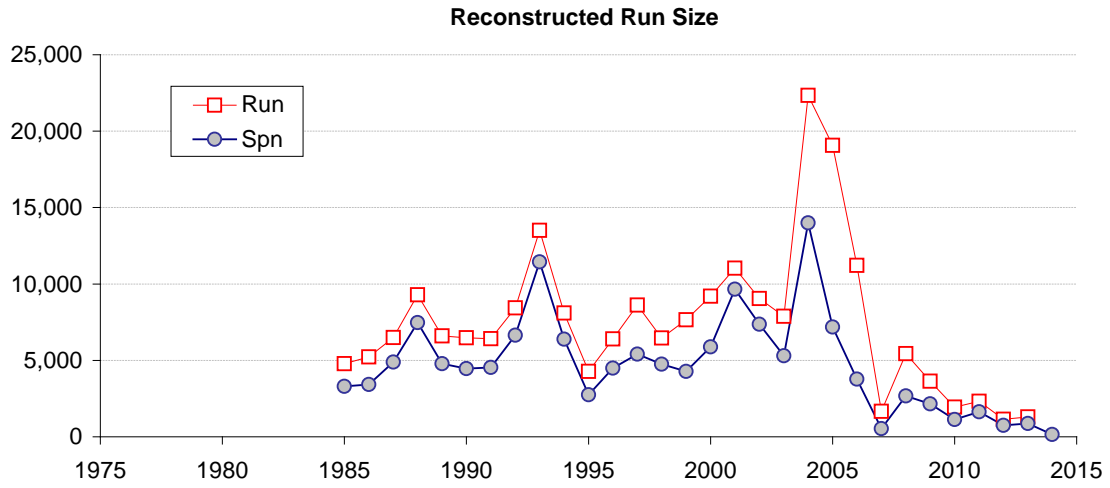


Figure C 5: Reconstructed run size, exploitation rate and catch by country.

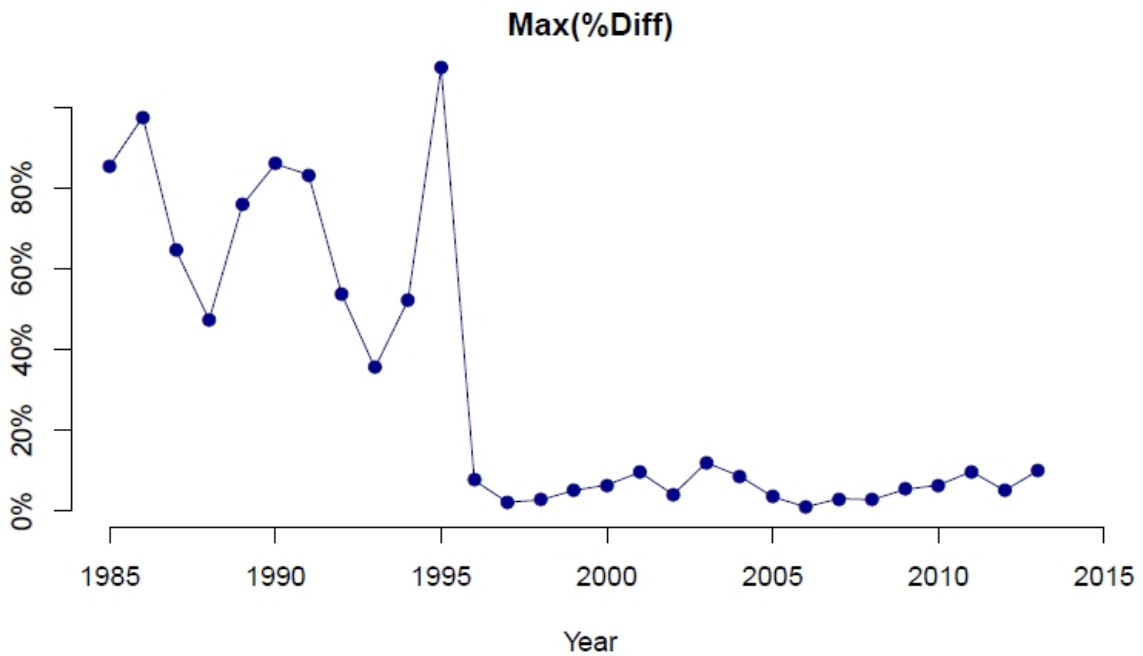
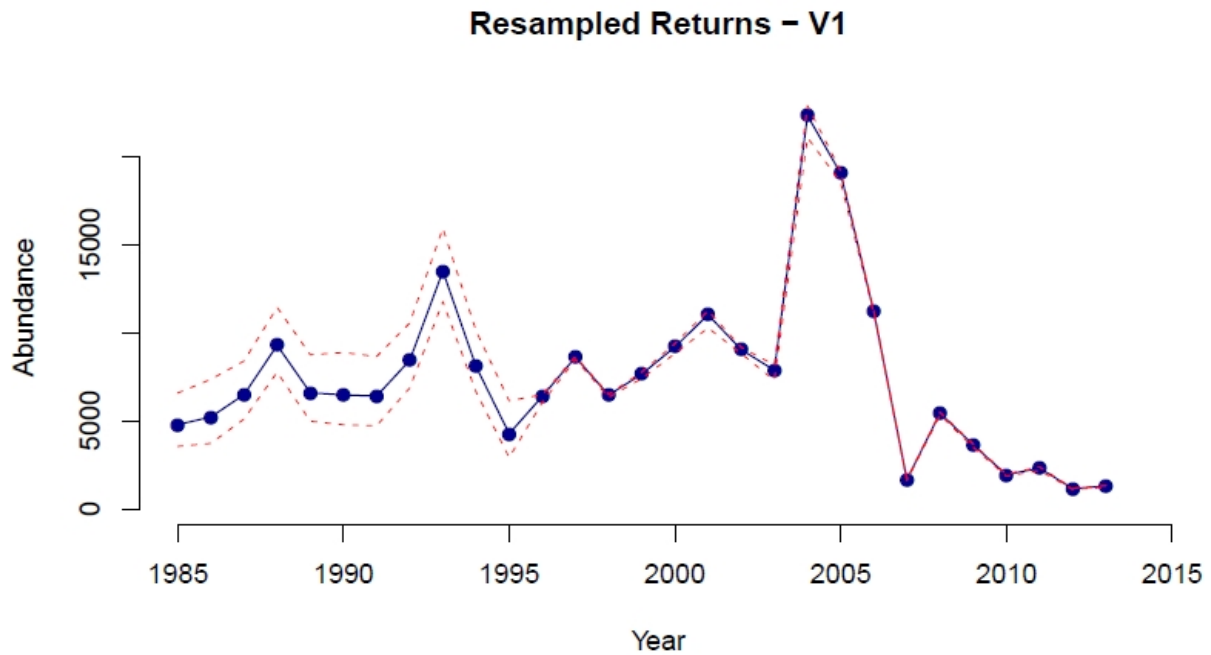


Figure C 6: Run reconstruction assumptions tested with resampling – Version 1. Top panel shows the range in total run size estimates introduced by resampling on 2 key assumptions: % small adults by age class (sample from 2000-2013 observations), % Little Tahltan in catches of total Stikine Chinook (infill pre-1996 by sampling from 1996-2013). Bottom panel shows % difference between smallest and largest estimates for each year.

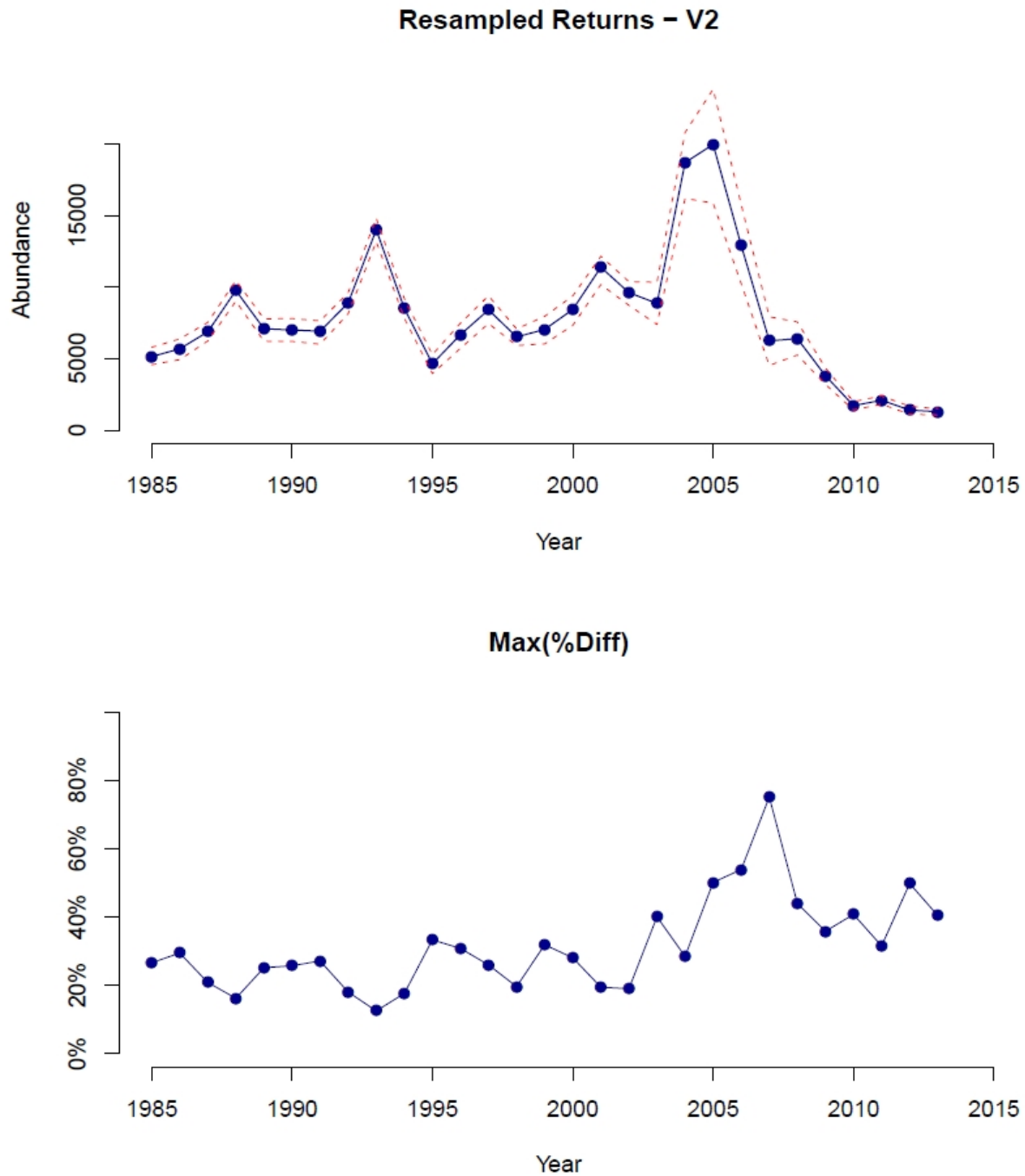


Figure C 7: Run reconstruction assumptions tested with resampling – Version 2. Top panel shows the range in total run size estimates introduced by resampling on 2 key assumptions: % jack by age class (sample from 2000-2013 observations) and % Little Tahltan in catches of total Stikine Chinook. For years up to 2009, sample from uniform distribution bounded by range of observed values, excluding the smallest and largest. For 2010 onward, sample from uniform distribution bounded by range of observed values. Bottom panel shows % difference between smallest and largest estimates for each year.

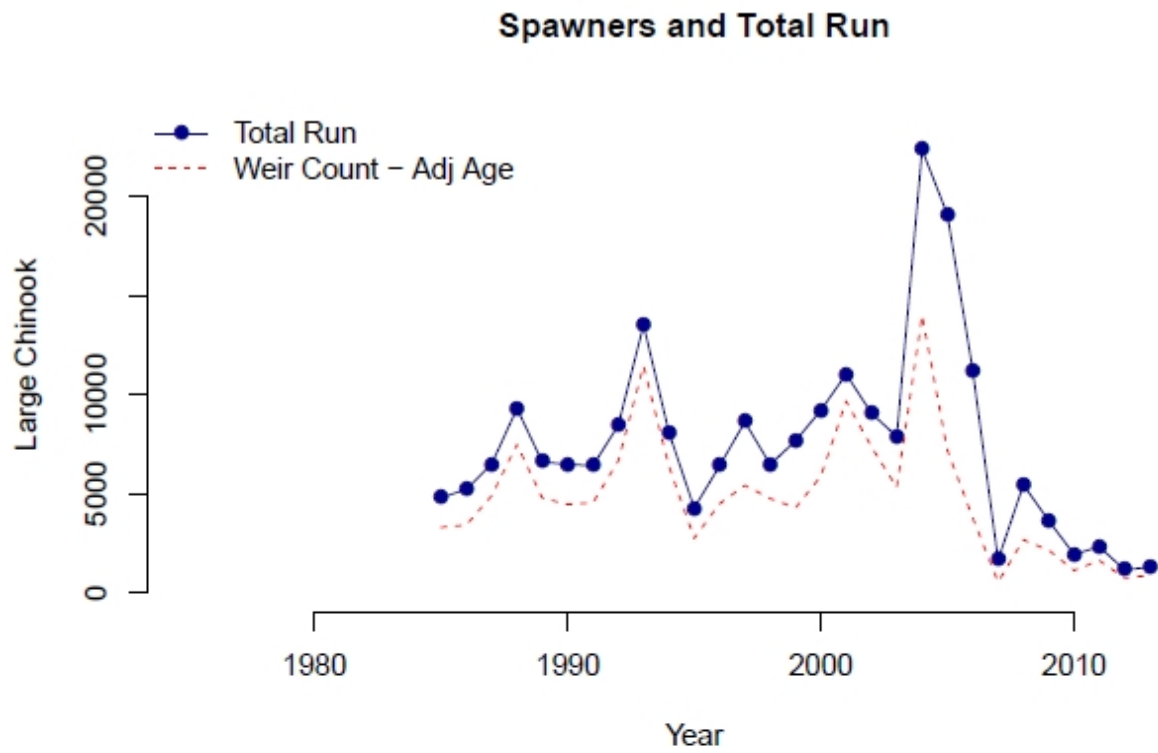


Figure C 8: Base case spawner-recruit time series.

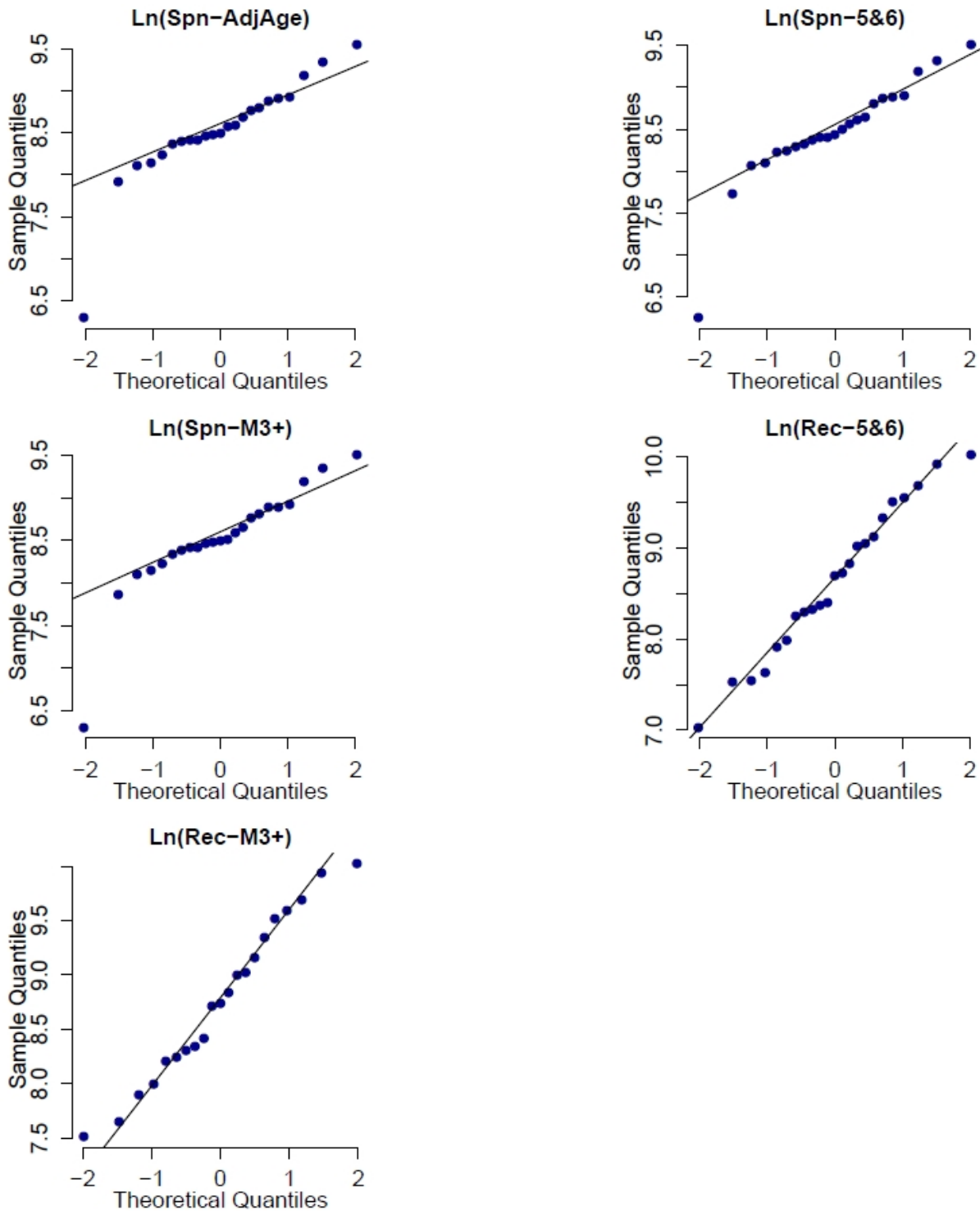


Figure C 10: QQnorm plots of Little Tahltan Chinook Data – SR Brood Years. Each panel compares the percentiles of a log-transformed data set to a theoretical normal distribution. If data is log-normally distributed, the $\log()$ of the estimates should resemble a normal distribution. If the distributions match, the points fall close to the diagonal line.

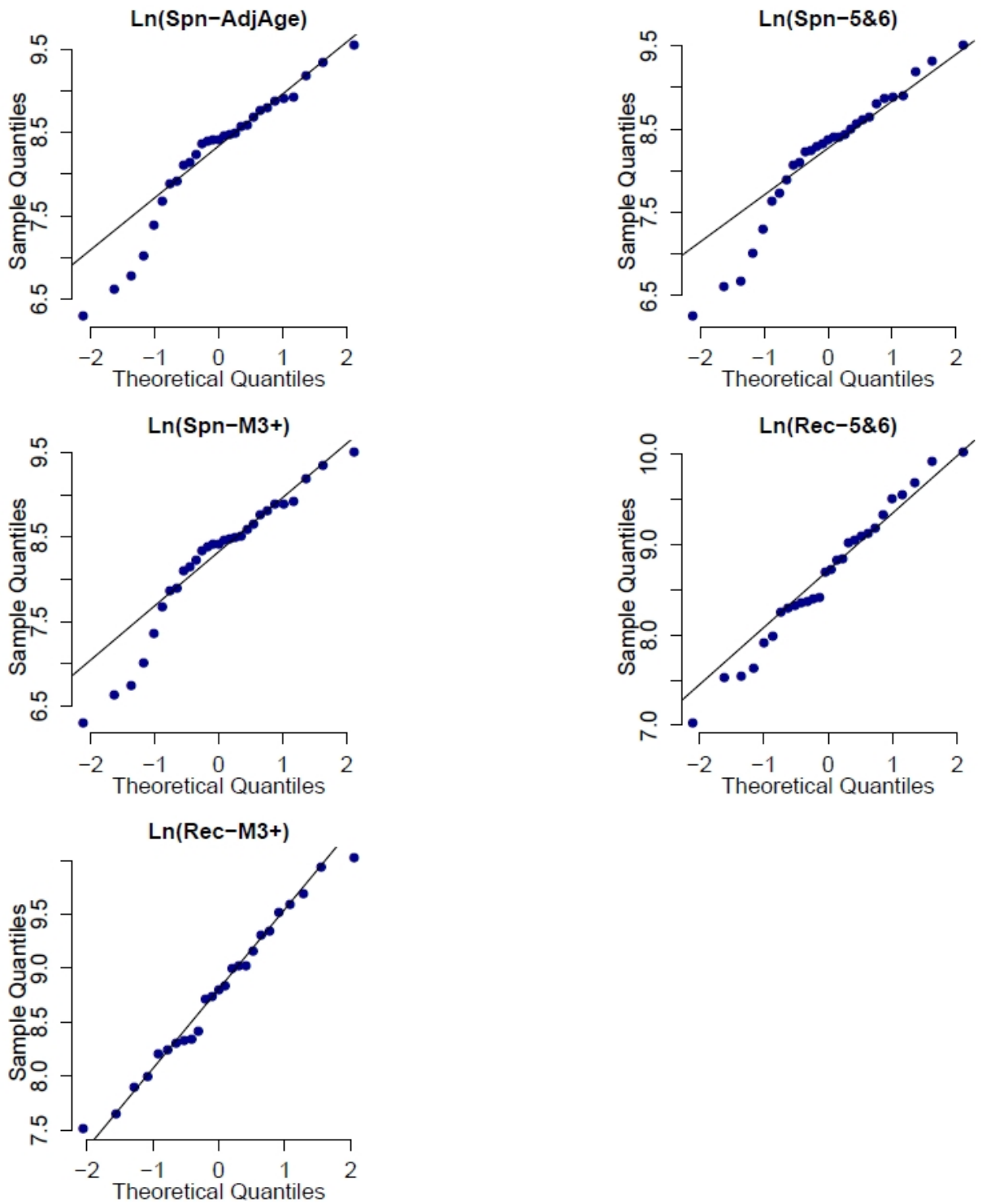


Figure C 11: QQnorm plots of Little Tahltan Chinook Data – All Years. Each panel compares the percentiles of a log-transformed data set to a theoretical normal distribution. If data is log-normally distributed, the $\log()$ of the estimates should resemble a normal distribution. If the distributions match, the points fall close to the diagonal line.

12 APPENDIX D: BUGS/JAGS MODEL FILES

12.1 SAMPLE DATA AND INITIS

```
# r2OpenBUGS and r2JAGS are called within R.
# This section shows the input objects for the base case data set.

# "Inits Object"
list(list(tau_R=3,C=2), list(tau_R=7,C=1))

# "Data Object"
$S
  Yr1985    Yr1986    Yr1987    Yr1988    Yr1989    Yr1990    Yr1991    Yr1992    Yr1993
3300.9193  3418.5775  4895.2459  7478.4068  4784.6609  4455.5033  4543.5675  6649.3491 11442.9131
  Yr1994    Yr1995    Yr1996    Yr1997    Yr1998    Yr1999    Yr2000    Yr2001    Yr2002
6384.2077  2750.6745  4487.4667  5416.5599  4755.8166  4282.6738  5877.6465  9660.7704  7360.8789
  Yr2003    Yr2004    Yr2005    Yr2006    Yr2007
5308.8534 13991.3949  7187.6150  3780.0564  541.7477

$R_Obs
Yr1985 Yr1986 Yr1987 Yr1988 Yr1989 Yr1990 Yr1991 Yr1992 Yr1993 Yr1994 Yr1995 Yr1996 Yr1997 Yr1998
  4345   9222  14073   8320   4121   2958  11319   6803   6023   8495   6188  16212   4028  13476
Yr1999 Yr2000 Yr2001 Yr2002 Yr2003 Yr2004 Yr2005 Yr2006 Yr2007
 20504  22744   1869   4444   3824   2733   2061   1901   1133

$N
[1] 23

$p.alpha
[1] 0

$p.beta
[1] 0

$tau_alpha
[1] 0.0001
```

```
$tau_beta
[1] 0.01
```

12.2 RICKER MODEL

```
# Ricker model
# taken from code package by Cass, Huang, Porszt, Grant, Macdonald, Michielsens
# parts that are not SR par estimation were moved to R to speed up the overall performance
# Notation translator: Y[] = "Ln(R.pred)" , RS[] = "Ln(RperS)", alpha = "ln.alpha"

model{
  for (i in 1:N) {
    R_Obs[i] ~ dlnorm(Y[i],tau_R)          #likelihood
    Y[i] <- RS[i] +log(S[i])              #calc log(R)
    RS[i] <- alpha - beta * S[i]          # ricker model
    log.resid[i] <- log(R_Obs[i]) - Y[i]  # tracking residuals for diagnostics
  }

  alpha ~ dnorm(0,0.0001)                 #prior for alpha
  beta <-1/C                               # prior for beta
  C~ dlnorm(1,0.1)                         # prior for beta

  tau_R ~ dgamma(0.001,0.001)             #prior for precision parameter

  sigma <- 1/sqrt(tau_R)                  # changed to this based on
                                          # Fleischman and Evenson (2010) ADFG FMS10-04
}
```

12.3 RICKER AR1 MODEL

```
# Ricker model with 1-yr autoregression term
# Adapted from code package by Cass, Huang, Porszt, Grant, Macdonald, Michielsens
# and expanded for AR1 based on Eq21 and 22 of Fleischman and Evenson (2010) ADFG FMS10-04
# parts that are not SR par estimation are handled in R to speed up the overall performance
# Notation translator: Y[] = "Ln(R.pred)" , RS[] = "Ln(RperS)", alpha = "ln.alpha"
```

```

model{

  # do first year
  R_Obs[1] ~ dlnorm(Y[1],tau_R)
  Y[1] <- log(S[1]) + RS[1]
  RS[1] <- alpha - beta * S[1] + phi * log.resid.0

  # do second year
  R_Obs[2] ~ dlnorm(Y[2],tau_R)
  Y[2] <- log(S[2]) + RS[2]
  RS[2] <- alpha - beta * S[2] + phi * log.resid[1]
  log.resid[1] <- log(R_Obs[1]) - Y[1]

  #loop over rest of N sample points (starting with the third)
  for (i in 2:N) { log.resid[i] <- log(R_Obs[i]) - Y[i] }
  for (i in 3:N) {
      R_Obs[i] ~ dlnorm(Y[i],tau_R) # likelihood
      Y[i] <- log(S[i]) + RS[i]
      RS[i] <- alpha - beta * S[i] + phi * log.resid[i-1]
  } # end for loop

  alpha ~ dnorm(0,0.0001) #prior for alpha
  beta <-1/C # prior for beta
  C ~ dlnorm(1,0.1) # prior for beta -> could change to dlnorm(p.beta, tau_beta)
  tau_R ~ dgamma(0.001,0.001) #prior for precision parameter
  phi ~ dnorm(0,0.0001)I(-1,1) # AR1 priors as per Fleishman and Evenson AppA2
  log.resid.0 ~ dnorm(0,tau.red) # I(-3,3) remove for jags WHY?
  tau.red <- tau.white * (1-phi*phi)
  tau.white ~ dgamma(0.01,0.01)
  sigma <- 1/sqrt(tau_R) # based on Fleishman and Evenson (2010) ADFG FMS10-04
} # end model description

```

12.4 BEVERTON-HOLT MODEL

```

# Beverton Holt Model
# Adapted from Bev-Holt STAN code by Mike Hawkshaw
# parts that are not SR par estimation were moved to R to speed up the overall performance

```

```

model{

```

```
for (i in 1:N) { ln_R_Obs[i] <- log(R_Obs[i])}

for (i in 1:N) {
  pred_rec[i] <- (exp(ln.alpha) * S[i]) / (exp(ln.beta) + S[i])
  Y[i] <- log(pred_rec[i])
}

for (i in 1:N) { ln_R_Obs[i] ~ dnorm(Y[i],tau_R) }

# NEW
alpha <- exp(ln.alpha)
beta <- exp(ln.beta)
ln.alpha ~ dnorm(p.alpha,tau_alpha)
ln.beta ~ dnorm(p.beta,tau_beta)

tau_R ~ dgamma(0.001,0.001) #prior for precision parameter
sigma <- 1/sqrt(tau_R)

} # end model description
```

13 APPENDIX E: R CODE

The R code used for this analysis, especially for the Bayesian model fits, builds on a library of functions that has been developed in collaboration with Bronwyn MacDonald and Sue Grant (DFO). The original code was developed by Al Cass (DFO). Other contributors to the code include Catherine Michielsens (PSC), Erin Porszt (DFO), Ann-Marie Huang (DFO), and Merran Hague (PSC).

All the code needed to fully replicate the analysis is very extensive and structured in a format that doesn't lend itself to compact documentation (i.e. function libraries and different scripts for reading in the data, doing the run reconstruction, running alternative model fits, creating plots and tables). Therefore we only provide key pieces to allow a review of estimation methods, rather than the fully reproducible code included in some recent ADFG publications (e.g. Bernard and Jones 2010).

13.1 MCMC WITH R2OPENBUGS / R2JAGS

The core module of this tool kit is a function that feeds a standard data object and BUGS model into different MCMC software through alternative R packages.

```
mcmc.sub <- function(data.obj, model.in, inits.in, settings.in ,pars.to.track.in,
                    out.label="PopA",prefix="", package="r2WinBUGS",
                    DIC.in=FALSE,debug.in=FALSE, save.history.in=FALSE,
                    tracing.in=FALSE, write.CODA.in=TRUE,
                    diag.plots.in=TRUE, CODA.diag.in=TRUE,
                    perc.vec=seq(5,95,by=5),output.type="default",
                    out.path=""){

# data.obj and inits.in as per example in Section 12.1
# model.in as per examples in Sections 12.2, 12.3, 12.4
# # settings.in is a list object with the specs for the mcmc:  $n.chains, $n.burnin, $n.thin, $n.samples,
# pars.to.track.in is a list of nodes to be monitored
# out.label = label for the output files the output (objects, coda files etc)
# package can be one of "r2JAGS", "r2WinBUGS", or "r2OpenBUGS"
# DIC.in can be TRUE or FALSE. If TRUE, then ....

# NOTE: details depend on chosen package!
# IMPORTANT NOTES:
# R2WinBUGS and R2JAGS handle thinning the same way, but R2OpenBUGS does the opposite!
```

```

# R2WINBUGS & R2JAGS: do n.burnin and n.samples, then thins based on n.thin, so that n.sample/n.thin
mcmc # samples are stored
# R2 OpenBUGS: does n.burnin*n.thin and n.samples*n.thin, then stores n.samples mcmc samples
# in the code below, this is fixed by adjusting the n.burnin and n.samples before calling R2OpenBUGS.
# This way, the results are almost the same for all 3 packages!
#However, there are still small differences:
# - R2WinBUGS rounds up when calculating n.iter/n.thin, then drops some of the final samples for some
#unknown reason
# - R2OpenBUGS rounds up when calculating n.iter/n.thin
# - R2JAGS behaves exactly like R2OpenBUGS *after* the above correction
# So, for settings.in = list(n.chains=2, n.burnin=20000, n.thin=60,n.samples=50000)
# R2OpenBUGS and R2JAGS each do 333 burnin (after thinning) plus 500 samples (after burnin), and spits out
# 1000 MCMC samples (500 * 2 chains)
# R2WinBUGS does 334 burnin (after thinning) plus 500 samples (after burnin), but spits out only 812 MCMC
# samples from the 2 chains.

if(!require(SOAR)) {install.packages("SOAR")}

if(!(package %in% c("r2JAGS", "r2WinBUGS","r2OpenBUGS"))){
  warning(paste("Package",package,"not implemented yet!"))
  stop()
}

# check and store current directory
base.dir <- getwd()

print(paste("STARTING MCMC ESTIMATION FOR,", paste(out.label,prefix,sep=""), "-----
-----"))

start.time <- proc.time()

# -----
if(package=="r2WinBUGS"){

# load library, install check happens earlier
library(R2WinBUGS)
print("Starting r2WinBUGS")

mcmc.obj <- bugs(data=data.obj, inits=inits.in, parameters.to.save=pars.to.track.in,

```

```

        model.file=model.in,
        program="winbugs",
        DIC=DIC.in,
        n.chains=settings.in$n.chains,
        n.burnin=settings.in$n.burnin,
        n.thin=settings.in$n.thin,
        n.iter=settings.in$n.samples,
        debug=debug.in, save.history=save.history.in) #,
        #bugs.directory = "c:/Program Files 2/WinBUGS14/"
        # NOTE: Potential Bug: Main Program Files folder locked on some OS)

print(paste("MCMC - r2WinBUGS took",summary(proc.time()-start.time)["elapsed"]))

MCMCsamples <- mcmc.obj$sims.matrix
MCMCsummary <- mcmc.obj$summary
MCMCsims <- mcmc.obj$n.sims

if(tracing.in){
  print("Output Elements"); print(names(mcmc.obj))
  #print("Model Fit"); print(mcmc.obj$model) # not informative because name of model file is created
internally in temporary cache
  print("MCMCsummary"); print(MCMCsummary)
  print("MCMCsamples");print(MCMCsamples[1:20,])
}

detach(package:R2WinBUGS)# detach library, to avoid conflicts with later MCMC runs using different package

#print(sessionInfo())

} # end if "r2winBUGS"

# -----
if(package=="r2OpenBUGS"){

# load library, install check happens earlier
library(R2OpenBUGS)

```

```

print("Starting r2OpenBUGS")

start.time <-proc.time()
mcmc.obj <- bugs(data=data.obj, inits=inits.in, parameters.to.save=pars.to.track.in,
                model.file=model.in,
                DIC=DIC.in,
                n.chains=settings.in$n.chains,
                n.burnin=round(settings.in$n.burnin / settings.in$n.thin) , # this is needed to fix
inconsistency across packages, see note in beginning
                n.thin=settings.in$n.thin,
                n.iter=round(settings.in$n.samples / settings.in$n.thin), # this is needed to fix
inconsistency across packages, see note in beginning
                debug=debug.in, save.history=save.history.in)

MCMCsamples <- mcmc.obj$sims.matrix
MCMCsummary <- mcmc.obj$summary
MCMCsims <- mcmc.obj$n.sims

print(paste("MCMC - r2OpenBUGS took",summary(proc.time()-start.time)["elapsed"]))

if(tracing.in){print("Output Elements"); print(names(mcmc.obj)); print("Model Fit"); print(mcmc.obj$model)
}

detach(package:R2OpenBUGS) # detach library, to avoid conflicts with later MCMC runs using different
package
#print(sessionInfo())

} # end if "r2OpenBUGS"

# -----
if(package=="r2JAGS"){

# load library, install check happens earlier
library(R2jags) # also attaches rjags package
print("Starting r2JAGS")

```

```

start.time <-proc.time()

if(debug.in){print("WARNING: debug = TRUE does not apply for R2JAGS and is ignored!")}

mcmc.obj <- jags(data=data.obj, inits=inits.in, parameters.to.save=pars.to.track.in,
               model.file=model.in,
               DIC=DIC.in,
               n.chains=settings.in$n.chains,
               n.burnin=settings.in$n.burnin,
               n.thin=settings.in$n.thin,
               n.iter=settings.in$n.samples)

print(paste("MCMC - r2JAGS took",summary(proc.time()-start.time)["elapsed"]))

# output
MCMCsamples <- mcmc.obj$BUGSoutput$sims.matrix
MCMCsummary <- mcmc.obj$BUGSoutput$summary
MCMCsims <- "Not yet implemented for R2jags, because it doesn't have n.sims output in R2jags (as in
R2OpenBUGS and R2 WinBUGS)"

if(tracing.in){
  print("Output Elements"); print(names(mcmc.obj))
  print("Model Fit"); print(mcmc.obj$model)
  print("r2jags BUGS Output Elements"); print(names(mcmc.obj$BUGSoutput))
  print("MCMC SubSample");print(MCMCsamples[1:20,]) # extract the first few rows of the chains for
alpha
} # end if tracing
detach(package:R2jags) # detach library, to avoid conflicts with later MCMC runs using different package
detach(package:rjags)

#print(sessionInfo())

} # end if "r2JAGS"

print(paste("STARTING OUTPUT SUMMARY FOR,", out.label, "-----"))

```

```

start.time <- proc.time()

# Save CODA in txt file (if turned on)
if(write.CODA.in){
  dir.create(paste("OUTPUT/CODA Files","/",out.path,sep=""),showWarnings=FALSE)
  # creates directory, if it already exists it does nothing
  setwd(paste("OUTPUT/CODA Files","/",out.path,sep=""))
  write.table(MCMCsamples,paste(prefix,out.label,"_pars.txt",sep=""))
  setwd(base.dir)
}

# create or append an array with the MCMC samplestats
# NOTE: SEEMS THAT THESE STORAGE ARRAYS DON'T NEED TO BE EXPLICITLY REMOVED.
# THEY DISAPPEAR WHEN THE SUBROUTINE CALL ENDS BECAUSE THEY ARE NOT RETURNED TO THE PARENT FUNCTION
# SHOULD HOWEVER MAKE THIS MORE ROBUST
if(!exists("mcmc.samplestats")){
  tmp.stats <- as.array(as.matrix(MCMCsummary))
  mcmc.samplestats <-
array(NA,dim=dim(tmp.stats),dimnames=list(dimnames(tmp.stats)[[1]],dimnames(tmp.stats)[[2]]))
} # end if creating new array

# save stats from current MCMC run
mcmc.samplestats[, ] <- as.matrix(MCMCsummary) # NOTE: INCLUDES JAGS DEFAULT THINNING FOR NOW

if(tracing.in){ print("mcmc.samplestats");print(paste(prefix,out.label)); print(mcmc.samplestats[, ])}

# create or append an array with the %iles for each tracked variable across chains
if(!exists("mcmc.percs")){
  vars.tmp <- dimnames(MCMCsamples)[[2]]
  mcmc.percs <-
array(NA,dim=c(length(perc.vec),length(vars.tmp)),dimnames=list(paste("p",perc.vec,sep=""),vars.tmp))
} # end if creating new array

mcmc.percs[, ] <- apply(MCMCsamples,MARGIN=2,quantile,probs=perc.vec/100)

```

```

# create or append list object with thinned MCMC chains
if(!exists("mcmc.samples")){
  mcmc.samples <-
array(NA,dim=dim(MCMCsamples),dimnames=list(1:dim(MCMCsamples)[[1]],dimnames(MCMCsamples)[[2]]))
}
mcmc.samples[,] <- MCMCsamples

# create or append list object with DIC

if(!exists("mcmc.dic")){
  mcmc.dic <- array(NA,dim=c(1,3),dimnames=list("",c("mean(Dev)","pD","DIC")))
} # end if creating new array

if(package=="r2JAGS"){mcmc.dic[,] <-
c(mcmc.samplestats["deviance","mean"],mcmc.obj$BUGSoutput$pD,mcmc.obj$BUGSoutput$DIC)}
if(package=="r2WinBUGS"|package=="r2OpenBUGS"){mcmc.dic[,] <-
c(mcmc.samplestats["deviance","mean"],mcmc.obj$pD,mcmc.obj$DIC)}

if(tracing.in){print("DIC ----");print(mcmc.dic[,])}

print(paste("Output processing took", summary(proc.time()-start.time)["elapsed"]))

# BUGS JAGS diagnostic plots

if (diag.plots.in){

start.time <- proc.time()

print(paste("STARTING BUGS/JAGS DIAGNOSTICS FOR,", out.label, "-----"))
# NOTE this calculates some diagnostics, and creates a pdf of plots if plotting is turned on

dir.create(paste("OUTPUT/Diagnostic Plots","/",out.path,sep=""),showWarnings=FALSE) # creates directory, if
it already exists it does nothing
setwd(paste("OUTPUT/Diagnostic Plots","/",out.path,sep=""));

```

```

pdf(paste(prefix,out.label,"_Diag_plots.pdf",sep=""),width=8.5, height=8.5, onefile=TRUE) ;
par(mfrow=c(1,1)) # change dir and start pdf for current pop

plot(mcmc.obj)# basic plot (SAME FOR BUGS AND JAGS, COULD MERGE)

# plot.jags does not include a density plot like the densplot() in the coda package
# could just do a hist() here?

if(package=="JAGS"){traceplot(mcmc.obj,ask=FALSE)}# traceplot() not in r2OpenBUGS
  dev.off(); setwd(base.dir) # close pdf and return to working folder

print(paste("BUGS/JAGS diagnostic plots took", summary(proc.time()-start.time)["elapsed"]))

} # end if JAGS.diag.plots

# OUTPUT - CODA

if (CODA.diag.in){

start.time <- proc.time()

print(paste("STARTING CODA DIAGNOSTICS FOR,", paste(prefix,out.label), "-----
--"))
# NOTE this calculates some diagnostics, and creates a pdf of plots if plotting is turned on

dir.create(paste("OUTPUT/Diagnostic Plots","/",out.path,sep=""),showWarnings=FALSE) # creates directory, if
it already exists it does nothing
setwd(paste("OUTPUT/Diagnostic Plots","/",out.path,sep=""));

pdf(paste(prefix,out.label,"CODA_diag_plots.pdf",sep="_"),width=8.5, height=8.5, onefile=TRUE) ;
par(mfrow=c(1,1)) # change dir and start pdf for current pop

# convert output to make usable for diagnostics from coda package
if(package=="r2JAGS"){
  coda.obj1 <- as.mcmc(mcmc.obj$BUGSoutput$sims.matrix)
  coda.obj2<- as.mcmc(mcmc.obj) #BUGSoutput)
}

```

```

if(package=="r2WinBUGS" | package=="r2OpenBUGS"){
    coda.obj1<- as.mcmc(mcmc.obj$sims.matrix)
    coda.obj2<- as.mcmc(mcmc.obj)
}

print("conversion to coda file successful")

#xyplot(coda.obj1) # -> not creating any plots WHY?
plot(coda.obj1)
#gelman.plot(coda.obj2) # NOT WORKING YET
crosscorr.plot(coda.obj1,main="crosscorr.plot")
cumuplot(coda.obj1)
densplot(coda.obj1)
geweke.plot(coda.obj1)

dev.off(); setwd(base.dir) # close pdf and return to working folder

print(paste("CODA diagnostic plots took", summary(proc.time()-start.time)["elapsed"]))

} # end if CODA.diag.plots

#####
print("CREATING OUTPUT OBJECT -----")

# CREATING OUTPUT LIST OBJECT (ONLY PARTLY IMPLEMENTED FOR NOW)
out.list <- list(mcmc.call=paste(prefix,out.label,sep="_"),mcmc.settings=unlist(settings.in))

if(output.type %in% c("short","default","full")){out.list<-c(out.list,list(SampleStats=mcmc.samplestats,
MCMC.Percentiles=mcmc.percs,Conv.Info="TBI",
DIC=mcmc.dic,PosteriorSamples=MCMCsims))}

if(output.type %in% c("default","full")){out.list<-c(out.list,list(Data=data.obj))}

if(output.type=="full"){out.list<-c(out.list,list(MCMC.samples=mcmc.samples))}

if(output.type=="all"){out.list<-c(out.list,list(MCMC.obj=mcmc.obj))}

```

```
return(out.list)
# not sure why return is necessary, but have run into error on some computers if return() is not there

} # end mcmc.sub
```

13.2 PERCENT RANK

The typical approach for displaying patterns that differ by several orders of magnitude (e.g. hundreds to millions of fish) is to plot the time series on a log scale. However this creates problems for visual interpretation, particularly with the diverse audiences in collaborative planning processes. The plots based on percent ranks are an experimental alternative.

Percent ranks rescale the smallest observation as 0, the largest observation as 1, and the median as 0.5. This puts all time series on the same vertical axis and gives the values a more direct interpretation.

[Code adapted from FigRs.](#)

```
# FUNCTION TO IMITATE EXCEL'S PERCENTRANK() FUNCTION
perc.rank<-function(x){
  rank.x<-rank(x, ties.method="min",na.last="keep") # keep NAs as NA value
  perc.rank.x <- (rank.x-1)/(max(rank.x,na.rm=TRUE)-1)
  perc.rank.x
}

# FUNCTION TO PLOT PERCENTRANKS AS DEVIATIONS FROM MEDIAN
perc.rank.plot<-function(x,ma=NULL,yrs=1990:2010,type="fancy"){
# x is a time series stored in vector
# ma specifies whether to plot a moving average. if ma is a number it defines the period

if(type=="spark"){barplot(perc.rank(x)-0.5, ylim=c(-0.5,0.5),col="darkblue",border="darkblue",
xlab="", ylab="",axes=FALSE,axisnames=FALSE)}

if(type=="fancy"){
x.ticks<-barplot(perc.rank(x)-0.5, ylim=c(0.6,0.5),col="lightblue",border="lightblue",
xlab="", ylab="",axes=FALSE,axisnames=FALSE)
abline(h=c(-0.5,0,0.5),col="gray")
  text(rep(-1.3,3), c(-0.5,0,0.5),adj=1,labels=c("Min","Median","Max"),xpd=NA,cex=0.9)
  if(!is.null(ma)){lines(x.ticks,filter(perc.rank(x)-
0.5,filter=rep(1/ma,ma),sides=1),col="red",lwd=2)}
```

```

    axis(side=1,at=x.ticks[seq(4,25,by=5)],labels= yrs[seq(4,25,by=5)])
  } # end type=fancy
}

```

13.3 PERCENTILE METHOD

```
# FUNCTION TO APPLY PERCENTILE METHOD AS DESCRIBED IN VOLK ET AL 2009 FMS 09-07
```

```
Percentile.Method <- function(spn,method="ADFG",rounding = TRUE, out.label="Data",
                             meas.error=NULL, ER=NULL){
```

```

# spn is a matrix with rows = years and 1 col labelled with the name of the dataset
perc.vec <- seq(0.05,0.95,by=0.05)
spn <- na.omit(spn) # remove NAs

```

```

if(rounding){ spn <- sapply(spn,FUN=roundup) }
contrast <- max(spn,na.rm=TRUE)/min(spn,na.rm=TRUE)

```

```
if(method=="DFO"){perc.vals <- c(0.25,0.75);perc.labels <- c("SEG_L","SEG_H")}
```

```

if(method=="ADFG"){
  if(contrast<4){perc.vals <- c(NA,0.15,1); perc.labels <- c("SEG_L_LowER","SEG_L","SEG_H")}
  if(contrast>=4 & contrast<=8 ){perc.vals <- c(NA,0.15,0.85)
    perc.labels <- c("SEG_L_LowER","SEG_L","SEG_H")}
  if(contrast>8){perc.vals <- c(0.15,0.25,0.75)
    perc.labels <- c("SEG_L_LowER","SEG_L","SEG_H")}}

```

```

if(method=="ADFG2"){
  if(is.null(meas.error) | is.null(ER)){
    print("ADFG2 %ile Method requires meas.error and ER as high/low"); stop()}
  if(contrast>8 & meas.error=="high"){perc.vals <- c(0.20,0.60); perc.labels <- c("SEG_L","SEG_H")}
  if(contrast>8 & meas.error=="low"){perc.vals <- c(0.15,0.65);perc.labels <- c("SEG_L","SEG_H")}
  if(contrast<=8 ){perc.vals <- c(0.05,0.65); perc.labels <- c("SEG_L","SEG_H")} # 5th %ile? YES
  if(contrast<=4 & meas.error=="high"){perc.vals <- c(NA,NA);perc.labels <- c("SEG_L","SEG_H")
    print("WARNING: ADFG2 %ile Method not applicable (Low contr, high ER)")}
  if(ER=="high"){perc.vals <- c(NA,NA);perc.labels <- c("SEG_L","SEG_H")
    print("WARNING: ADFG2 %ile Method only applicable if ER<40%!")}
}

```

```

matrix.labels <- c("contrast",perc.labels,"min",paste("p",perc.vec*100,sep=""),"max")
out.matrix<- matrix(NA,nrow=length(matrix.labels),ncol=1,dimnames=list(c(matrix.labels), out.label))
out.matrix["contrast",] <- contrast
out.matrix[c("min","max"),] <- c(min(spn,na.rm=TRUE),max(spn,na.rm=TRUE))
out.matrix[perc.labels,] <- quantile(spn,probs=perc.vals,na.rm=TRUE)
out.matrix[paste("p",perc.vec*100,sep=""),] <- quantile(spn,probs=perc.vec,na.rm=TRUE)

```

```
out.matrix
```

```
} # end Percentile.Method
```

```
# ROUNDING SUB FUNCTION AS DESCRIBED IN VOLK ET AL 2009 FMS 09-07
```

```

roundup <- function(x){
  x.out <- signif(x,digits=2) # round to 2 significant figures
  if(x.out<x) { # if it was rounded down, then add 1 to the second sig fig
    x.out <- x.out + as.numeric(paste(1,paste(rep(0,trunc(log10(x)-1)),collapse=""),sep="")) }
  x.out}

```

13.4 REGRESSION (MLE) FIT OF BASIC RICKER MODEL

```
# FUNCTION TO FIT LINEAR FORM OF BASIC RICKER MODEL
```

```

ricker.fit <- function(Rec,Spn,sigma.type="default",var.labels=c("Log(R/S)","Spawners"),bm=TRUE,
  rec.units="Rec",bm.alpha.correct=FALSE){
# Rec = recruits time series // # Spn = spawner time series (any variation: EFS, ETS, TS, Smolts)
# sigma.type = specifies the calculation to be used for sigma. "default" = R default residual sq error
# bm = if TRUE, calculate various population benchmarks
# bm.alpha.correct= if TRUE, use ln(alpha) +(sigma^2/2) instead of ln(alpha)
# rec.units = "Rec" is default, but can also feed in "lnRpS"
# Note: BM code replicates the calculations in a spreadsheet provided by Ed Jones (ADFG)
if(rec.units=="Rec"){lnRpS <- log(Rec/Spn)} # convert to log recruits per spawner
if(rec.units=="lnRpS"){lnRpS <- Rec } # if function input is already in units of ln(Rec/Spn)

fit <- lm(lnRpS~Spn) # fit simple linear regression model
ln.alpha.par <- fit$coefficients[1] # extract intercept
beta.par <- -fit$coefficients[2] # extract slope
if(sigma.type=="default"){sigma.par <- summary(fit)$sigma} # OTHER VARIATIONS TO BE IMPLEMENTED

```

```

if(bm){      Smax.bm <- 1/beta.par
  if(bm.alpha.correct){
    Seq.bm <- (ln.alpha.par + sigma.par^2/2) / beta.par
    Smsy.bm <- (ln.alpha.par + sigma.par^2/2) / beta.par *(0.5-0.07*(ln.alpha.par + sigma.par^2/2))
  }
  if(!bm.alpha.correct){
    Seq.bm <- ln.alpha.par / beta.par
    Smsy.bm <- ln.alpha.par / beta.par *(0.5-0.07*ln.alpha.par)
  }
  Umsy.bm <- Smsy.bm * beta.par
} # end if bm
out.pars <- c(exp(ln.alpha.par),beta.par,sigma.par); names(out.pars) <- c("alpha","beta","sigma")
out.bm<- c(Smax.bm,Seq.bm,Smsy.bm,Umsy.bm); names(out.bm) <- c("Smax","Seq","Smsy","Umsy")
out.list <- list(Model="Ricker", Pars=out.pars, BM=out.bm, sigma.type=sigma.type, var.labels=var.labels,
residuals=fit$residuals) # NOTE: the residuals are in lnRpS not R
out.list
} # end function ricker.fit

```

13.5 MEASURES OF FIT AND PRECISION

Non-parametric Coefficient of Variation (NPCV) = $(p_{69.15}-p_{38.85})/p_{50}$, which is the range that captures roughly the middle third of # the samples divided by median. An estimate is considered precise if NPCV<25% (Clark et al. 2009)

```

npcv.fn <- function(x) {
  x <- na.omit(as.vector(x))
  attributes(x)$na.action <- NULL
  quants <- quantile(x,probs=c(0.6915,0.3885,0.5))
  npcv <- (quants[1] - quants[2]) / quants[3]
  if(sign(min(x))<>sign(max(x))){npcv<-NA} # NPCV only works if sample range doesn't span 0
  npcv
}

```

Standardized Interquartile Range (SIQR)= $(p_{75}-p_{25})/p_{50}$, which is the range that covers the middle half of the samples (i.e. the width of the box in standard boxplots), rescaled by median.

```

siqr.fn <- function(x) {
  x <- na.omit(as.vector(x))
  attributes(x)$na.action <- NULL

```

```
quants <- quantile(x,probs=c(0.75,0.25,0.5))
siqr <- (quants[1] - quants[2]) / quants[3]
if(sign(min(x))<>sign(max(x))){siqr<-NA} # SIQR only works if sample range doesn't span 0
siqr
}
```

Standardized Median Absolute Deviation (SMAD) = median of absolute residuals from median, divided by median.

```
smad.fn <- function(x) {
  x <- na.omit(as.vector(x))
  attributes(x)$na.action <- NULL
  smad <- median(abs(x - median(x)))/median(x)
  smad
}
```