

**Estimation of Chinook Salmon Escapement,
Distribution and Run Timing in the Togiak
River Watershed Using Radio Telemetry,
Togiak National Wildlife Refuge, Alaska, 2010**

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Estimation of Chinook Salmon Escapement, Distribution and Run Timing in the Togiak River Watershed Using Radio Telemetry, Togiak National Wildlife Refuge, Alaska, 2010

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Abstract

Radio telemetry was used to determine distribution and run timing of Chinook salmon *Oncorhynchus tshawytscha* in the Togiak River watershed. Additionally, mark-recapture techniques were employed to estimate Chinook salmon abundance. In 2010, 211 radio transmitters were implanted into Chinook salmon from the lower 5 km of the Togiak River as part of the marking event. A total of 159 fish (75%) were successfully tracked to spawning locations. Twenty-four (12%) had an indeterminate fate, 22 (10%) were harvested, and six (3%) were assigned a fate of dead/regurgitated. Eighty percent ($n = 127$) of the tracked fish selected spawning locations in the mainstem of the Togiak River, and 20% ($n = 32$) selected spawning locations in the tributaries, primarily Gechiak Creek (6%, $n = 9$). A resistance-board weir was installed in Gechiak Creek to serve as the recapture event for the mark-recapture effort. A total of 373 unmarked and 8 marked Chinook salmon were counted through the weir, but a complete enumeration for the season was not possible due to multiple high water events rendering the weir inoperable for multiple days. Six age classes were identified from scales collected in 2010, with the majority of the samples consisting of age 1.3 fish (74% of marked fish and 55% of fish sampled through the weir). Females comprised 55% of the marked fish and 45% of the fish sampled through the weir. Chinook salmon lengths ranged from 455 to 991 mm for marked fish and from 319 to 980 mm for fish sampled through the weir. The spawning population estimate for Chinook salmon greater than 450 mm in length that entered the Togiak River between 22 June and 5 August is 10,096 fish (90% CI = {5,709 ; 18,849}). Simulation modeling suggests that due to differences in run timing between tributary and mainstem spawning populations, the sampling protocol employed may have resulted in differential tagging rates across subpopulations in the overall stock complex for which an abundance estimate was desired, potentially biasing the abundance estimate downward. An alternative tagging protocol is recommended to reduce abundance estimate biases.

Introduction

Chinook salmon *Oncorhynchus tshawytscha* returning to spawn in the Togiak River watershed are harvested in subsistence, sport, and commercial fisheries. The Alaska Department of Fish and Game (ADFG) established a lower bound Sustainable Escapement Goal in the Togiak River watershed of 9,300 Chinook salmon based on aerial surveys (Baker et al. 2006). This goal has been regularly achieved since 1996, mainly through regulation of the commercial fishery (Sands et al. 2008). Average estimated Chinook salmon spawning escapement from 1996 to 2005 was 11,862 fish, and average harvest was 11,273 fish, representing a 49% exploitation rate. The harvest includes 9,213 fish harvested in the commercial fishery, 902 harvested in the sport fishery, and 1,158 harvested in the subsistence fishery (Sands et al. 2008).

Current monitoring of Chinook salmon escapement into the Togiak River watershed is limited to aerial surveys. Total escapement is estimated by expanding visual counts with correction factors. The accuracy of aerial survey counts is greatly affected by stream life, variable run timing, observer efficiency, weather, water conditions, aircraft characteristics (type, speed, altitude, and pilot experience), and other factors (Bue et al. 1998). Aerial survey estimates within the Togiak River watershed have not been verified or compared with other methods, and the accuracy with which the observations index actual abundance is unknown. Aerial survey efforts have been scaled back since 2005, and Chinook salmon total escapement estimates have not been calculated (Salomone et al. 2009). The Office of Subsistence Management, through its strategic planning process, has identified a need to obtain reliable escapement estimates for Chinook salmon in the Togiak River (OSM 2005). The Bristol Bay Regional Advisory Council has voiced support for this need since 2003, and development of a reliable estimate of Chinook salmon escapement into the Togiak River was explicitly requested in the 2008, 2010 and 2012 Request for Proposals for the Fisheries Resource Monitoring Program. Improving long-term escapement monitoring of all species of adult Pacific salmon in the Togiak River has been a top priority issue with the Togiak National Wildlife Refuge, Togiak Traditional Council, and ADFG. Accurate monitoring of Chinook salmon abundance is needed to ensure that adequate escapements are achieved so that healthy Chinook salmon populations are sustained and subsistence harvests and other needs are maintained.

Subsistence harvest and Chinook salmon spawning and rearing habitat in the Togiak River occur within the Federal Conservation System boundaries of the Togiak National Wildlife Refuge. Providing a harvest priority to subsistence users in these waters is mandated under Title VIII of ANILCA.

This is the second year of a three-year radio telemetry study to estimate Chinook salmon abundance in the Togiak River watershed.

Objectives for the project were:

1. estimate the proportion of Chinook salmon migrating past a weir on Gechiak Creek;
2. estimate the abundance of Chinook salmon escaping into the Togiak River watershed such that the estimate will have a 90% probability of being within 25% of the true abundance;
3. estimate the weekly age and sex composition of spawning Chinook salmon in Gechiak Creek, such that simultaneous 90% confidence intervals have a maximum width of 0.20;
4. estimate the mean length of Chinook salmon by sex and age; and
5. document Chinook salmon spawning locations in the Togiak River watershed.
6. evaluate the effectiveness of aerial spawning ground surveys for monitoring Chinook salmon abundance in the Togiak River watershed; and
7. measure and document water temperature throughout the main stem and lower tributaries in the Togiak River watershed.

Objective 6 could not be met in 2010 due to poor flying conditions and limited aircraft availability, which did not allow ADFG staff to obtain aerial counts and calculate an abundance estimate. Objective 7 was the responsibility of Bristol Bay Native Association, and will be reported separately.

Study Area

The Togiak River is located in southwest Alaska and lies within the Togiak National Wildlife Refuge (Figure 1). The watershed encompasses 5,178 km², comprises nine major lakes and five major tributaries, and is bounded on the east by the Wood River Mountains and on the west by the Ahklun Mountains. The Togiak River originates at the outlet of Togiak Lake and flows 93 km to Togiak Bay. The watershed upstream of Pungokebuk Creek is part of a congressionally designated Wilderness Area. Detailed descriptions of the lakes and tributaries can be found in the Togiak Refuge Fisheries Management Plan (USFWS 1990).

Five species of Pacific salmon *Oncorhynchus* spp. are found in the Togiak River watershed along with rainbow smelt *Osmerus mordax*, rainbow trout *O. mykiss*, Dolly Varden *Salvelinus malma*, Arctic char *S. alpinus* and Arctic grayling *Thymallus arcticus* (USFWS 1990).

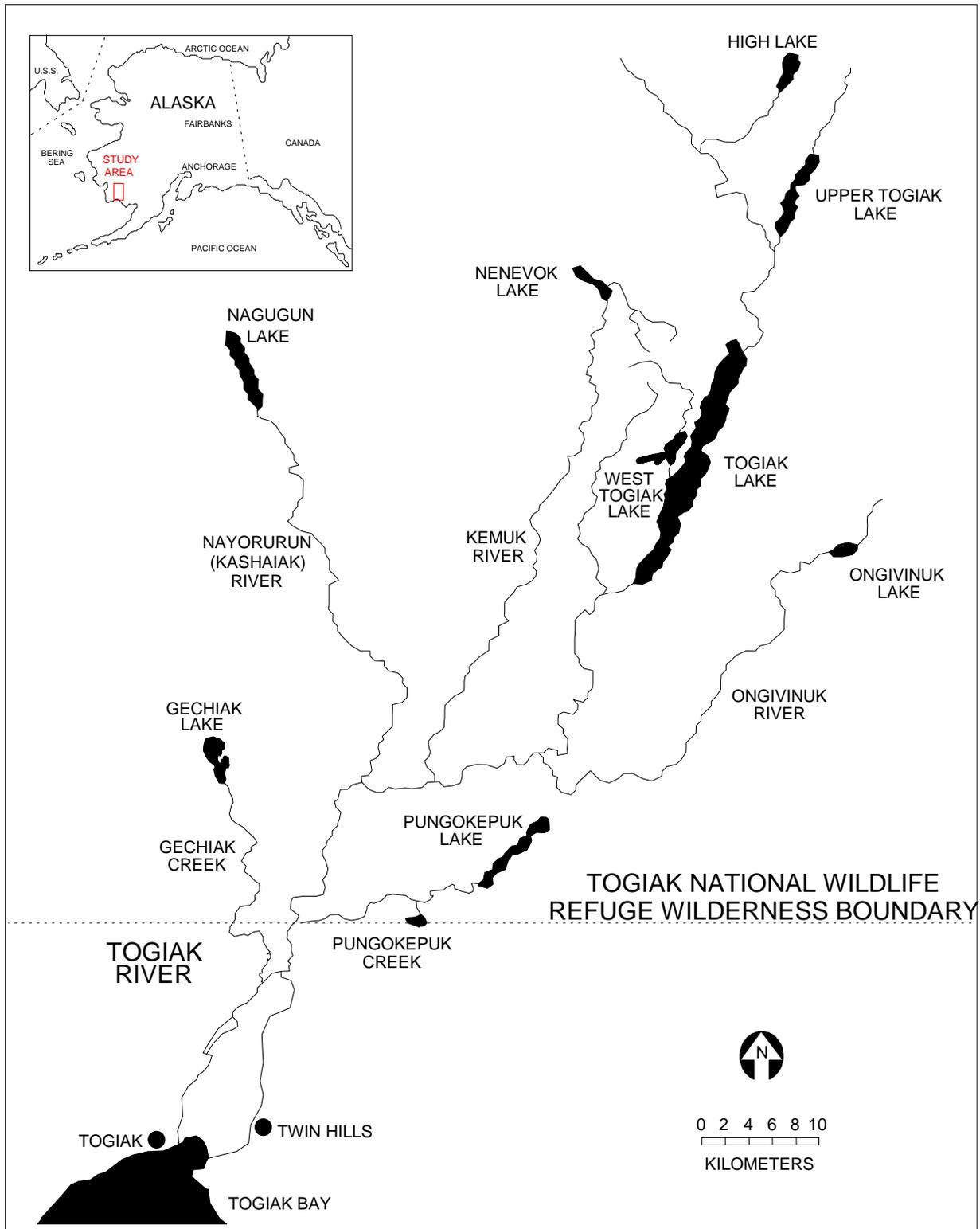


Figure 1. Map of the Togiak River watershed in Southwest Alaska.

Methods

A radio telemetry experiment was conducted to estimate the abundance, distribution and run timing of Chinook salmon in the Togiak River watershed. Fish were captured and marked with radio transmitters in the lower 5 km of the mainstem. A resistance-board weir was installed in Gechiak Creek to enumerate fish passage and to obtain a proportion of marked to unmarked Chinook salmon. Movements and final spawning destinations of radio tagged fish were documented using a combination of fixed data logging receiver stations and aerial- and ground-based mobile tracking.

Mark-Recapture Procedures

Marking Event.---A three person crew fished a drift gillnet (18.3 m long, 4.6 m deep, 20.3 cm stretched mesh size), with one crew member piloting the boat and the other two positioned in the bow tending the net. The gillnet was deployed from the bow of the boat, and the boat motor was idled in reverse to keep the net perpendicular to the shore while drifting downstream in the center or deepest sections of the river. Each sampling area is less than 1 km in length, and fishing continued until the end of the area was reached or a fish became entangled in the net. Drift time was monitored and recorded with a stopwatch. All fish except Chinook salmon caught in the net were identified to species, counted and immediately released. Statistical weeks defining temporal strata were used for sampling (Table 1). Sampling was conducted until the radio transmitter allocation was reached.

Table 1. Allocation schedule for Chinook salmon radio transmitters in the Togiak River, 2010.

Strata Dates	Radio Transmitter Allocation
20 June – 3 July	45
4 – 10 July	45
11 – 17 July	45
18 – 24 July	45
25 July – 7 August	20
<i>Total</i>	200

Chinook salmon longer than 450 mm (mid-eye to tail fork) were tagged with radio transmitters manufactured by Advanced Telemetry Systems, Incorporated[®] (ATS; Model No. F1840B). Transmitters were encapsulated in a biologically inert polypropylene copolymer and equipped with a stainless steel nylon coated whip antenna. Transmitters weighed 22 g, which never exceeded 2% of the fish's body weight (Winter 1983). Radio transmitters were implanted through the esophagus using a plunger as described by Burger et al. (1985). Two hundred radio tags with unique pulse-codes were dispersed over sixteen radio frequencies between 163.3 and 164.0 MHz and each frequency had from 3 to 26 different codes. The combination of codes on each frequency allowed for the identification of individual fish. A mortality code was transmitted after 8 hours of inactivity. In addition to the radio tags, 30.5 cm serially numbered spaghetti tags (Floy Tag and Manufacturing, Inc.; Model No. FT-4) in international orange color were applied near the rear base of the dorsal fin between the interneural bones using a hollow

needle. The tag was secured to the back of the fish with a Nico press sleeve, and served as a highly visible secondary mark.

Efforts were made to minimize stress to Chinook salmon during capture and handling. Captured fish were removed from gillnets as quickly as possible, and gillnet meshes were cut if the fish could not be easily removed from the net. Chinook salmon were then placed in a padded tagging cradle alongside the boat to allow the fish to be processed without removal from the water. The general health and appearance of each fish was recorded and injured or severely stressed fish were not tagged. Radio tagged Chinook salmon were immediately released into the river after tagging. Total handling time for each tagged fish was about two minutes or less.

The assumptions used for calculating sample size were that: 1) capture and tagging of Chinook salmon did not change their ultimate spawning locations, 2) fish destined for the various spawning locations had an equal probability of capture within each stratum, and 3) tagged fish behaved independently. The binomial probability distribution (Johnson et al. 1992) provided a useful model based on these assumptions, and allowed determination of the number of Chinook salmon that had to be observed at a particular spawning location to satisfy the statistical criteria specified in Objective 3. Prior to the season, 20 to 45 radio transmitters were allocated to each of five tagging strata (Table 1).

Radio transmitters were deployed over the shortest time period possible within each stratum. This was the most efficient deployment strategy given our limited knowledge of the abundance and run timing of Chinook salmon in the Togiak River. Tagging fish as quickly as the field crew could capture them increased the likelihood that all tags could be deployed within each stratum, and if fewer than the allotted tags were deployed in a particular stratum, the crew attempted to deploy the remaining tags in the subsequent stratum.

Recapture Event---A resistor board weir (Tobin 1994; Stewart 2002) was installed in Gechiak Creek (59.2218°N, 160.25049°W), approximately 2 rkm upstream from Togiak River. Weir panels were constructed of 2.5 cm inside-diameter schedule 40 polyvinyl chloride electrical conduit. Resistor boards were attached to each panel to aid floatation. Panel dimensions were 5.8 m long by 0.9 m wide with 7.62 cm center to center picket spacing. The panels were attached to the substrate by way of a steel substrate rail and a 10 mm cable running from bank to bank (Figure 2). An apron of 1.2 m mesh chain link fence served to stabilize the substrate and acted as a barrier to fish passage beneath the rail. A fish passage panel designed as a chute was positioned near the deepest part of the channel, allowing fish to pass into a live trap to facilitate biological sampling and passing adult salmon through the weir. Two panels positioned in the thalweg of the creek allowed for boat passage. The boat passage panels were marked with orange buoys on either side, and were not maintained with their resistor boards deployed.

The weir served to recapture radio tagged fish marked in the lower river and to enumerate all fish moving up the creek. Fish were counted intermittently throughout the daylight hours from roughly 0600 through to 2400 hours. The duration of each counting session varied depending on the number of fish arriving at the weir. A contrasting substrate was placed on the stream bottom in front of the counting panel to enhance visibility of fish and to facilitate species identification as they were passed through the counting panel. For the hours the weir went unmanned, the live trap was closed to passage. The weir was cleaned of debris and inspected daily for integrity. Repairs were made as needed.



Figure 2. A resistor-board weir installed in Gechiak Creek, 2010. A remote telemetry station was co-located on top of the bluff .

Biological sampling--- For all Chinook salmon radio tagged in the marking event, length was measured to the nearest mm (mid-eye to fork of tail) and sex was determined from external characteristics (Mecklenburg et al. 2002). Three scales from the preferred area on the left side of each fish (Jearld 1983) were removed, cleaned, and mounted on gummed scale cards. After the field season, scale impressions from the gum cards were made on acetate blanks using a heated hydraulic press. Scale impressions were viewed with a microfiche reader and aged using standards and guidelines of Mosher (1968). Ages were reported according to the European method described by Jearld (1983) and Mosher (1968), where the number of winters the fish spent in fresh water and in the ocean are separated by a decimal. Fish with scales that could not be aged were not included in the age analyses.

Chinook salmon passing through the weir at the recapture event were sampled for age, sex, and length (ASL) data using a temporally stratified sampling design (Cochran 1977), with statistical weeks defining strata. A sample of 155 fish was drawn weekly for ASL information. If run strength was not sufficient for the weekly sampling goal to be reached, about 20% of the weekly escapement was sampled. Samples were dispersed throughout the week and taken periodically during the day. All fish within the trap were included in the sample to avoid potential bias caused by the selection or capture of individual fish, even if the target number of fish was exceeded. Non-target fishes captured in the live trap were identified to species, enumerated, and

released above the weir. Lastly, tissue samples were collected from the axillary process. These samples were archived for later genetic analysis.

Data Analysis

Radio telemetry tracking methods---Radio tagged Chinook salmon were tracked throughout the Togiak River watershed using a combination of six fixed monitoring stations (Table 2; Figure 3) and mobile tracking from boats and fixed-wing aircraft. Four of the fixed monitoring stations were located on the mainstem, and two were located on tributaries. One station was co-located at the field camp site and weir on Gechiak Creek, and the other station was located approximately 1 km upstream from the Nayorurun River mouth. The first fixed station on the mainstem was placed above the capture and tag deployment site to help delineate lower mainstem spawning locations. This was done because tracking results from 2008 raised the concern that capture and tag deployment activities may have occurred in spawning areas.

Fixed monitoring stations were used to record up and downstream movement of individual tagged fish. Each fixed station included a single receiver-datalogger (ATS model R4500C or R4520C), a single 4-element Yagi antenna, antenna mast, 12-volt deep cycle battery, solar panel, voltage regulator, and strongbox. Data from fixed receiver stations were downloaded weekly to a notebook computer.

Aerial surveys were used to identify specific spawning locations in the Togiak River and its tributaries. Aerial surveys were conducted from a fixed-wing aircraft equipped with an H-antenna mounted on each wing strut. Aerial surveys were flown at altitudes of approximately 100–400 m above ground along the Togiak River and its tributaries. A global positioning system (GPS) built in to the receiver-datalogger (ATS model R4500C or R4520C) was used during aerial surveys to record latitude and longitude coordinates of each transmitter located.

Boat surveys were used to more precisely locate spawning in the mainstem Togiak River. Boat surveys were conducted using a portable receiver-datalogger (ATS model R4500C or R4520C) and a 4-element Yagi antenna. A hand held GPS was used during boat surveys to record latitude and longitude coordinates for each transmitter located.

Table 2. Names and locations (decimal degrees) of fixed telemetry stations in the Togiak River watershed, 2010.

Station Name	Latitude	Longitude
Entry	59.11683	-160.35385
Second	59.18333	-160.27858
Gechiak	59.22188	-160.25049
Ranger	59.26767	-160.20892
Nayorurun	59.37212	-160.09810
Kemuk	59.36909	-159.98770

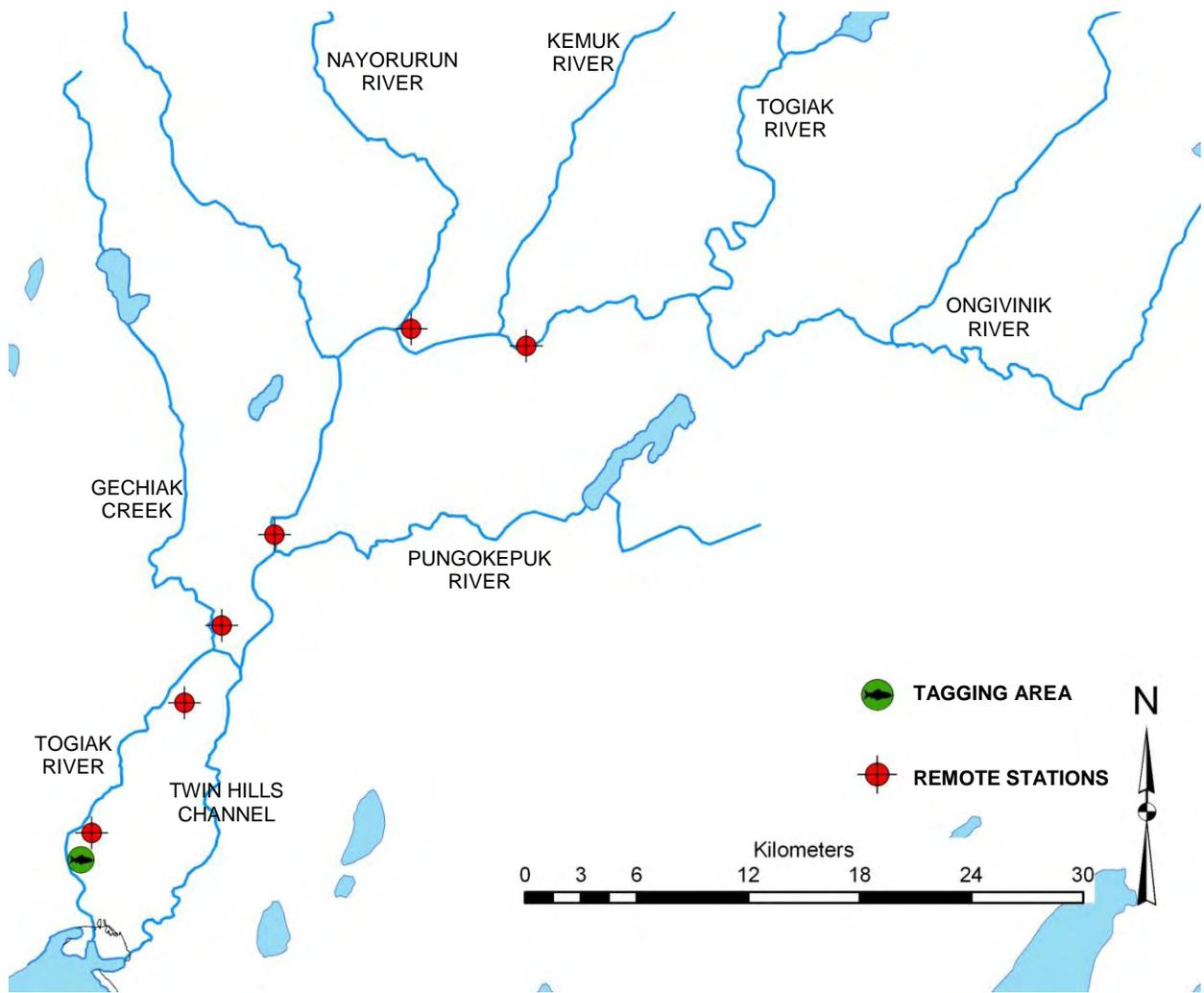


Figure 3. Remote data logging receiver station locations and tagging area in the Togiak River, 2010.

Radio telemetry data interpretation---Each radio tagged Chinook salmon was assigned one of six possible fates based on information collected from mobile and fixed receivers (Table 3). Fish whose spawning locations could be identified based on tracking results were assigned a fate of either mainstem or tributary spawner. Mainstem spawners were assigned to one of six river sections (Figure 4). The boundaries of these (A-F) corresponded with aerial survey segments used by ADFG (Brookover et al. 1996). Tributary spawners were assigned to one of six tributaries. In addition to the tributary survey areas designated by ADFG, in 2010 we added the Twin Hills Channel as a possible spawning tributary. Chinook salmon whose spawning location could not be determined with reasonable certainty were placed into an unknown category. The unknown category was further divided into two groups: fish that were unsuccessfully located post-tagging; and fish that were successfully tracked within the system, but disappeared after at least two to three weeks of movement. Fish assigned a fate of harvested or dead/regurgitated were censored from the sample.

Table 3. Fate of Chinook salmon radio-tagged in the Togiak River, 2010.

Fate	Description
<i>Spawning Location:</i>	
Mainstem (1 of 6 river sections)	A fish that spawned in Togiak River.
Tributary (1 of 6 tributaries)	A fish that spawned in a tributary of the Togiak River.
<i>Unknown Fate:</i>	
Insufficient location information	A fish that could not be located by either fixed or mobile telemetry tracking.
Suspected harvest	A fish that was tracked to multiple locations over a 2-4 week period before disappearing from the system.
<i>Removed From Study:</i>	
Harvested	A fish that was harvested in either the commercial, sport, or subsistence fisheries.
Dead/Regurgitated	A fish that did not complete its spawning migration because it either died or regurgitated its radio tag.

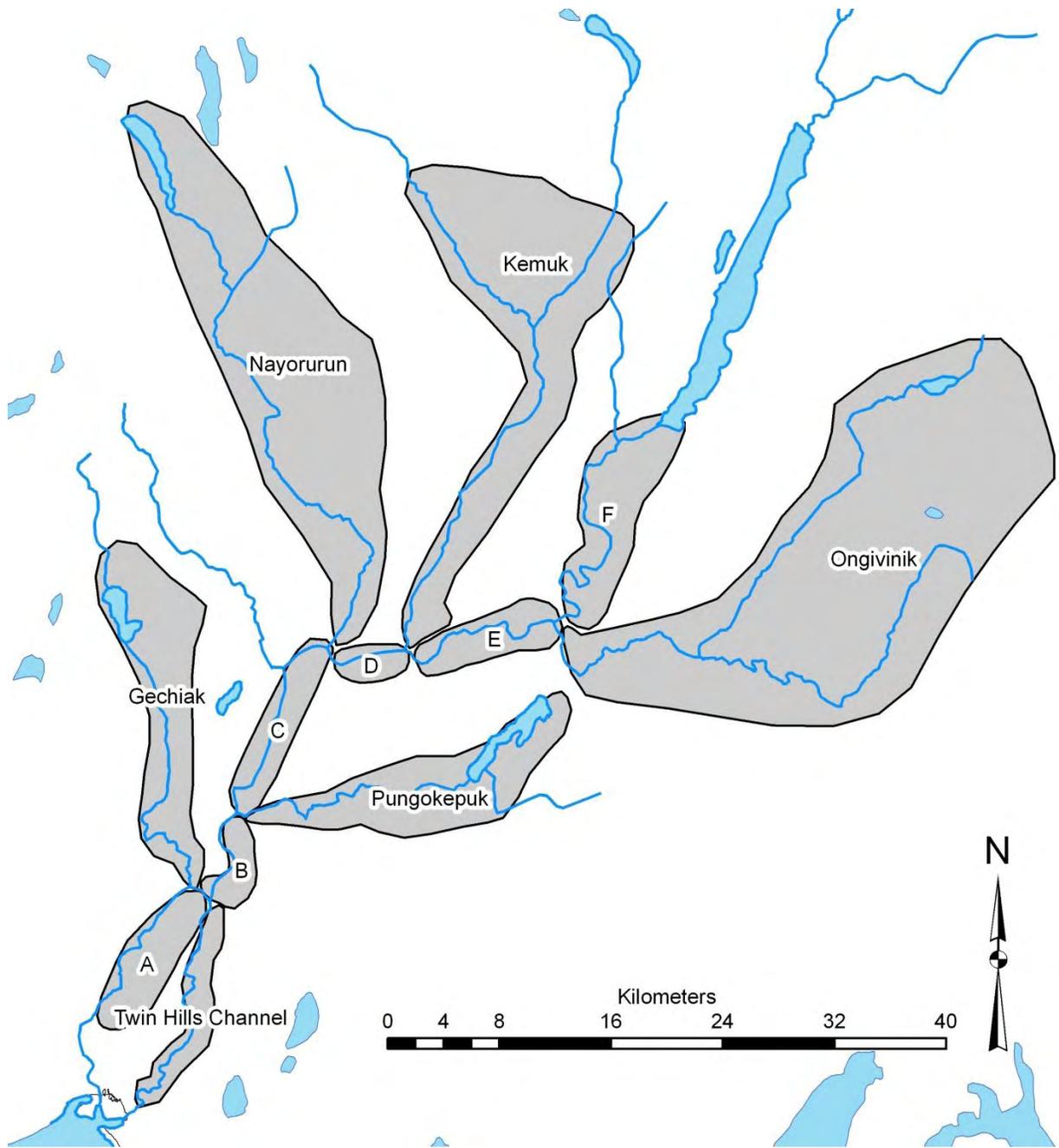


Figure 4. Mainstem river sections corresponding to ADFG aerial survey delineations and tributary fates assigned to radio tagged Chinook salmon in the Togiak River, 2010. The exception is the Twin Hills Channel, which was designated as a possible spawning fate for the first time in 2010.

Spawning abundance estimation and simulation--- Chinook salmon were marked at one tagging site over seven weeks, and systematically recaptured at another site over a period of several weeks. However, the data were treated as a single release and recapture event and analyzed using a single release, single recapture closed population abundance estimator, which is the classic Lincoln-Petersen type estimator (e.g. Krebs 1998). Seber (1982) suggested using the Chapman variant of the Lincoln Peterson estimator to reduce bias when sample and population sizes are small. This estimator is built upon a formal likelihood model using the hypergeometric distribution and is based on sampling without replacement to mark individuals. A Chapman abundance estimate, N , was calculated as:

$$N = \frac{(n_1 + 1)(n_2 + 1)}{(m_2 + 1)} - 1$$

where n_1 is the number of Chinook salmon tagged and released at the tagging site over all time strata, n_2 is the number of Chinook salmon counted passing the Gechiak Creek weir (the recapture event), and m_2 is the number of Chinook salmon captured at the weir that were found to be marked. The sampling distribution of the Chapman estimator is approximately normally distributed for large sample sizes, but Krebs (1998) suggested that in some cases, depending upon the number of marked and recaptured individuals, the Poisson and Binomial distributions provide better approximations. An “accurate” approximation of the sampling distribution of the Chapman abundance estimate is necessary to get $\alpha\%$ confidence intervals that correctly brackets the true population abundance estimate with probability equal to α . Following Krebs (1998), because the fraction of marked recaptures (m_2/n_2) was less than 0.1 and the number of recaptures was < 50 , the Poisson distribution was used to model m_2 and to approximate the sampling distribution of the Chapman estimator for confidence interval construction. To construct a confidence interval, the *pois.exact* function in the R statistical programming language (R Development Core Team 2010) package *epitools* (Aragon 2010) was used to calculate a confidence interval for m_2 , which was then substituted into the Chapman abundance estimator to calculate a confidence interval for N . For comparisons, we also computed confidence intervals using two other methods: 1) a parametric bootstrap routine with 100,000 bootstrap samples from a hypergeometric distributed Chapman abundance estimator, and 2) a naive normal approximation to the sampling distribution of N using Chapman’s approximate formula for the variance of N (Seber 1982)

Lincoln-Petersen estimators rely on the following assumptions (e.g. Pollock et al. 1990):

1. the population is closed (no additions or deletions);
2. marks are not lost or misidentified;
3. all animals are equally likely to be captured at each sampling occasion.

If these assumptions are satisfied, then the Lincoln-Petersen estimator for population abundance will be unbiased for large samples and populations; otherwise, the Chapman variant is more robust for small samples and populations. For this study, both assumptions 1 and 2 appear to be valid, while assumption 3 may not be. We felt the population can be treated as closed because 1) Togiak River has only one entrance, so all Chinook salmon entering the river must pass the tagging site; 2) Chinook salmon are anadromous and semelparous, so additions to the population

prior to and after the study period were not a concern as long as tagging spanned the run duration; 3) while some salmon may die after passing the tagging site, we thought tagging-induced mortality would be low (and could be monitored) and that mortality would be randomly distributed throughout the marked and unmarked population. We felt that tag loss and misidentification would be negligible with the methods used for this study, and we were able to track the fate of all tagged individuals to determine this. We thought it was most likely that Assumption 3 would be violated, resulting in biased abundance estimates, and much of the closed-population literature deals with the problem of heterogeneous probability of capture (e.g. Otis et al. 1978, Pollock et al. 1990).

There are at least two processes by which this study's marking and recapture design could introduce heterogeneous capture probabilities either at the tagging site, the recapture site (Gechiak Creek weir) or both. First, gillnet gear was used to collect Chinook salmon for tagging, and this gear is size selective. The gill net mesh size used will only capture a certain size segment of the population. Fish larger than this segment cannot become enmeshed and escape capture (unless they become tangled), while fish smaller than this segment pass through the meshes. Therefore, very large and very small individuals would not be included in the tagged population. However, using different gear for the recapture event that either has different or no selectivity would tend to make resulting population estimates unbiased. Our recapture event was essentially a census, since all fish passing the weir, regardless of size, were sampled for tags when the weir was operated. Thus, the capture probability heterogeneity imposed by the gillnet gear during tagging was not the same as that imposed by our recapture methods.

The second potential source of capture heterogeneity was differential run timing of the various spawning populations within the total Chinook salmon run. To examine this problem, we conducted two analyses. First, we constructed tests for differences in run timing among populations. Similarity in run timing provides indirect support to the assumption that tributary and main stem populations were mixed at the tagging site, which reduces the potential for heterogeneous capture probabilities. Run timing curves were not available for the Togiak Chinook salmon run because escapement counts for populations other than the Gechiak Creek population were unavailable and counts at the Gechiak Creek weir were incomplete. However, some run timing information was available from the fate of radio-telemetry tagged individuals. Two methods were used to examine this using R-code (Appendices 3 and 4).

First, we constructed four different tests using a contingency table approach and computed either Chi Square or Fisher exact goodness of fit tests (Sokal and Rolf 1994) to examine the following questions:

1. Are there differences in the run timing between pooled tributary and pooled mainstem populations (H_0 : There is no difference in run timing between tributary and mainstem spawners)?
2. Are there differences in the run timing amongst the tributary subpopulations (H_0 : There is no difference in run timing between tributary subpopulations)?
3. Are there differences in the run timing amongst the mainstem subpopulations (H_0 : There is no difference in run timing between mainstem subpopulations)?
4. Are there differences in the run timing between the Gechiak subpopulation and the pooled "rest-of-river" population (H_0 : There is no difference in run timing between the Gechiak tributary subpopulation and the rest-of-river population)?

R code to run these tests is presented in Appendix 3.

Second, we constructed a simulation model, to understand how differences in run timing among up to three populations (two tributaries and “rest-of-river”) can affect the Lincoln-Petersen (or Chapman variant) abundance estimation under a sampling design similar to the one used in this study: one marking area (mouth of the Togiak mainstem) and a systematic recapture sample (Gechiak Creek weir). Results were used to identify the direction of any bias from plausible run timing scenarios relevant to this study and determine whether the selection of tagging or recapture protocols could be used to reduce the bias. The simulation model contained the following elements:

1. The run of interest, for which an abundance estimate is sought, is comprised of up to three populations.
2. Run timing for each population is modeled as a normal curve and timing parameters could be changed to result in:
 - a) complete mixing of populations in the tagging area (populations have identical run timing curves),
 - b) no mixing in tagging area (populations have run timing curves that do not overlap), or
 - c) incomplete mixing in tagging area (populations have run timing curves that partially overlap).
3. Tag release rates and absolute numbers of tag released could be modeled as constant or varying across populations and time, and the number and timing of tagging events was controllable.
4. Sampling within the model for marking and recapture could be simulated as deterministic or probabilistic through binomial or multinomial sampling processes, and random error for specific tag rates could be varied to simulate random variations in gear efficiency or other effects.
5. The following parameters were used as inputs : individual population abundance (the sum of which was total run size), individual population run timing and compression parameters, number of and timing of tagging strata, tagging rates per stratum or numbers of tag released per stratum, choice of deterministic or probabilistic sampling processes, and random error level, if any, imposed on tagging.

Simulations were run under two different tagging release protocols and three different run timing scenarios to identify potential biases for 2010 Togiak field data and to determine whether changes to the tagging protocol were needed for future years. We populated the model with a single tributary population run of 400 fish to represent the Gechiak Creek population and a rest-of-river run of 10,000 fish. Two tagging release simulations were tested: set tag releases and tagging in proportion to abundance. In both simulations, the same approximate total number of tags was released over five tagging strata. Similar to our study, we used about 210 total tags, which corresponded to a population tagging rate of about 2% for the model. In simulations examining set tag releases, which mirrored realized tagging outcomes in the 2010 Togiak field season, a set number of tags were released in each of five tagging strata (Table 14). In simulations examining tagging in proportion to abundance, which resulted in different numbers of tags being released in each tagging stratum, we used a constant tagging rate of 6% of fish available per stratum. Run timing tests suggested that tributary populations may have earlier run timing than main stem spawners. Thus, there is some suggestion that the Gechiak Creek population has either similar or slightly earlier run timing through the tagging area compared to

the rest-of-river population, which would be comprised mostly of mainstem spawners. To account for possible differences in run timing that went undetected, we simulated complete mixing of a tributary and rest-of-river population on the tagging grounds as well as low-levels of run timing differences. Tributary run timing was varied by +/- half a stratum, representing a run-peak timing difference of about +/- four days. For this analysis, we constrained all tagging and recapture events to be deterministic and did not include random error on tagging rates. This allowed specified tagging rates to represent proportions of the available populations that were tagged, weir counts to represent a complete census, and tag recovery to represent all tagged fish that entered the tributary.

Results

Gillnet sampling for Chinook salmon was conducted over a total of 43 hours between 22 June and 7 August, and a total of 260 Chinook salmon were captured between 22 June and 5 August (Figure 5). The highest total catches occurred on 7 and 18 July when 21 and 30, respectively, Chinook salmon were caught. Eleven Chinook salmon were damaged in the gill net sufficient to result in gill bleeding. These injured fish were not marked. Other species captured included chum *O. keta* ($n = 38$) and sockeye *O. nerka* ($n = 56$) salmon, rainbow trout ($n = 2$), and Dolly Varden/Arctic char ($n = 10$).

Four age classes of Chinook salmon were expected to occur in the Togiak River run (1.2, 1.3, 1.4, and 1.5), although only two of these (1.3 and 1.4) were expected to comprise the majority of the run.

From the marking event in the lower Togiak River, age data were obtained from 212 Chinook salmon, of which 25 (11%) fish could not be aged because of illegible or regenerated scales. Six age classes were present in 2010, with age 1.3 (74%), and 1.4 (12%) comprising 86% of the sample (Table 4). Sex was determined for 197 Chinook salmon, and 15 of the fish sampled could not be sexed using secondary sexual characteristics. Females comprised 55% of Chinook salmon sampled (Table 5; Figure 6). Lengths were measured from 212 Chinook salmon, and lengths ranged from 699 to 991 mm for females and 455 to 900 mm for males (Table 6).

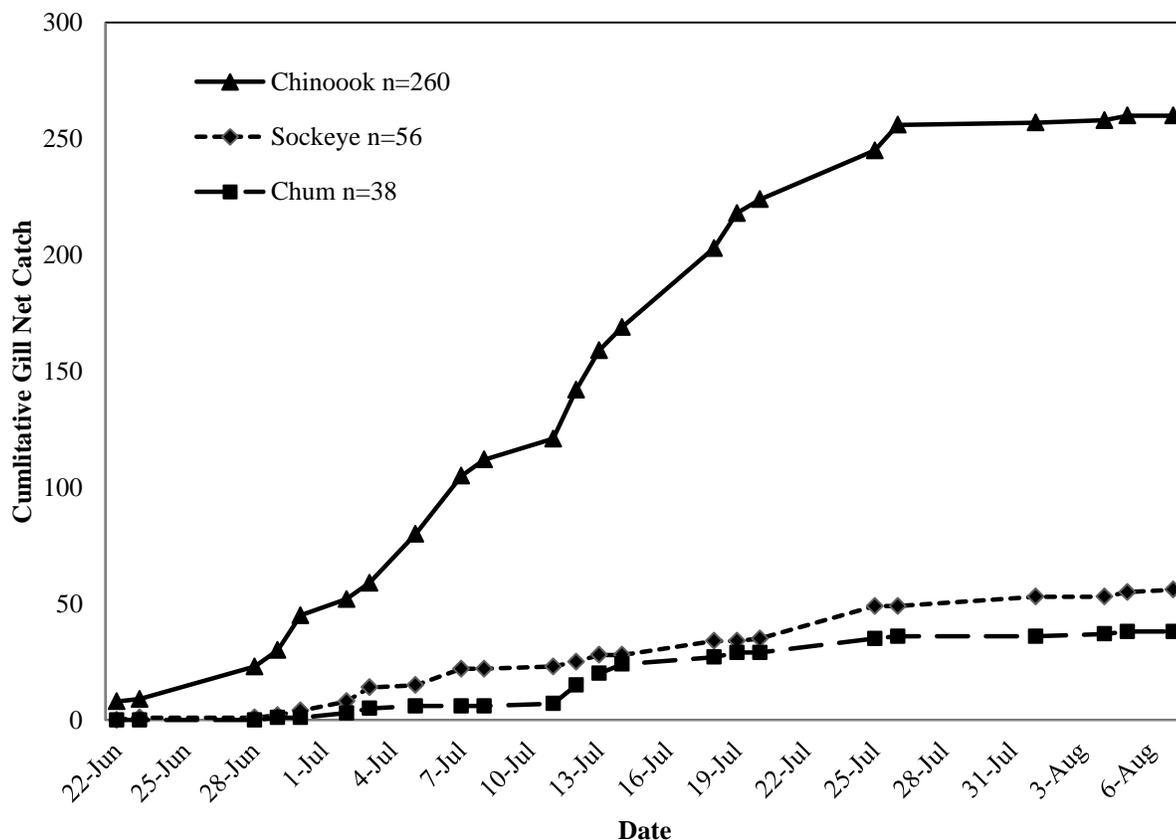


Figure 5. Cumulative total catch of Chinook, sockeye, and chum salmon caught by gillnet in the lower Togiak River, 2010.

Table 4. Age composition of Chinook salmon radio tagged in the lower Togiak River, 2010.

Age	<i>n</i>	%	SE(%)
1.2	17	9	0.02
1.3	138	74	0.03
1.4	22	12	0.02
2.1	1	1	0.01
2.2	3	2	0.01
2.3	6	3	0.01
Total ^a	187	100	

^aTotal number sampled does not include fish whose age could not be determined (*n*=25).

Table 5. Sex composition of Chinook salmon radio tagged in the lower Togiak River, 2010.

Sex	<i>n</i>	%	SE(%)
Female	108	55	0.04
Male	89	45	0.04
Total ^a	197	100	

^aTotal number sampled does not include fish whose sex could not be determined (*n*=15).

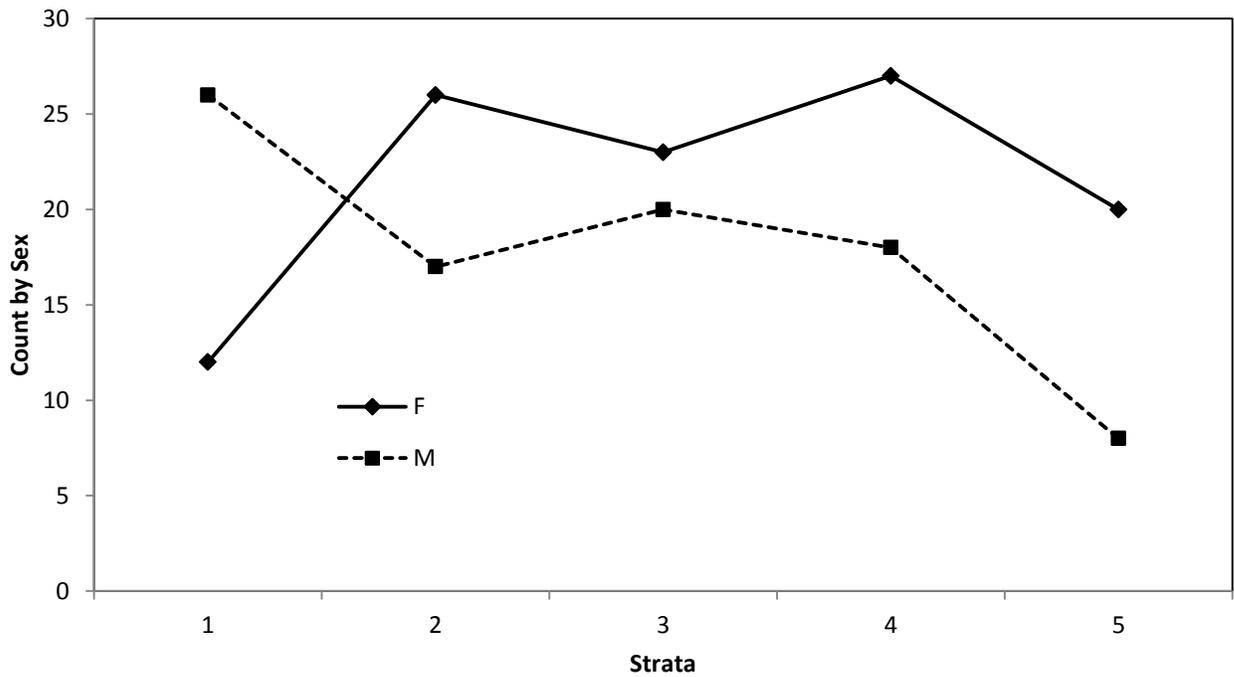


Figure 6. Sex composition of Chinook salmon radio tagged in the lower Togiak River, 2010, by strata. Total: Female *n*=108; Male *n*=89; Unknown Sex *n*=15.

Table 6. Mean length (mm), SE, range, and sample size by age of Chinook salmon radio tagged in the lower Togiak River, 2010.

Length	Age Class					
	1.2	1.3	1.4	2.1	2.2	2.3
Mean	716	816	862	860	758	819
SE	31	4	14	-	49	31
Minimum	455	690	750	860	670	734
Maximum	870	973	991	860	840	940
<i>n</i>	17	138	22	1	3	6

^aNumber sampled does not include fish whose length and age could not be determined (*n*=25).

The resistance-board weir was installed in Gechiak Creek on 27 June. Daily operations began at 0600 hours on 28 June. Multiple high water events occurred throughout the summer, causing disruption in weir operation. The weir was deemed to be either unsafe to operate or not fish tight from 30 July through 3 August; 10 – 11 August; and from 15 August until the water levels were low enough to pull the weir at the end of the field season.

In total, 381 Chinook salmon were counted through the weir, with the highest daily count occurring on 29 July (Appendix 1). Of the 381 Chinook salmon enumerated, 373 were unmarked and 8 were radio tagged. Other species captured included Coho *O. kisutch* (*n* = 127), chum (*n* = 15,097), and sockeye (*n* = 11,131) salmon (Figure 7), rainbow trout (*n* = 44), and Dolly Varden/Arctic char (*n* = 779), whitefish (*n* = 5), and Arctic grayling (*n* = 1). An additional 83 fish were counted through the weir that were not identified. The whitefish counted through the weir were not all identified to species; however, one of the whitefish counted was identified as a round whitefish *Prosopium cylindraceum*.

From the recapture event in Gechiak Creek, age data were obtained from 92 unmarked Chinook salmon sampled from the weir, of which 9 (1%) fish could not be aged because of illegible or regenerated scales. Seven age classes were present in 2010, with ages 1.3 (55%) and 1.2 (13%) comprising 68% of the sample (Table 7). Sex was determined for 91 Chinook salmon, and 2 of these could not be sexed using secondary sexual characteristics. Females comprised 45% of Chinook salmon sampled (Table 8; Figure 8). Lengths were measured from 92 Chinook salmon, and lengths ranged from 703 to 980 mm for females and 319 to 734 mm for males (Table 9).

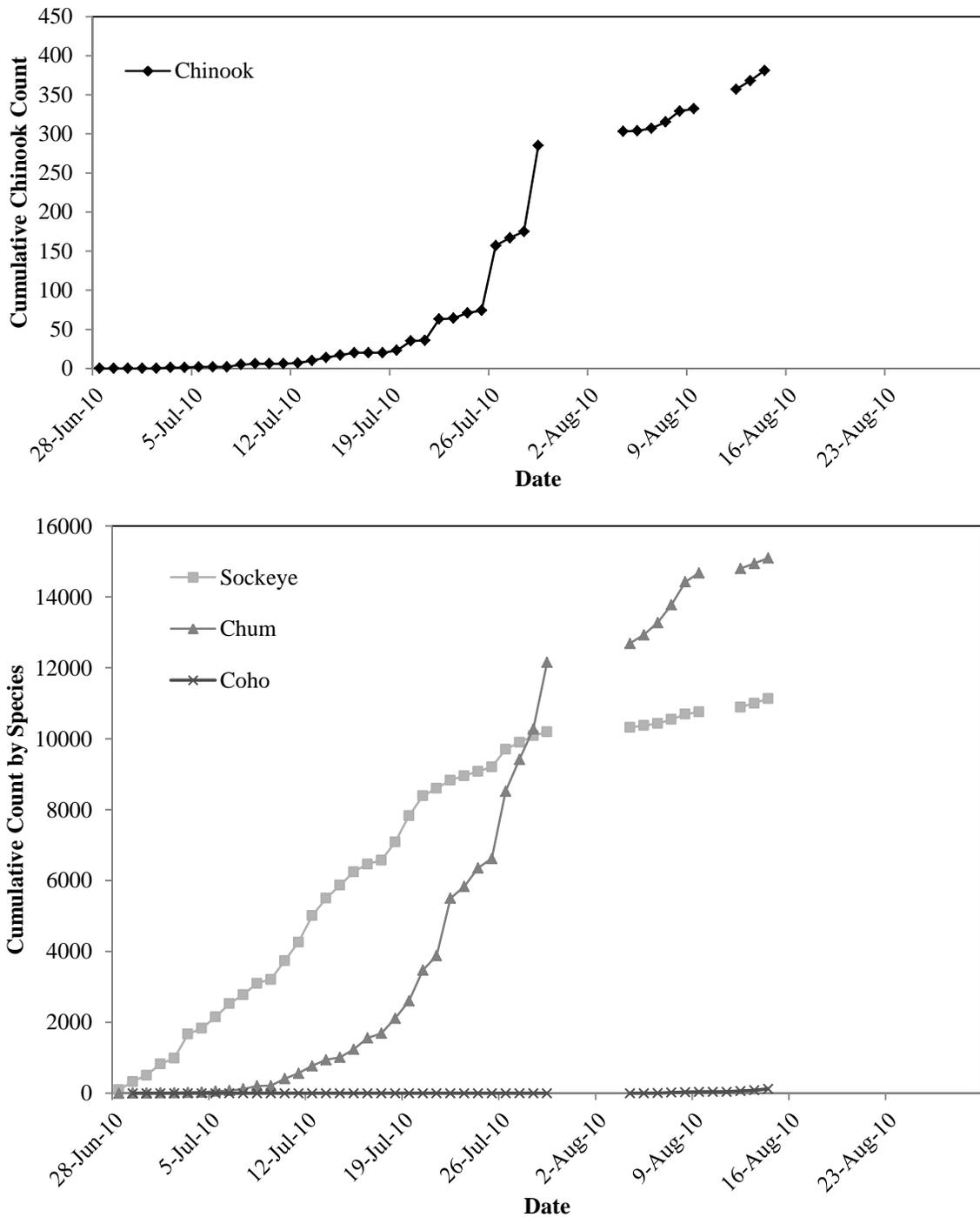


Figure 7. Cumulative count of Chinook salmon ($n=381$) counted through the Gechiak Creek weir (top) and cumulative count of sockeye ($n=11,131$), chum ($n=15,097$), and coho ($n=127$) salmon counted through the Gechiak Creek weir by species (bottom), 2010. Breaks in data series indicate dates the weir was inoperable due to high water.

Table 7. Age composition of unmarked Chinook salmon sampled through the Gechiak Creek weir, 2010.

Age	<i>n</i>	%	SE (%)
1.1	5	6	2.6
1.2	13	15	4.0
1.3	46	55	5.5
1.4	12	14	3.8
2.1	4	5	2.3
2.2	1	1	1.2
2.3	3	4	2.0
Total ^a	84	100	

^aTotal number sampled does not include fish whose age could not be determined (*n*=9).

Table 8. Sex composition of unmarked Chinook salmon sampled through the Gechiak Creek weir, 2010.

Sex	<i>n</i>	%	SE(%)
Female	41	45	5.2
Male	50	55	5.2
Total ^a	91	100	

^aTotal number sampled does not include fish whose sex could not be determined (*n*=2).

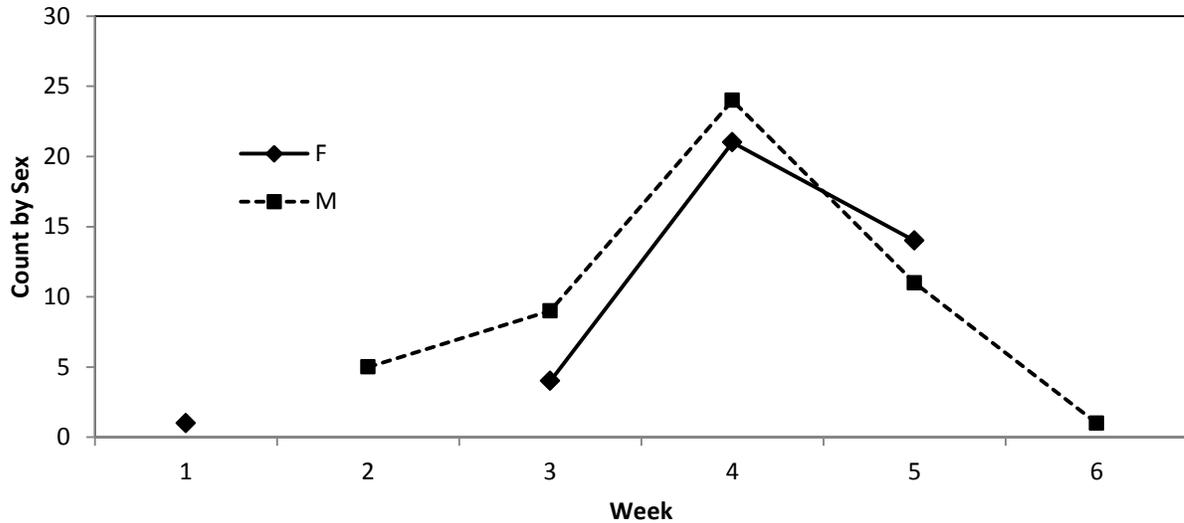


Figure 8. Weekly sex composition of unmarked Chinook salmon sampled through the Gechiak Creek weir, 2010. Total: Female $n=40$; Male $n=50$; Unknown Sex $n=2$. Sampling occurred 3 July – 5 August in 2010.

Table 9. Mean length (mm), SE, range, and sample size by age of unmarked Chinook salmon sampled through the Gechiak Creek weir, 2010.

Length	Age Class						
	1.1	1.2	1.3	1.4	2.1	2.2	2.3
Mean	369	537	801	827	568	741	812
SE	12	32	9	22	76	-	38
Minimum	319	410	665	715	470	741	760
Maximum	400	770	932	980	718	741	885
Total ^a	6	13	46	12	3	1	3

^aNumber sampled does not include fish whose age could not be determined ($n=9$).

All fixed telemetry stations were operational by 19 June. Several sustained high water events which resulted in three of the remote stations being flooded (Entry and Second stations on 16 August and Nayorurun station on 17 August), prematurely ending their operation. The Kemuk station was shifted to higher ground in its same location on 17 August, and continued to operate through 4 September. The Ranger station receiver was removed on 18 August to replace the malfunctioning receiver used for aerial tracking. The Gechiak receiver remained in place through 2 September.

Thirty-three boat searches were conducted from 18 July to 31 August, and five aerial searches were conducted through 5 July and 31 August.

Radio transmitters were implanted into 211 Chinook salmon between 22 June and 5 August. Initially, 40 radio transmitters were allocated to each of the first 4 strata and 20 radio transmitters were allocated to the fifth and final stratum. However, fisherman returned radio tags to us that were harvested in the sport, subsistence, or commercial fisheries, allowing us to redeploy the harvested tags (Table 10; Appendix 2). Of the 211 tagged Chinook salmon, a total of 159 fish (75%) were successfully tracked to spawning areas, 24 (12%) were not successfully tracked to a spawning location, 22 (10%) were harvested, and six (3%) were assigned a fate of dead/regurgitated (Table 11, Appendix 2). One Chinook salmon was recaptured during gill net sampling.

Table 10. Adjusted allocation for distribution of Chinook salmon radio transmitters in the Togiak River, 2010.

Stratum	Week(s)	Transmitters Allocated	Transmitters Deployed
1	June 20 – 26	45	45
	June 27 – July 3		
2	July 4 – 10	45	45
3	July 11 – 17	45	45
4	July 18 – 24	45	46 ^a
5	July 25 – 31	20	30 ^a
	August 1 – 7		
Total		200	211

^aIncludes radio tags that were harvested, returned to the field crew, and then redeployed in another Chinook salmon.

Table 11. Fate of Chinook salmon radio-tagged in the Togiak River, 2010.

Fate	Number	Percentage
<i>Spawning Location:</i>		
Mainstem (1 of 6 river sections)	127	60
Tributary (1 of 6 tributaries)	32	15
<i>Total</i>	<i>159</i>	<i>75</i>
<i>Unknown Fate:</i>		
Undetermined/insufficient location information	8	4
Undetermined/suspected harvest	16	8
<i>Total</i>	<i>24</i>	<i>12</i>
<i>Removed From Study:</i>		
Harvested	22	10
Dead/Regurgitated	6	3
<i>Total</i>	<i>28</i>	<i>13</i>
Total Tagged:	211	100

Eighty percent ($n = 127$) of the Chinook salmon tracked selected spawning locations in mainstem areas of the Togiak River, with 9% ($n = 15$) in the lower mainstem below Gechiak Creek (Table 12). Twenty percent ($n = 32$) selected spawning locations in tributaries, with 6% ($n = 9$) selecting locations in Gechiak Creek.

The percentages of Chinook salmon tracked to sections A (9%) and F (18%) of the mainstem in 2010 were inverse to the percentages of radio tagged fish assigned to the same locations (30% to section A and 7% to section F) in 2009. The gradient of distribution of spawning in the mainstem in 2010 reflects the 1987-2005 ADFG aerial survey averages more closely than the telemetry results from 2008 or 2009 (Table 12).

The proportions of Chinook salmon tracked to Gechiak Creek, Pungokepuk Creek, Nayorurun River, and Kemuk River in 2010 were not markedly different from the 2009 telemetry results (Table 12). However, Chinook salmon were tracked to Ongivinik River ($n = 3$) in 2010, unlike in 2008 or 2009, neither year having tracked Chinook salmon to that tributary. Additionally, the channel draining from the Togiak River at rkm 21 past the village of Twin Hills (Figure 4) was identified as a spawning location for the first time in 2010 ($n = 2$). The Twin Hills Channel (also identified as the Twin Hills Cutoff) was not included in the 1995-2005 ADFG aerial surveys.

Tests for run timing (Appendix 3) were complicated by low counts of tags released for some subpopulations. Data pooling and Fisher exact tests were conducted to provide some robustness to low cell counts in contingency table analyses; however, we caution that these run timing goodness of fit tests may have low power to detect a difference in run timing in all cases except for the test of pooled tributary fish vs. pooled mainstem fish which resulted in acceptable counts in contingency table cells (see Appendix 3). Results indicated no statistically significant difference between groups tested at the 5% type I error level (i.e. all tests had p -values > 0.05)

except for the test of pooled tributary populations vs. pooled mainstem populations (Chi Square test p-value: 0.023, Fisher exact test p-value: 0.024). This test suggests a difference in the timing at which tributary and mainstem spawning fish arrive at the tagging site, where it appears that the tributary spawners hit the tagging area earlier than mainstem spawning fish.

Table 12. Distribution of Chinook salmon within ADFG spawning survey river sections in the Togiak River drainage based on radio tracking in 2008, 2009, and 2010; and ADFG average aerial survey estimates during 1987 to 2005.

River Section	Number (Percent)			
	2008 Radio Tracking	2009 Radio Tracking	2010 Radio Tracking	1987-2005 Aerial Surveys ^a
<u>Mainstem</u>				
Mainstem A	26 (34)	35 (30)	15 (9)	162 (4)
Mainstem B	11 (14)	14 (11)	18 (11)	221 (6)
Mainstem C	17 (22)	22 (19)	26 (16)	547 (15)
Mainstem D	0 (0)	7 (6)	13 (8)	289 (7)
Mainstem E	2 (3)	18 (15)	28 (18)	503 (13)
Mainstem F	1 (1)	8 (7)	28 (18)	957 (24)
<u>Total</u>	57 (74)	104 (88)	127 (80)	2,679 (69)
<u>Tributary</u>				
Gechiak Creek	10 (13)	6 (5)	9 (6)	392 (10)
Pungokepuk Creek	2 (3)	3 (3)	8 (5)	159 (4)
Nayorurun River	6 (7)	3 (2)	6 (4)	213 (5)
Kemuk River	2 (3)	2 (2)	4 (3)	274 (7)
Ongivinuk River	0 (0)	0 (0)	3 (2)	202 (5)
Twin Hills Channel ^b	-	-	2 (1)	-
<u>Total</u>	20 (26)	14 (12)	32 (20)	1,240 (31)
<u>Drainage Total</u>	77	118	159	3,919

^aADFG 1987-2005 average aerial survey estimates from Westing et al. (2007).

^bTwin Hills Channel not included in surveys prior to 2010; "-" is no data.

Table 13. Number of radio-tagged Chinook salmon tracked by strata to ADFG spawning survey river sections in the Togiak River drainage ($n=159$), 2010.

Strata	River Section											
	Mainstem						Tributary					
	A	B	C	D	E	F	Gechiak	Pungokepuk	Nayorurun	Kemuk	Ongivinuk	Twin Hills Channel
1	2	0	1	2	4	6	2	1	2	3	0	0
2	3	3	4	3	6	4	3	3	3	1	1	0
3	2	4	3	3	7	10	3	2	0	0	2	0
4	5	7	6	5	9	5	1	2	0	0	0	1
5	2	4	11	0	2	3	0	0	1	0	0	1
Total	15	18	25	13	28	28	9	8	6	4	3	2

For 2010, the point estimate and confidence intervals (Poisson approximation for the sampling distribution of the Chapman abundance estimator) for the abundance of Chinook salmon in the Togiak River is $N = 10,096$, with 95% CI (N) = {5,237 ; 21,176} and 90% CI (N) = {5,709 ; 18,849}. To be specific, this estimate is for the population of salmon at risk of tagging: adult Chinook salmon greater than 450 mm in length that entered the Togiak River between 22 June and 5 August 2010. For comparison, we computed 90 and 95% confidence intervals using a parametric bootstrap routine with 100,000 bootstrap samples from a hypergeometric distributed Chapman abundance estimator (95% CI = {5,399 ; 20,246}, 90% CI = {5,785 ; 16,197}) and confidence intervals based upon a naive normal approximation to the sampling distribution of N using Chapman's approximate formula for the variance of N (Seber 1982; 95% CI = {3,686 ; 16,506} , 90% CI = {4,716 ; 15,476}).

Simulation results (Table 14) demonstrate that even small discrepancies between run timings between the systematic recapture sample population, the Gechiak fish, and the rest of river population can result in population abundance estimates that are potentially biased downward. Simulations under a set number of tags released per stratum, following the same sampling protocol as was used for the 2010 field study, suggest that if the Gechiak population had a run timing that peaked approximately four days before the rest of river run complex, abundance estimates could be biased downward (Table 14). Even in cases where the smaller Gechiak tributary run and the rest of river stock complex had completely overlapping run timing curves, the estimate was still biased downward. Our results imply that tagging rates over the 2010 marking effort were probably not the same between Gechiak and rest-of-river fish, which suggests that the 2010 estimate of abundance may be biased downwards (Table 14). Note that bias was greatly reduced when simulating tagging in proportion to abundance (lower half, Table 14), even when the tributary population modeled after the Gechiak subpopulation had different run timing than the rest-of-river population. We caution that simulation results are suggestive of the direction of biases, and are not directly comparable to the 2010 Togiak field project because the model is a severe abstraction of reality. For example, we simulated tagging processes as deterministic instead of using a binomial or multinomial sampling process; as such, modeling results could be interpreted as the expected outcome over many different probabilistic (binomial

or multinomial sampling) realizations. Absolute levels of biases reported by modeling exercises are not to be taken as truth.

Table 14. Simulation results for a population modeled after the Togiak-Gechiak Chinook salmon populations, 2010.

		Differences in tributary subpopulation run timing peak (in units of tagging strata)		
			fully mixed (no difference)	
		-0.5 stratum		+0.5 stratum
Set Tag Releases*	True total population	10400	10400	10400
	Estimated total population	6044	8461	6044
	90% CI***	(3905, 9737)	(5065, 14857)	(3905, 9737)
	Bias	-42%	-19%	-42%
	Tag rate tributary	0.0325	0.0225	0.0325
	Tag rate rest-of-river	0.0197	0.0201	0.0197
Tagging in Proportion to Abundance**	True total population	10400	10400	10400
	Estimated total population	9268	9268	10376
	90% CI***	(5404, 16746)	(5404, 16746)	(5867, 19370)
	Bias	-11%	-11%	1%
	Tag rate tributary	0.02	0.02	0.0175
	Tag rate rest-of-river	0.0199	0.0199	0.0199

* Simulation model parameters (Appendx 4). All trib2 parameters set to 0 (only simulating main and trib1); ERROR OPTIONS: tag.probalistic = 0, tag.rate.sd=0, recapture.probs= 1.0; TAG OPTION A is chosen, with constant.num.tag = c(45,45,45,45,30). Specific simulation runs: 1) fully mixed: Ntrib1 = 400, Nmain = 10000, run.mean.trib1 = -0.15, run.mean.main = -0.15, run.sd.trib1=0.75, run.sd.main = 0.75, run.scaling.lo = -4.0, run.scaling.hi = 3.0, strata = 21, tag.strata = c(6,9,12,15,18). 2) -0.5 stratum: same as fully mixed except: run.mean.trib1 = -0.75. 3) +0.5 stratum: same as fully mixed except run.mean.trib1 = 0.65.

** Simulation model parameters. All trib2 parameters set to 0 (only simulating main and trib1); ERROR OPTIONS: tag.probalistic = 0, tag.rate.sd=0, recapture.probs= 1.0; TAG OPTION B is chosen, with constant.tag.rate = 0.06. All other parameters specified as with predefined tag release simulation runs.

*** Confidence intervals were generated using the Poisson approximation for sampling distribution of the Chapman abundance estimator.

Discussion

Based on prior experience, we began fishing to capture Chinook salmon for tagging on 22 June 2010 and were surprised to capture eight Chinook salmon on that date. In contrast, we began fishing on 20 June in 2008 and did not capture a Chinook salmon until 26 June (Anderson 2009), and on 25 June in 2009 and only captured and tagged two Chinook salmon (Anderson 2010). In 1988 and 1990, results of a sonar project stationed on the Pungokebuk River estimated the Chinook salmon run start date to be approximately 25 June (Irving et. al 1995). While we still think the 2010 marking event covered most of the run, the earliest portion of the run may have been slightly underrepresented in the tagged population.

Not all Chinook salmon passing the Gechiak Creek weir may have been counted due to interruptions caused by flooding events. These interruptions resulted in missed or incomplete counts for a total of seven days from 28 June through 14 August. A final flood event caused us to suspend weir operations on 15 August, and by the time water levels receded enough to resume operations on 29 August, we had decided to end the season. Despite repeated high water events, the integrity of the weir structure remained intact. The substrate on the river right side of the weir was softer against the bank than is ideal for a weir site, and some scouring occurred around and under the right bulkhead. However, sandbag coverage was increased in this area to mitigate erosion, and we did not observe any Chinook salmon being able to swim around the weir without being counted.

Our simulation results implied that tagging rates during 2010 were probably not the same between Gechiak Creek and rest-of-river Chinook salmon, and suggest that the 2010 estimate of abundance may be biased downwards (Table 14). However, we caution that simulation results can only be used to suggest the likely direction of biases and cannot be used to adjust the 2010 estimate. Results do suggest that deployment of tags in proportion to abundance would result in less biased estimates than deployment of a set numbers of tags each week, as was done in 2010.

From 2008 through 2010, the sex ratios of tagged Chinook salmon in lower river samples had greater percentages of females than males: 69% in 2008, 59% in 2009, and 55% in 2010 (Anderson 2009, 2010). This finding was consistent with the selectivity of the gill net mesh size used, since it favored capture of larger-bodied Chinook salmon that tend to be female. In contrast, most tagged Chinook salmon sampled at the weir were males (55%), while the sex ratio of all tagged fish that spawned in Gechiak Creek was roughly equal (4 males, 4 females, and 1 unknown). The dominant age class in 2010 was age 1.3 (74% of marked fish and 55% of fish sampled through the weir), which was consistent with the 2008 study (54% of marked fish). However, in 2009, age 1.4 fish (49%) dominated the sample of marked fish (Anderson 2009, 2010). Our age results are in keeping with those reported by MacDonald (1997) and MacDonald and Lisac (1997).

In contrast to aerial survey information, spawning distribution based on our telemetry information has consistently shown greater use of spawning areas within the main stem than in the tributaries (Tables 12 and 13). This difference is probably due to effects of water clarity on aerial survey observations, since much of the main stem is turbid. While main stem spawning appears to be much more important than previously estimated, spawning distribution within the main stem in 2010 was different than that previously documented. In 2010, most tagged Chinook salmon tracked to main spawning areas were found in the lower portion of the Togiak River (Section A), while in the 2008 and 2009, most were found in the upper portion of the river (sections E and F). In 2010, we also recorded tagged Chinook salmon in tributaries that were not used by radio tagged fish in 2008 and 2009: the Ongivinik River and the Twin Hills Channel. Togiak Village residents informed us that the spawning distribution recorded in 2010 is more

commonly seen in high water years, which is consistent with what we observed in the field regarding spawning locations and water levels.

Anderson (2010) reported that both sport and subsistence fishing occurred in areas where Chinook salmon hold and spawn within the lower river. Tagged Chinook salmon appear to hold in the lower main stem until around 20 July, after which they move rapidly upstream to various spawning destinations. This holding behavior increases the likelihood of tagged fish being harvested by either sport or subsistence fishermen. Of our 211 radio tagged fish, 16 were successfully tracked to different locations over a period of 2-4 weeks before they seemingly disappeared from the system, resulting in a fate assignment of unknown (Table 11). Though these 16 Chinook salmon were not reported to have been harvested, we suspect that they were captured and removed from the system in one of the fisheries. If we include these 16 Chinook salmon with 22 that were known to have been harvested, then 18% rather than 10% of all tagged Chinook salmon were harvested.

Recommendations

In 2010, the field crew concluded fishing once all of the allotted radio tags were deployed as assigned by strata. This resulted in our inability to construct an estimate of run timing based on catch per unit effort (CPUE) data. In order to better describe overall run timing, we advise crews to continue fishing for a set amount of time every day once the transmitter allocation for a stratum has been met, much like a test fishery. The same capture and fish handling procedures should be followed in order to ensure consistency in fishing effort.

Based on the results of our mark-recapture simulation analyses, we recommend that the number of tags deployed be increased and that tagging be conducted in proportion to Chinook salmon abundance within each time stratum. Increasing the number of tags deployed would improve the precision of all abundance estimates. However, because the number of radio tags available is cost-limited, we suggest using spaghetti tags for the primary mark. If these tags were color-coded by time strata, resulting counts of different colored tags at the weir would allow us to develop a run timing curve for this population. Tagging Chinook salmon in proportion to abundance would reduce the bias of the total abundance estimate. To achieve this, sampling effort would be standardized across strata and the number of tags released would equal the number of Chinook salmon caught. This would be much easier to achieve using spaghetti tags. As was done in 2010, Chinook salmon injured during fishing would not be tagged.

We recommend that paired abundance estimates from the mark-recapture experiment and aerial counts be used to develop a more precise aerial survey program as an appropriate and affordable management tool. Our results show that mark-recapture is a viable approach for estimating Chinook salmon abundance in the Togiak River under appropriate sampling protocols. However, this approach is expensive in both time and resources, and is not viewed as a method to use for long-term annual monitoring.

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Appendix 1. Count of Chinook marked with radio tags and unmarked Chinook salmon through the Gechiak Creek weir, 2010.

Date	No. Untagged Counted	No. Tagged Counted	Total Daily Count	Cumulative Total Count
28-Jun-10	0	0	0	0
29-Jun-10	0	0	0	0
30-Jun-10	0	0	0	0
1-Jul-10	0	0	0	0
2-Jul-10	0	0	0	0
3-Jul-10	1	0	1	1
4-Jul-10	0	0	0	1
5-Jul-10	1	0	1	2
6-Jul-10	0	0	0	2
7-Jul-10	0	0	0	2
8-Jul-10	3	0	3	5
9-Jul-10	1	0	1	6
10-Jul-10	0	0	0	6
11-Jul-10	0	0	0	6
12-Jul-10	1	0	1	7
13-Jul-10	3	0	3	10
14-Jul-10	4	0	4	14
15-Jul-10	3	0	3	17
16-Jul-10	3	0	3	20
17-Jul-10	0	0	0	20
18-Jul-10	0	0	0	20
19-Jul-10	3	0	3	23
20-Jul-10	12	0	12	35
21-Jul-10	1	0	1	36
22-Jul-10	27	0	27	63
23-Jul-10	1	0	1	64
24-Jul-10	7	0	7	71
25-Jul-10	3	0	3	74
26-Jul-10	83	0	83	157
27-Jul-10	10	0	10	167
28-Jul-10	8	0	8	175
29-Jul-10	104	6	110	285
30-Jul-10	-	-	-	-
31-Jul-10	-	-	-	-
1-Aug-10	-	-	-	-
2-Aug-10	-	-	-	-
3-Aug-10	-	-	-	-
4-Aug-10	18	0	18	303
5-Aug-10	1	0	1	304
6-Aug-10	3	0	3	307
7-Aug-10	8	0	8	315
8-Aug-10	14	0	14	329
9-Aug-10	3	0	3	332

Appendix 1. Continued.

Date	No. Untagged Counted	No. Tagged Counted	Total Daily Count	Cumulative Total Count
10-Aug-10	-	-	-	-
11-Aug-10	-	-	-	-
12-Aug-10	24	1	25	357
13-Aug-10	11	0	11	368
14-Aug-10	12	1	13	381
15-Aug-10	-	-	-	-
...
29-Aug-10	-	-	-	-
Total	373	8	381	381

“-“ denotes days the weir was inoperable due to high water. “...” denotes a continuation of inoperable weir conditions from 16 – 28 August in 2010.

Appendix 2. Summary of biological data and tracking history for radio tagged Chinook salmon in the Togiak River, 2010.

Tagging Stratum	Date Tagged	Fish ID	Age	Sex	Length (mm)	Fate ^a	Number of Detections
1	22-Jun	1	--	F	862	Harvested	7
1	22-Jun	2	1.3	U	782	F	20
1	22-Jun	3	1.4	M	890	Harvested	6
1	22-Jun	4	1.3	F	810	Dead/Regurgitated	0
1	22-Jun	5	1.3	U	830	D	17
1	22-Jun	6	1.2	M	606	Unknown†	2
1	22-Jun	7	2.3	M	760	Harvested	2
1	23-Jun	8	1.3	M	728	Harvested	3
1	28-Jun	9	1.3	F	855	E	24
1	28-Jun	10	1.3	U	827	Harvested	3
1	28-Jun	11	1.2	U	522	Nayorurun	8
1	28-Jun	12	1.4	M	752	Harvested	7
1	28-Jun	13	1.3	U	839	Unknown†	4
1	28-Jun	14	1.2	M	737	F	17
1	28-Jun	15	1.3	M	832	Dead/Regurgitated	6
1	28-Jun	16	1.3	M	875	Unknown†	1
1	28-Jun	17	1.3	M	764	Harvested	3
1	28-Jun	18	1.3	F	903	Kemuk	11
1	28-Jun	19	1.4	F	991	A	19
1	28-Jun	20	1.4	F	937	A	11
1	29-Jun	21	1.3	M	728	E	12
1	29-Jun	22	1.3	M	827	Unknown†	6
1	29-Jun	23	1.3	M	762	Gechiak	17
1	29-Jun	24	--	M	781	E	9
1	29-Jun	25	--	M	770	C	19
1	30-Jun	26	--	F	929	Harvested	21
1	30-Jun	27	--	M	706	Pungokepuk	6
1	30-Jun	28	1.3	M	815	D	21
1	30-Jun	29	1.3	M	785	Nayorurun	15
1	30-Jun	30	1.3	F	810	Harvested	1
1	30-Jun	31	1.3	M	790	Kemuk	12
1	30-Jun	32	1.3	F	810	Harvested	7
1	30-Jun	33	1.3	M	823	E	26
1	30-Jun	34	--	U	760	Kemuk	10
1	2-Jul	35	1.4	U	845	Harvested	4
1	2-Jul	36	1.3	M	795	Unknown	1
1	2-Jul	37	1.3	F	895	Gechiak	20
1	2-Jul	38	1.3	M	710	F	21
1	2-Jul	39	1.3	M	790	Unknown†	6
1	2-Jul	40	1.3	F	830	F	18

Appendix 2. Continued.

Tagging Stratum	Date Tagged	Fish ID	Age	Sex	Length (mm)	Fate ^a	Number of Detections
1	3-Jul	41	1.3	M	865	F	17
1	3-Jul	42	1.3	M	777	Dead/Regurgitated	0
1	3-Jul	43	1.3	F	740	Dead/Regurgitated	0
1	3-Jul	44	1.3	U	724	F	30
1	3-Jul	45	1.3	M	810	Unknown†	13
2	5-Jul	46	1.3	F	832	D	17
2	5-Jul	47	1.3	F	737	B	16
2	5-Jul	48	1.3	F	790	Ongiviniak	7
2	5-Jul	49	1.3	M	750	E	43
2	5-Jul	50	2.3	M	734	Pungokepuk	9
2	5-Jul	51	1.3	F	800	Pungokepuk	7
2	5-Jul	52	1.3	M	850	Harvested	1
2	5-Jul	53	2.3	F	781	A	19
2	5-Jul	54	1.3	M	786	C	24
2	5-Jul	55	1.2	U	715	F	18
2	5-Jul	56	1.3	F	699	Nayorurun	11
2	5-Jul	57	1.3	F	857	Unknown	12
2	5-Jul	58	1.3	F	835	E	25
2	5-Jul	59	--	F	807	Unknown†	11
2	5-Jul	60	1.3	M	869	Harvested	2
2	5-Jul	61	1.2	F	729	Kemuk	21
2	5-Jul	62	1.3	F	766	B	3
2	5-Jul	63	1.3	F	845	Harvested	11
2	5-Jul	64	1.3	F	809	C	30
2	5-Jul	65	1.4	M	809	Pungokepuk	9
2	7-Jul	66	1.3	F	845	Harvested	1
2	7-Jul	67	--	F	776	Gechiak	17
2	7-Jul	68	1.2	F	843	D	17
2	7-Jul	69	--	F	840	E	23
2	7-Jul	70	1.3	F	825	B	11
2	7-Jul	71	1.3	M	760	Harvested	3
2	7-Jul	72	1.3	M	765	D	9
2	7-Jul	73	1.3	M	860	E	11
2	7-Jul	74	1.3	M	800	Gechiak	25
2	7-Jul	75	1.3	M	780	Harvested	21
2	7-Jul	76	1.2	F	790	F	13
2	7-Jul	77	1.2	M	870	Nayorurun	16
2	7-Jul	78	--	M	500	Harvested	4
2	7-Jul	79	--	F	858	C	17
2	7-Jul	80	1.3	F	790	A	20
2	7-Jul	81	1.3	F	845	Harvested	7

Appendix 2. Continued.

Tagging Stratum	Date Tagged	Fish ID	Age	Sex	Length (mm)	Fate ^a	Number of Detections
2	7-Jul	82	1.3	F	875	F	17
2	7-Jul	83	--	M	900	Unknown	10
2	7-Jul	84	1.3	M	775	Gechiak	12
2	7-Jul	85	--	F	835	C	14
2	7-Jul	86	1.3	M	745	F	15
2	8-Jul	87	1.3	M	789	E	13
2	8-Jul	88	1.4	F	826	A	12
2	8-Jul	89	1.2	F	798	Nayorurun	11
2	8-Jul	90	1.2	U	762	E	14
3	11-Jul	91	2.1	F	860	A	9
3	11-Jul	92	1.3	F	844	F	9
3	11-Jul	93	1.3	F	756	D	21
3	11-Jul	94	1.4	F	834	D	21
3	11-Jul	95	1.3	M	716	C	33
3	11-Jul	96	1.3	M	842	Unknown†	2
3	11-Jul	97	1.3	F	784	C	22
3	12-Jul	98	1.4	M	905	Pungokepuk	6
3	12-Jul	99	1.2	M	455	Dead/Regurgitated	6
3	12-Jul	100	1.3	F	821	E	18
3	12-Jul	101	--	M	755	B	19
3	12-Jul	102	1.3	F	815	F	11
3	12-Jul	103	1.3	M	855	E	24
3	12-Jul	104	--	F	845	Unknown†	8
3	12-Jul	105	1.4	F	910	E	16
3	12-Jul	106	1.2	M	771	B	24
3	12-Jul	107	1.2	F	822	Ongivinik	13
3	12-Jul	108	1.3	F	782	F	26
3	12-Jul	109	1.3	M	828	F	9
3	12-Jul	110	1.3	M	830	Unknown†	2
3	12-Jul	111	1.3	F	896	F	20
3	12-Jul	112	1.3	M	910	F	15
3	12-Jul	113	1.3	M	945	F	17
3	12-Jul	114	1.3	M	716	F	32
3	13-Jul	115	1.3	F	784	Gechiak	17
3	13-Jul	116	2.2	M	764	E	13
3	13-Jul	117	--	M	754	Gechiak	18
3	13-Jul	118	1.3	U	855	Ongivinik	11
3	13-Jul	119	1.3	M	855	E	15
3	13-Jul	120	1.3	F	779	F	22
3	13-Jul	121	--	F	791	E	28
3	13-Jul	122	1.3	M	779	Harvested	5

Appendix 2. Continued.

Tagging Stratum	Date Tagged	Fish ID	Age	Sex	Length (mm)	Fate ^a	Number of Detections
3	13-Jul	123	1.3	U	815	B	20
3	13-Jul	124	1.3	F	845	Pungokepuk	9
3	13-Jul	125	1.3	M	719	F	19
3	13-Jul	126	1.3	M	930	E	12
3	14-Jul	127	1.3	F	765	Gechiak	12
3	14-Jul	128	1.3	F	835	Unknown†	6
3	14-Jul	129	1.3	M	794	Unknown	2
3	14-Jul	130	1.3	F	795	C	16
3	14-Jul	131	--	F	795	A	12
3	14-Jul	132	1.3	F	850	D	20
3	14-Jul	133	1.3	F	865	B	11
3	14-Jul	134	1.3	F	860	Unknown†	7
3	14-Jul	135	1.3	M	715	Unknown†	9
4	18-Jul	136	1.4	F	868	F	13
4	18-Jul	137	1.3	F	834	E	23
4	18-Jul	138	1.3	M	867	E	11
4	18-Jul	139	1.4	F	878	B	22
4	18-Jul	140	2.3	M	940	F	11
4	18-Jul	141	1.3	M	834	Twin Hills Channel	8
4	18-Jul	142	1.3	F	840	C	15
4	18-Jul	143	1.3	F	837	B	18
4	18-Jul	144	1.2	M	695	Harvested	3
4	18-Jul	145	1.3	M	815	Pungokepuk	12
4	18-Jul	146	1.3	M	844	A	13
4	18-Jul	147	1.4	F	800	B	15
4	18-Jul	148	1.3	M	814	C	18
4	18-Jul	149	--	F	849	F	18
4	18-Jul	150	1.3	F	823	E	25
4	18-Jul	151	1.3	M	810	E	24
4	18-Jul	152	1.3	M	973	B	11
4	18-Jul	153	1.3	F	814	E	13
4	18-Jul	154	1.4	M	900	E	16
4	18-Jul	155	--	F	880	E	21
4	18-Jul	156	1.4	M	891	D	21
4	18-Jul	157	1.2	U	757	Gechiak	10
4	18-Jul	158	1.4	F	950	B	11
4	18-Jul	159	1.3	F	898	Pungokepuk	20
4	18-Jul	160	--	F	853	Dead/Regurgitated	0
4	18-Jul	161	1.3	F	872	A	14
4	18-Jul	162	1.2	F	826	C	17
4	18-Jul	163	1.4	F	809	A	14
4	18-Jul	164	--	F	900	E	15

Appendix 2. Continued.

Tagging Stratum	Date Tagged	Fish ID	Age	Sex	Length (mm)	Fate ^a	Number of Detections
4	18-Jul	165	1.3	F	804	Unknown	5
4	19-Jul	166	1.3	F	834	C	18
4	19-Jul	167	1.3	M	835	D	17
4	19-Jul	168	1.3	M	800	D	21
4	19-Jul	169	2.2	M	670	C	25
4	19-Jul	170	1.3	F	869	A	11
4	19-Jul	171	1.3	M	882	F	17
4	19-Jul	172	1.3	F	845	C	20
4	19-Jul	173	1.3	F	908	A	6
4	19-Jul	174	--	M	835	Harvested	4
4	19-Jul	175	2.3	F	842	D	19
4	19-Jul	176	1.3	F	750	B	11
4	19-Jul	177	1.3	M	880	E	23
4	20-Jul	178	1.3	F	805	B	8
4	20-Jul	179	1.3	F	859	D	25
4	20-Jul	181	1.3	M	836	F	12
4	20-Jul	180*		F	835	Unknown	9
5	25-Jul	182	1.3	F	870	Unknown	1
5	25-Jul	183	1.3	M	755	B	12
5	25-Jul	184	1.4	M	750	F	16
5	25-Jul	185	--	U	735	B	23
5	25-Jul	186	1.4	F	801	C	11
5	25-Jul	187	1.3	F	858	C	10
5	25-Jul	188	1.3	F	860	C	19
5	25-Jul	189	1.3	M	710	Unknown†	11
5	25-Jul	190	1.3	M	826	C	16
5	25-Jul	191	1.3	F	845	A	9
5	25-Jul	192	1.3	U	767	F	10
5	25-Jul	193	1.3	F	835	C	7
5	25-Jul	194	1.4	F	845	C	9
5	25-Jul	195	--	F	857	A	4
5	25-Jul	196	1.3	M	879	Nayorurun	12
5	25-Jul	197	1.3	F	794	B	10
5	26-Jul	199	1.3	F	860	C	17
5	26-Jul	200	1.3	F	845	E	17
5	26-Jul	201	2.3	F	855	Unknown	1
5	26-Jul	203	1.4	F	795	C	10
5	26-Jul	204	1.3	M	780	C	15
5	26-Jul	206	1.3	F	760	Unknown†	14
5	26-Jul	207	1.3	F	790	F	19
5	26-Jul	198*	1.3	F	790	E	26
5	26-Jul	202*	1.4	M	985	C	22

Appendix 2. Continued.

Tagging Stratum	Date Tagged	Fish ID	Age	Sex	Length (mm)	Fate ^a	Number of Detections
5	26-Jul	205*	1.3	F	885	Unknown†	16
5	26-Jul	208*	1.3	F	865	C	8
5	4-Aug	209	1.3	M	690	A	9
5	5-Aug	210*	2.2	F	840	B	6
5	5-Aug	211*	1.3	F	790	Twin Hills Channel	2

†Denotes fish whose fate is unknown but are suspected to have been harvested.

*Denotes fish that were marked with a redeployed radio tag (tag was returned to us early in the season from harvested fish).

^aMainstem spawning fates are as follows:

A = From the first fixed telemetry station to Gechiak Creek

B = Gechiak Creek to Pungokepuk Creek

C = Pungokepuk Creek to Nayorurun (Kashaiak) River

D = Nayorurun River to Kemuk River

E = Kemuk River to Ongivinik River

F = Ongivinik River to Togiak Lake

Appendix 3. R code used to test run timing differences in radio tagged Chinook salmon tracked to spawning areas within the Togiak River drainage, 2010.

```
# Goodness of fit tests to examine run timing differences between salmon populations
# In all tests, the null hypothesis is, H_0 : no difference in run timing at the marking site between
# populations. In terms of the goodness of fit tests, acceptance of the null hypothesis indicates that
# the test fails to reject the hypothesis that the two compared samples
# (run timing data between two compared salmon populations) came from the same distribution.
# See the main text for an explanation of the data used to infer run timing at the marking site.

# Data entry: tag releases by stratum
# pooled, mainstem vs. tributary releases: for test, H_0: No difference in tag release rate timings between
# mainstem and tributary pooled populations main-stem and trib. pooled releases by stratum 1-5
m. <- c(15,23,29,37,23) # fated mainstem spawners releases by stratum 1-5
t. <- c(8,11,7,4,2) # fated tributary spawner data
# set up the data into contingency table cells
dat.pool <- matrix(c(m.,t.),nrow=5,ncol=2,byrow=F,dimnames=list(c("s1","s2","s3","s4","s5"),c("main","trib")))
# look at the contingency table
dat.pool

# individual spawning location releases by stratum 1-5; convert to percent total released tags by stratum
a. <- c(2,3,2,5,3)
b. <- c(0,3,4,7,4)
c. <- c(1,4,3,6,11)
d. <- c(2,3,3,5,0)
e. <- c(4,6,7,9,2)
f. <- c(6,4,10,5,3)
gech <- c(2,3,1,0)
pung <- c(1,3,2,2,0)
nayo <- c(2,3,0,0,1)
kemuk <- c(3,1,0,0,4)
ongi <- c(0,1,2,0,0)
THC <- c(0,0,0,1,1)

# Set up the contingency table for a test: H_0: No difference in tag release rate timings between tributary subpopulations
dat.trib.pops <- matrix(c(gech,pung,nayo,kemuk,ongi),nrow=5,ncol=5,byrow=F,dimnames=list(c("s1","s2","s3","s4","s5"),
c("gech","pung","nayo","kemuk","ongi")))

# Set up the contingency table for a test: H_0: No difference in tag release rate timings between mainstem subpopulations
dat.main.pops <- matrix(c(a.,b.,c.,d.,e.,f.),nrow=5,ncol=6,byrow=F,dimnames=list(c("s1","s2","s3","s4","s5"),
c("a.", "b.", "c.", "d.", "e.", "f.")))

# Set up the contingency table for test H_0: No difference in tag release rate timings between Gechiak vs. pooled rest of river
rest <- a. + b. + c. + d. + e. + f. + pung + nayo + kemuk + ongi + THC
dat.Gech.rest <- matrix(c(rest,gech),nrow=5,ncol=2,byrow=F,dimnames=list(c("s1","s2","s3","s4","s5"),
c("rest","gech")))

# Goodness of fit tests (Chi squared and Fisher Exact tests). Note, a rule of thumb for Chi square tests is that all cells in
# a contingency table should contain counts of 5 or greater. In this case, the test statistic will be well approximated
# by the Chi square distribution. Violations of this rule of thumb indicates that the test statistic may not be well approximated
# by the Chi Square distribution, and inference may be incorrect. Thus, while Chi Square tests are provided, Fisher exact tests
# are also provided which may be robust to small- or zero- cell counts.

# Test 1: H_0: No difference in tag release rate timings between mainstem and tributary pooled populations
chisq.test(dat.pool) # p-value: 0.023
fisher.test(dat.pool) # p-value: 0.024
# indicates a significant difference at a 5% Type I error rate that in fact, mainstem and tributary populations appear
# to represent samples from different distributions. In examining the data, it appears that tributary fish run
# earlier than mainstem spawning fish, as inferred by higher tag release rates early on for tributary populations
# relative to mainstem spawning populations.

# Test 2: H_0: No difference in tag release rate timings between tributary subpopulations
chisq.test(dat.trib.pops) # p-value: 0.087
fisher.test(dat.trib.pops) # p-value: 0.118

# Test 3: H_0: No difference in tag release rate timings between mainstem subpopulations
chisq.test(dat.main.pops) # p-value: 0.116
fisher.test(dat.main.pops) # note: test may be too memory-hungry due to large number of cells and low count values, p-value: 0.118

# Test 4: H_0: No difference in tag release rate timings between Gechiak vs. pooled rest of river
# *** NOTE *** : very low cell counts for all of Gechiak column; the power of this test to detect differences in run timing is
# not reliable.
chisq.test(dat.Gech.rest) # p-value: 0.387
fisher.test(dat.Gech.rest) # p-value: 0.336
```

Appendix 4. R code for the simulation model.

```

# Single release, single recapture abundance estimation using the Chapman variant of the Lincoln-Petersen estimator
# on mixed subpopulations of in-migrating salmon with potentially different run timings and population sizes, and
# systematic recapture sampling only on tributary subpopulations.
# v. 5.16.11

# Description: This simulator generates three "runs" of salmon that enter a tagging area: i) subpopulations bound for tributaries
# ii) a river-wide population, that is not bound for the tributary. Marking takes place in the mouth of the river, and recapture occurs
# systematically, only on tributary subpopulations (e.g. at weirs). Options are available to alter the run timing, run compression, run size,
# tagging effort (with option to specify pre-set numbers of tags released per tagging event, or option to specify tagging rates such that
# numbers of tags released per strata varies), and sampling can be simulated as deterministic or probabilistic. Point estimates
# and confidence intervals are produced, and a plot of run curves and tagging events. Users must step through the parameter section to
# specify a number of simulation options: confidence interval alpha levels, 'true' abundances, 'true' run timing characteristics,
# number and timing of tagging strata, tag release options, and sampling/implementation error options.

##### Specify population and tagging sampling parameters #####

# Confidence interval tail probabilities (e.g. 90% CI:(alpha.lo,alpha.hi)=(.05,.95) or 95% CI: (alpha.lo,alpha.hi)=(.025,.975)
alpha.lo <- .05 # this is prob. for alpha/2 % lower tail region for an alpha % CI
alpha.hi <- .95 # this is prob. for (1 - alpha/2) % upper tail region for an alpha % CI

# abundances
Ntrib1 <- 400 # the tributary 1 sub population true abundance
Ntrib2 <- 0 # the tributary 2 sub population true abundance
Nmain <- 10000 # the non-tributary population
Ntotal <- Ntrib1 + Ntrib2 + Nmain

# run timing (need to choose these to get sensible overlapping population run timings; set means and sd's equal to simulate complete
mixing)
# for simulation testing of Gechiak, Togiak mainstem populations, set run.mean.trib1 <- -.75 for early, and .65 for late.
run.mean.trib1 <- -.75 # location parameter for the normal distribution cumulative dist. function
run.mean.trib2 <- 0 # location parameter for the normal distribution cumulative dist. function
run.mean.main <- -.15
run.sd.trib1 <- .75 # spread parameter for the normal distribution cumulative dist. function
run.sd.trib2 <- 0 # spread parameter for the normal distribution cumulative dist. function
run.sd.main <- .75
run.scaling.lo <- -4 # scaling factors for total run length, affects the "x-axis" of a run timing plot, see below
run.scaling.hi <- 3

# Tagging events: Multiple parameters to be specified:

# The number of strata to divide up total sampling time, and selection of specific strata for tag events
strata <- 21 # number of temporal strata (intervals) to divide up the run curve into (not necessarily number
tagging events)
tag.strata <- c(6,9,12,15,18)# vector of tagging event timings (selection of the strata intervals above)

# There are 3 options to specify how tags are administered: Specify ONE option below, set all other parameters to ZERO
otherwise
### TAG OPTION A: A set number of tags are released per tagging event.
# define a set number of tags to release in each tagging release strata (timing of tagging strata and length of strata specified
with
# 'strata' and 'tag.strata' above. The tags released in each specific tag stratum will be allocated according to the relative
proportion
# with which subpopulations are present (either deterministically or probabilistically as specified under ERROR OPTION
1, see below).
constant.num.tag <- 0# c(45,45,45,45,30) # define vector of targets (tag releases will be either the target or
the number of fish

# present if it is < the target), OR set to ZERO otherwise

### TAG OPTION B: Specify tagging rate, so number of tags released within a tag stratum is not constant, rather varies in
abundance is
# proportion to abundance of all salmon present across all subpopulations. In this option, the tag rate in proportion to
# constant across all tagging strata. As is the case with option A, tags released in any specific tag stratum will be allocated
# according to the relative proportion with which subpopulations present (either deterministically or probabilistically as
# specified under ERROR OPTION 1, see below).
constant.tag.rate <- .06 # define a constant rate (on the (0,1) interval), i.e. the percentage of fish present to tag
OR set to zero

### TAG OPTION C: Specify tagging rate, so number of tags released within a tag stratum is not constant, rather varies in
each tag strata

```

Appendix 4. Continued.

```

# individually, allowing tag rate to vary across strata. As is the case with option A, tags released in any specific tag
# stratum will be allocated according to the relative proportion with which subpopulations present (either deterministically
# or probabilistically as specified under ERROR OPTION 1, see below).
tag.rate.trib1 <- c(.8,.0585,.02375,.0575,.625) # tagging rate on marking grounds for trib subpop
tag.rate.trib2 <- c(.8,.0585,.02375,.0575,.625) # tagging rate on marking grounds for trib subpop
tag.rate.main <- c(.8,.0585,.02375,.0575,.625) # tagging rate on marking grounds for rest of river subpop

# Options to introduce error in the process of sampling fish for tagging and recapture
# ERROR OPTION 1: probabilistic tagging capture process
# Should the tagging sampling process be deterministic (e.g tags released = # present * tag rate (a proportion)); or #
# Should the tagging sampling process be probabilistic (e.g. number tags released = binomial or multinomial sampling
with
# success rate = tag rate, introduces probabilistic sampling error)
tag.probablilistic <- 0 # set to 1 for probabilistic sampling, OR set to ZERO otherwise

# ERROR OPTION 2: tag rate implementation error for TAG OPTIONS B & C
# If tagging is deterministic ('tag.probablilistic <- 0'; see above), an alternative option to add error in tagging rates can be
specified
# for tag release options where tag rates are specified (TAG OPTIONS B & C above; if TAG OPTION A is chosen, then
no such option exists).
# This option could be used to simulate error
# in the relationship between tagging effort and tagging success such that specified tag rates will not be exact. This could
be used to simulate
# non constant catchability in a Catch-effort relationship for example if gear effectiveness randomly varied over the study
period.
# This options imposes bias-corrected lognormal deviates to specified tag rates:
tag.rate.sd <- 0.0 # set spread of log normal deviates (e.g. 0.25) OR set to ZERO for no error
# Should error vary across subpopulations and by tagging event (err.by.strata.time=1)? or only by tagging event
(err.by.strata.time=0)?
# Option to impose tag.rate implementation error as constant across all subpopulations within a tagging strata
(err.by.strata.time=0), OR
# implementation error not only varies across tagging strata, but also across subpopulations within tagging strata
(err.by.strat.time=1)
err.by.strata.time <- 0 # setting this to 0 impose tag implementation error that varies across tagging strata but is
constant amongst populations
# within strata is probably more realistic to
mimic gillnet efficiency varying randomly over time but not across subpopulations.

# ERROR OPTION 3: probabilistic recapture sampling process
# Recapture an enumeration at the weir is assumed to be complete, but a probabilistic sampling process, which would
introduce sampling error
# into the detection of marked and unmarked fish that pass the weir (e.g. if you want to simulate the chance that tags are
missed at the weir),
# can be simulated. Recapture sampling is coded as a binomial sampling process with the probability of success =
recapture.probs.
# Setting 'recapture.probs' = 1.0 ensures that all unmarked and marked fish that pass the weir are correctly detected (no
error), while
# setting 0.0 < 'recapture.probs' < 1.0 introduces weir detection error. For example, recapture.probs <- .9 means that any
fish passing the weir
# has a 90% chance of being counted and examined for tags.
recapture.probs <- 1.0 # set to 1.0 for not weir detection error OR set <1.0 to simulate weir detection error

# storage
Ntrib1 later
pop.strata.pct.trib1 <- 1: strata # the percentages of the run that occur over a discrete time interval, to be multiplied by
Ntrib2 later
pop.strata.pct.trib2 <- 1: strata # the percentages of the run that occur over a discrete time interval, to be multiplied by
Nmain later
pop.strata.pct.main <- 1: strata # the percentages of the run that occur over a discrete time interval, to be multiplied by

marks.trib1 <- 1: length(tag.strata) # storage vectors for number of marks released by strata
marks.trib2 <- 1: length(tag.strata)
marks.main <- 1: length(tag.strata)

# Comments on TAG OPTIONS
# Similar scenarios can be obtained

##### END specify parameters #####
##### The simulation model #####
    
```

Appendix 4. Continued.

```

# Divide the run curves into strata; divide the "time" or x-axis into equal spacing from run.scaling.lo to run.scaling.hi which
# encompasses the total st. normal cum. curve from 0 to 100%, e.g. plot(pnorm(seq(from=-3,to=3,by=.1)))
strata.index <- seq(from=run.scaling.lo,to=run.scaling.hi,length.out=(strata+1) )
for (i in 1:strata )
    {
        pop.strata.pct.trib1[i] <-pnorm(strata.index[i+1],mean=run.mean.trib1,sd=run.sd.trib1)-
pnorm(strata.index[i],mean=run.mean.trib1,sd=run.sd.trib1)
        pop.strata.pct.trib2[i] <-pnorm(strata.index[i+1],mean=run.mean.trib2,sd=run.sd.trib2)-
pnorm(strata.index[i],mean=run.mean.trib2,sd=run.sd.trib2)
        pop.strata.pct.main[i] <-pnorm(strata.index[i+1],mean=run.mean.main,sd=run.sd.main)-
pnorm(strata.index[i],mean=run.mean.main,sd=run.sd.main)
    } # end i loop
# Visualize run timing curves and tagging events
plot(pop.strata.pct.main*Nmain,type="l",col="red",xlab="temporal strata, (t)",ylab="abundance (t)",lwd=2)
points(pop.strata.pct.trib1*Ntrib1,type="l",col="blue",lty=1,lwd=2)
points(pop.strata.pct.trib2*Ntrib2,type="l",col="green",lty=2,lwd=2)
abline(v=tag.strata)
legend("topleft",legend=c("Main run", "Trib 1", "Trib 2", "Tag
event"),col=c("red","blue","green","black"),lty=c(1,1,2,1),lwd=c(2,2,2,1),bty="n")

# Override tagging rates if TAG OPTION B is chosen above (constant tag rate across all three populations), this code forces constant
tag rates
if (constant.tag.rate !=0)
    {
        tag.rate.trib1 <- rep(constant.tag.rate,times=length(tag.strata))
        tag.rate.trib2 <- rep(constant.tag.rate,times=length(tag.strata))
        tag.rate.main <- rep(constant.tag.rate,times=length(tag.strata))
    } # end if

# Modify tag rates to add error under ERROR OPTION 2, if TAG OPTION B or C is chosen
# Option to add error on proposed tagging rates (tag release OPTION B & C only_ when sampling is a "deterministic" process rather
# than probabilistic binomial or multinomial sampling. This updates proposed deterministic tag rates with error, if any
# (set by 'tag.rate.sd' ), and only if tag.probablilistic has been set to ZERO
# Lognormal deviates w/ bias correction (e.g. Maudner, M.N. 2006. ICES, 63:969-979):
err.v1 <- exp( rnorm(n=length(tag.rate.trib1),mean=0,sd=tag.rate.sd) - .5*tag.rate.sd^2 )
err.v2 <- exp( rnorm(n=length(tag.rate.trib2),mean=0,sd=tag.rate.sd) - .5*tag.rate.sd^2 )
err.v3 <- exp( rnorm(n=length(tag.rate.main),mean=0,sd=tag.rate.sd) - .5*tag.rate.sd^2 )
if (tag.probablilistic == 0)
    {
        if (err.by.strata.time==0) # if option is chosen above, fix error to be same across subpopulations in
any tagging event
            {
                err.v2 <- err.v1
                err.v3 <- err.v1
            } #end if
        tag.rate.trib1 <- tag.rate.trib1 * err.v1
        tag.rate.trib2 <- tag.rate.trib2 * err.v2
        tag.rate.main <- tag.rate.main * err.v3
    }

# Simulate tagging at the marking site by strata, using TAG OPTION specified above, and probabilistic or deterministic sampling as
specified
# through ERROR OPTION 1 above
for (j in 1:length(tag.strata) )
    {
        if ( sum(constant.num.tag) != 0) # constant release of tags per tagging strata (TAG OPTION A above)
            {
                sum.runs <- round(Ntrib1*pop.strata.pct.trib1[ tag.strata[j]
])+round(Ntrib2*pop.strata.pct.trib2[ tag.strata[j] ])+
                round(Nmain*pop.strata.pct.main[
tag.strata[j] ] )

                p.trib1 <- round(Ntrib1*pop.strata.pct.trib1[ tag.strata[j] ] ) / sum.runs
                p.trib2 <- round(Ntrib2*pop.strata.pct.trib2[ tag.strata[j] ] ) / sum.runs
                p.main <- round(Nmain*pop.strata.pct.main[ tag.strata[j] ] ) / sum.runs
                if (tag.probablilistic == 1) # ERROR OPTION 1, probabilistic tagging process
                    {
                        temp.multinom <- rmultinom(n=1, size=constant.num.tag[j], prob
=c(p.trib1,p.trib2,p.main))

                        marks.trib1[j] <- temp.multinom[1]
                        marks.trib2[j] <- temp.multinom[2]
                    }
            }
    }

```

Appendix 4. Continued.

```

                                marks.main[j] <- temp.multinom[3]
                                } # end if
                                if (tag.probabilistic == 0) # Deterministic tagging process option (but can add error if
ERROR OPTION 2 is chosen, see above)
                                {
                                    marks.trib1[j] <- round(p.trib1 * constant.num.tag[j])
                                    marks.trib2[j] <- round(p.trib2 * constant.num.tag[j])
                                    marks.main[j] <- constant.num.tag[j]-sum(marks.trib1[j] +
marks.trib2[j]) # this line ensures sum tags = constant.num.tag[j]
                                } # end if
                                } # end if
                                if ( sum(constant.num.tag) == 0 ) # tagging is in proportion to abundance (TAG OPTION B & C above)
                                {
                                    if (tag.probabilistic == 1) # ERROR OPTION 1, probabilistic tagging process
                                    {
                                        marks.trib1[j] <-
rbinom(n=1,size=round(Ntrib1*pop.strata.pct.trib1[ tag.strata[j] ]),prob=tag.rate.trib1[j])
                                        marks.trib2[j] <-
rbinom(n=1,size=round(Ntrib2*pop.strata.pct.trib2[ tag.strata[j] ]),prob=tag.rate.trib2[j])
                                        marks.main[j] <-
rbinom(n=1,size=round(Nmain*pop.strata.pct.main[ tag.strata[j] ]),prob=tag.rate.main[j])
                                    } # end if
                                    if (tag.probabilistic == 0) # Deterministic tagging process option (but can add error if
ERROR OPTION 2 is chosen, see above)
                                    {
                                        marks.trib1[j] <- round(
tag.rate.trib1[j]*(Ntrib1*pop.strata.pct.trib1[ tag.strata[j] ] ) )
                                        marks.trib2[j] <- round(
tag.rate.trib2[j]*(Ntrib2*pop.strata.pct.trib2[ tag.strata[j] ] ) )
                                        marks.main[j] <- round(
tag.rate.main[j]*(Nmain*pop.strata.pct.main[ tag.strata[j] ] ) )
                                    } # end if
                                } # end j loop

                                # The recapture event (can make this process deterministic by setting 'recapture.probs =1.0' in the parameters section (ERROR
OPTION 3,
                                # see above), or probabilistic by setting 'recapture.probs < 1.0')
                                # the number of true tributary population fish that are detected going through the weir
                                weir1 <- rbinom(n=1,size=round( sum(pop.strata.pct.trib1*Ntrib1) ),prob=recapture.probs)
                                weir2 <- rbinom(n=1,size=round( sum(pop.strata.pct.trib2*Ntrib2) ),prob=recapture.probs)
                                # the number of true tagged tributary fish that are detected going through the weir
                                recaptures1 <- rbinom(n=1,size=sum(marks.trib1),prob=recapture.probs)
                                recaptures2 <- rbinom(n=1,size=sum(marks.trib2),prob=recapture.probs)

                                # Estimate abundance, report confidence intervals and simulation output

                                # The Chapman variant of the Lincoln Petersen estimator: point estimates and CI's using an exact poisson and parametric bootstrap
                                n1 <- sum(marks.trib1) + sum(marks.trib2) + sum(marks.main) # number of released marks
                                n2 <- weir1 + weir2 # total number of recaptures
                                m2 <- recaptures1 + recaptures2 # total number of recaptures that were marked
                                N <- round((n1+1)*(n2+1)/(m2+1)) # The Chapman point estimate

                                # Confidence interval Method 1: parametric bootstrap with hypergeometric distribution
                                nn.<- 100000 # the number of random draws
                                m. <- n1 # n1 in the Chapman estimator, the number of marks ("white balls" by R) in the urn
                                n. <- N-n1 # the number of unmarked fish in the urn at time of recapture
                                k. <- n2 # the number of balls drawn from the urn, the recapture sample
                                m2.sim <- rhyper(nn=nn. , m=m. , n=n. , k=k. )
                                N.sim <- round((n1+1)*(n2+1)/(m2.sim+1)) # bootstrap point estimate
                                CI.Bootstrap <- quantile(N.sim,probs=c(alpha.lo,alpha.hi)) # bootstrap confidence interval

                                # Confidence interval Method 2: Poisson approximation, using m2 as the "entering" variable, with Poisson exact measures
from eiptools
                                # see Krebs (1998) section 2.1.1, and note these quantities are wider by quite a bit from CI's using values
reported in Krebs
                                # and are closer to those using the information in A1 in Seber 1982, but narrower.
                                require(eiptools)
                                temp.m2 <- pois.exact(m2,conf.level = (alpha.hi-alpha.lo) )

```

Appendix 4. Continued.

```
CI.PoissonExact <- c(round((n1+1)*(n2+1)/(temp.m2$upper+1)),round((n1+1)*(n2+1)/(temp.m2$lower+1)))  
  
# Print output:  
# abundances: estimated, true, %bias  
N; Ntotal; signif((N-Ntotal)/Ntotal,digits=2)  
# Confidence intervals: poisson exact, bootstrap version  
CI.PoissonExact; CI.Bootstrap  
# tag rates: trib1, trib 2, main  
sum(marks.trib1) / Ntrib1; sum(marks.trib2) / Ntrib2; sum(marks.main)/Nmain  
# total tag release by subpopulation: trib1, trib 2, main, total  
sum(marks.trib1); sum(marks.trib2); sum(marks.main); (sum(marks.trib1)+sum(marks.trib2)+sum(marks.main) )  
# tag release by subpopulation by strata: trib 1, trib 2, main  
marks.trib1; marks.trib2; marks.main  
# tag rates by strata: trib 1, trib 2, main  
tag.rate.trib1; tag.rate.trib2; tag.rate.main
```