Regional Operational Plan SF.2A.2014.03

Kenai River Chinook Salmon Abundance and Migratory Timing

by

Adam Reimer

May 2014

Alaska Department of Fish and Game **Divisions of Sport Fish and Commercial Fisheries**

Symbols and Abbreviations

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Weights and measures (metric)

centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)

cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature

day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry

all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General

Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat. or long.
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Mathematics, statistics

all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_2$, etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

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by

Adam Reimer

Alaska Department of Fish and Game, Division of Sport Fish, Soldotna

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Division of Sport Fish
May 2014

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PURPOSE

The primary purpose of this research is to provide an estimate of Chinook salmon abundance entering the Kenai River that is independent of existing sonar programs. Both estimates of abundance have been used to develop escapement goals for Kenai River Chinook salmon (Fleischman & McKinley, 2013; McKinley & Fleischman, 2013). A secondary purpose of this research is to monitor Chinook salmon migration within the Kenai River drainage for the purpose of informing management decisions with respect to time and area.

BACKGROUND

The Kenai River watershed encompasses approximately 2,200 square miles of the Kenai Peninsula including diverse landscapes such as glaciers, large lakes, high mountains, and vast lowlands. The Kenai River mainstem is approximately 82 miles long including a 15 mile stretch where it flows through Skilak Lake (Figure **1**). Tidal influence extends up to rivermile (rm) 12.

Populations of Chinook salmon *Oncorhynchus tshawytscha*, coho salmon *O. kisutch*, sockeye salmon *O. nerka*, pink salmon *O. gorbuscha*, Dolly Varden *Salvelinus malma*, and rainbow trout *O. mykiss* live in the Kenai River and support valuable commercial and recreational fisheries. For example, Kenai River Chinook salmon support the largest recreational fishery for this species in Alaska. (Jennings, Sundet, & Bingham, 2009). Kenai River fisheries will likely support substantial angler effort into the foreseeable future due to its reputation, easy accessibility and location near major Alaskan population centers.

For management purposes, Kenai River Chinook salmon are separated temporally into two runs; early-run fish are those that enter the river prior to July 1 and late-run fish are those that enter the river on or after July 1. The estimated total annual run of early-run Chinook salmon has ranged from 5,605 (cv=0.09) to 23,800 (cv=0.12) Chinook salmon (McKinley & Fleischman, 2013). Early-run fish are harvested primarily by the inriver sport fishery, but also by a marine sport fishery in Cook Inlet and a small subsistence fishery in the estuary. The estimated total annual run of late-run Chinook salmon has ranged from 28,550 (cv=0.09) to 99,690 (cv=0.10) Chinook salmon (Fleischman & McKinley, 2013). Late-run fish are harvested primarily by an inriver sport fishery and a marine commercial set gillnet fishery in Cook Inlet, but also by marine sport, commercial drift gillnet, subsistence and personal use fisheries. The largest potential biases in estimates of early and late run abundance apply to species apportionment of the sonar based inriver run estimate.

Biologically, Kenai River Chinook salmon are separated into tributary and mainstem spawning populations. Most populations of tributary spawning Chinook salmon arrive from late-April to early-July (T. N. Bendock & Alexandersdottir, 1992; Burger, Wangaard, Wilmot, & Palmisano, 1983; A. M. Reimer, 2013) although some tributaries (Russian River and Grant Creek) have demonstrated later return timing. Tributaries of the Kenai River (Figure **1**) which support populations of Chinook salmon include Beaver Creek, Slikok Creek, Funny River, Moose River, Killey River, Russian River, Juneau Creek, Quartz Creek, Ptarmigan Creek, and Grant Creek (T. N. Bendock & Alexandersdottir, 1992; Burger et al., 1983; Johnson & Daigneault, 2013; A. M. Reimer, 2013). Benjamin Creek, tributary of the Killey River, and Crescent and Dave's creeks, tributaries of Quartz Creek, also contain Chinook salmon. Mainstem spawning Chinook salmon

arrive from late-June to mid-August (T. N. Bendock & Alexandersdottir, 1992; Burger et al., 1983; Hammarstrom, Larson, Wenger, & Carlon, 1985; A. M. Reimer, 2013). The entire Kenai River mainstem upstream of the intertidal area (rm12) is suitable spawning habitat for Chinook salmon (Burger et al., 1983; A. M. Reimer, 2013).

Thus the biological and management divisions are roughly synonymous. Details regarding the overlap in the run timing of tributary- and mainstem-spawning Chinook salmon as well as the spatial and temporal distributions of the inriver sport harvest of these two groups of fish are reported elsewhere (McKinley, Barclay, & Jasper, 2013).

ABUNDANCE ESTIMATION

During the 1988 Alaska Board of Fisheries (BOF) meeting, management policies were adopted to govern management of both runs. These policies, amended many times since, established escapement goal ranges for both runs and prescribed the management actions available to achieve those goals. The early-run optimum escapement goal range (OEG) is currently 5,300 to 9,000 Chinook salmon. The late run sustainable escapement goal range (SEG) is currently 15,000-30,000 Chinook salmon. The management plans for each run require timely predictions of escapement, as well as age composition data to develop brood tables necessary for stock-recruit assessment. Implementation of these management plans has been contentious and attracts much public scrutiny. In the past 20 years, the 1997, 1998, 2000, 2002, and 2010-2013 early runs, and the 1998, 2011- 2013 late runs were restricted to meet escapement goals.

The size of the inriver run is a key component for estimating spawning escapement and implementing management plans. Daily and seasonal estimates of Chinook salmon abundance at rm 8.6 have been generated since 1987 using hydroacoustic techniques. Acoustic assessment of Chinook salmon in the Kenai River is complicated by the presence of more abundant sockeye salmon, which migrate concurrently with Chinook salmon. From 1986 to 2012, sockeye salmon passage estimates generated by the rm 19 sockeye sonar project ranged from 645,906 to 2,295,576 (Westerman & Willette, 2013) while late-run Chinook salmon passage estimates generated by the Chinook sonar project ranged from 23,250 (CV=0.09) to 85,110 (CV=0.13) (Fleischman & McKinley, 2013). Because of these difficulties, acoustic assessment of Chinook salmon abundance in the Kenai River has used continuously refined technologies and techniques in an effort to improve fish species classification. Most recently, dual-frequency identification sonar (DIDSON) has been used to assess Kenai River Chinook salmon abundance passing upstream midriver at rm 8.6 since 2010 (Miller, Burwen, & Fleischman, 2013).

In 2011, it became evident that additional Chinook salmon migrate shoreward of the DIDSON transducers at rm 8.6 (Burwen, Miller, & Fleischman, 2014). In 2012 and 2013, more small Chinook salmon were counted at tributary weirs than could be explained by apportioning rm 8.6 sonar counts with rm 8.6 netting data (both collected midriver). In 2013, experimental netting near shore at rm 8.6 caught a disproportionate number of small Chinook salmon compared to the standard midriver netting and fish captured nearshore were similarly sized to fish sampled at tributary weirs (Figure **2**). These findings have motivated considerable revisions to Chinook salmon sonar and netting programs in the Kenai River.

Data from this project has been used to produce post-season estimates (Table **1**) of total inriver Chinook salmon abundance, based on a Stock Specific Abundance and Run Timing model (SSART). Such estimates have been used to develop new escapement goals (Fleischman & McKinley, 2013; McKinley & Fleischman, 2013) based on expanded DIDSON estimates. This operational plan describes total inriver Chinook salmon abundance estimation using the SSART model in 2014.

ADF&G began testing an additional sonar site at rm 13.7 during 2013. The original (and current) site located at rm 8.6 has the advantage of being located downstream of all spawning Chinook salmon. However, water level at the site is tidally influenced, and sonar transducers situated to be submerged near shore at low tide are much farther offshore during high tide. Consequently, a variable proportion of passing fish are detected, depending upon fish spatial distribution by tide stage. The new site is above tidal influence and is designed to count the vast majority of migrating fish. Abundance estimates from the rm 13.7 sonar and from this project will provide valuable cross-checks with one another, thereby facilitating an enhanced understanding of Chinook salmon abundance, run-timing, and behavior that will be useful to fisheries managers.

MIGRATORY DISTRIBUTION AND TIMING

Radio tags have been deployed in conjunction with the SSART model to improve the precision of stock composition estimates. However, radio-tagged Chinook salmon also provide general information that is valuable for fisheries management. A major source of management uncertainty involves implementing stock specific fishing regulations during mixed stock sport fisheries. For example, overlap in the run timing of tributary- and mainstem-spawning Chinook salmon within the Kenai River makes restrictions or liberalizations directed at one stock difficult. Radio tags deployed during this study will update spatial and temporal distribution information for Kenai River Chinook salmon stocks. This information has been summarized from 2010-2013 (A. M. Reimer, 2013).

Telemetry data from this project will also provide an estimate of the proportion of Chinook salmon that spawn between sonar counters at rm 8.6 and rm 13.7. A separate project is responsible for estimating harvest downstream of the rm 13.7 site[1].

OBJECTIVES

OBJECTIVES

1. Estimate the inriver abundance of early-run Chinook salmon entering the Kenai River from 16 May through 30 June and late-run Chinook salmon entering Kenai River from 1 July through 10 August, such that both bounds of the 95% Bayesian credibility intervals are within 25% of the corresponding posterior medians.
2. Estimate the proportion of mainstem-spawning Chinook salmon that migrated upstream of Kenai river mile 13.7 such that the estimate is within 8 percentage points of the true value 95% of the time.

[1] The Kenai River Inriver Gillnetting Study and the Kenai River Creel Survey are described in another operational plan (McKinley FY14/FY15 Operational Plan, Kenai River Creel Survey, Inriver Gillnetting and Age Composition Study).

SECONDARY OBJECTIVES

1. Count the number of radio-tagged Chinook salmon that entered the Killey River and the number of radio-tagged Chinook salmon that migrated above the Killey River weir.
2. Determine the spawning distribution for radio-tagged Chinook salmon captured during the early and late runs.
3. Determine the dates when radio-tagged Chinook salmon that spawned in the Funny River enter the Funny River.
4. Determine the dates when radio-tagged Chinook salmon that spawned in the Killey River enter the Killey River.
5. Estimate the percentage of radio-tagged Chinook salmon sampled prior to July 1 that were in waters open to sport fishing upstream of Slikok Creek on July 1.
6. Estimate the percentage of radio-tagged Chinook salmon sampled prior to July 1 that were in waters open to sport fishing upstream of Slikok Creek on July 16.

METHODS

STUDY DESIGN

Inriver Abundance

The Stock Specific Abundance and Run Timing model (SSART) was developed by the USFWS (Bromaghin, Gates, & Palmer, 2010) and later modified by ADF&G[2]. The model creates a space-time matrix of relative abundance where the genetic reporting groups ("stocks": Killey River-Benjamin Creek, Funny River-Slikok Creek, Grant Creek, mainstem Kenai River-Juneau Creek, Quartz Creek-Crescent Creek, and Russian River) represent the space (stock) component and 2-week strata represent the time component. Information about relative abundance by stock is obtained from two data sources: genetic stock identification (GSI) estimates of inriver gillnetting samples, and final destinations from radio telemetry. Information about relative abundance over time is obtained using the CPUE of an inriver gillnetting program located near rm 8.6. The matrix is converted from relative abundance to actual fish by having known escapements for one or more of the genetic reporting groups. For the 2014 season we will have known escapements for 4 of 6 reporting groups and partial information about one other (Killey River / Benjamin Creek).[3] Harvest is accounted for, by stock, by collecting genetic samples from harvested fish, and weighting by estimates of harvest by time strata. Because the SSART model reconstructs the entire run through space and time, it provides stock-specific estimates of abundance, harvest rate, and harvest by time period.

For traditional mark-recapture experiments, and for estimates like those obtained by Bromaghin et al (2010), the migration success of marked fish can be affected by the act of handling and marking (Reimer & Fleischman, 2012). Here, we derive stock composition for the SSART model primarily from GSI analysis of tissue samples, which are unaffected by fish behavior after sampling. This removes a large source of potential bias. Since 2010, GSI estimates of stock composition have been supplemented with known stock IDs from radio telemetry final destinations, which improve the precision of the resulting estimates of abundance.

[2] The current methods differ from those of Bromaghin et al. (2010) in the use of GSI allele frequency data, the inclusion of harvest, and in the adoption of a Bayesian, rather than maximum likelihood, framework.

[3] In 2014, the only stock component with no stand-alone estimate of escapement will be mainstem Kenai River-Juneau Creek.

Another advantage of the SSART model over traditional mark-recapture is that it accommodates differential sampling fractions across time. Stratification over the time dimension permits application of different levels of sampling effort during each time stratum.

The SSART model relies on information collected by several projects to achieve its objectives. While each of these projects is described fully in separate operational plans, specific features relevant to our objectives are discussed herein. The department has completed a memorandum of agreement with the United States Fish and Wildlife Service (USFWS) (COOP-12-070) and a fish resource permit with McMillen, LLC (SF2013-105d[4]) that cover the activities described herein including sharing of data between organizations.

Inriver run stock composition and index of abundance

The temporal index of abundance used for the SSART model is taken from the Kenai River Chinook Salmon Inriver Gillnetting Study. Stock composition of the inriver run is estimated from GSI and radio telemetry data collected by the Kenai River Chinook Salmon Inriver Gillnetting Study.

Kenai River Chinook Salmon Inriver Gillnetting Study

The Kenai River Inriver Gillnetting Study has fished a standardized location defined by the rm 8.6 Chinook salmon sonar site's ensonified zone (offshore) since 2002. In 2013, a second crew netted the "nearshore" area between each bank and the ensonified zone. The proportion of Chinook salmon less than 750 mm MEF was larger for fish captured nearshore than for fish captured offshore during both runs (early run P=0.002, late run P=0.055).

During 2014, the gillnetting project will be redesigned and expanded to capture fish migrating bank to bank at rm 8.6. Sampling will occur for 12 hours per day from May 16 to August 15. Additional sampling may occur at other sites.[5] Age, sex and length (ASL) samples and genetic samples will be taken from every Chinook salmon captured. Radio tags will be deployed on every fish sampled prior to July 1 and on a subset of those sampled on or after July 1 (see Radio Tag Deployments section below). Every Chinook salmon captured will receive a hole punch in the upper caudal fin to prevent resampling.

The project has used two mesh sizes (5.0" and 7.5", stretched) since 2002, chosen to reduce the size selectivity of the sample and also to reduce the probability of damage to gill filaments during capture. In 2014, 4-panel nets with 2 alternating panels of each mesh size will be deployed systematically with respect to bank and distance offshore to ensure that fish of all sizes, throughout the sampling area have a reasonable possibility of capture.

We anticipate approximately double the sample size from the Kenai River Chinook Salmon Inriver Gillnetting Study relative to past years, based simply on twice as much sampling effort. From 2010-2013 between range 231-645 genetic samples have been collected by Kenai River Inriver Gillnetting Study staff (Table **2**). However, we expect the 2014 run size to approximate the 2013 run size and therefore expect to collect less than 500 genetic samples in 2014.

[4] SF2013-105d is the 2013 fish resource permit number. The 2014 fish resource permit had not been issued by the time of publication.

[5] Sampling is scheduled near rm 12 with 3 mesh sizes during the early run, however such plans are subject to change if the abundance of early-run Chinook salmon substantially exceed the preseason forecast.

Escapement by reporting group

Killey River Weir

The Killey River weir provides an escapement estimate for part of the Benjamin Creek/Killey River genetic reporting group to the SSART model. The weir has been operated by the USFWS since 2012. Upstream migrating fish swim freely through a fish passage chute in the resistance board weir where they are recorded by a motion-activated digital video recording device. The video footage from the site is reviewed by a technician to determine upstream passage. The weir will be operational from early-June until mid-August.

Migrating Chinook salmon will be sampled for ASL by closing the fish passage chute and allowing migrating Chinook salmon to collect within a sampling enclosure between 1500 and 1800 nearly every day. This system resulted in sampling 10 to 20 percent of the run during each quarter of the migration in 2013.

Because the weir is located approximately 2 miles downstream from the confluence of Benjamin Creek with the Killey River, we expect significant spawning both upstream and downstream of the weir. Radio tags will be used to determine the fraction of Killey River fish that migrated upstream of the weir. During 2013, the USFWS observed 1,881 Chinook salmon at the Killey River weir. Of the 38 radio tagged Chinook salmon that entered the Killey River drainage in 2013, 19 migrated upstream of the Killey River weir.

Funny River Weir

The Funny River weir provides an escapement estimate for the Funny River part of the Funny River-Slikok Creek genetic reporting group to the SSART model. The weir has been operated by the USFWS since 2006. Upstream migrating fish swim freely through a fish passage chute in the resistance board weir where they are recorded by a motion activated digital video recording device. The video footage from the site is reviewed by a technician to determine upstream passage. The weir will be operational from late-May until mid-August.

Migrating Chinook salmon will be sampled for ASL by periodically closing the fish passage chute and allowing migrating Chinook salmon to collect within a sampling enclosure. Sampling effort will be scaled in real time to sample at least twenty percent of the run during each calendar week.

The weir is located approximately 0.75 miles upstream from the Funny River confluence with the Kenai River. A limited amount of spawning does occur downstream of the weir[6]. During 2013, the USFWS observed 1,027 Chinook salmon at the Funny River weir.

Escapement from the Slikok Creek component of the Funny River-Slikok Creek reporting group will be estimated based on the historic relationship between the Funny River and Slikok Creek escapements from 2008-2012[7].

[6] Between 2010 and 2013, 40 radio tagged Chinook salmon spawned within the Funny River drainage. Thirty eight fish spawned upstream of the weir, one fish spawned immediately downstream of the weir and one fish that spawned near the weir was not confirmed as upstream or downstream.

Grant Creek Weir

The Grant Creek weir provides an escapement estimate for the Grant Creek genetic reporting group to the SSART model. The Grant Creek weir has been operated by the McMillen, LLC on behalf of the Grant Lake Hydro Project (FERC # 13212) only since 2013. The weir will be operational from break-up to freeze-up. Upstream migrating fish will be passed manually after sampling for ASL. Spawning is not known to occur downstream of the weir. During 2013, 33 Chinook salmon were counted at the Grant Creek weir.

Quartz Creek Weir

The Quartz Creek weir provides an escapement estimate for the Quartz Creek/Crescent Creek genetic reporting group to the SSART model. The weir has been operated by the USFWS only since 2013. Upstream migrating fish swim freely through a fish passage chute in the resistance board weir where they are recorded by a motion activated digital video recording device. The video footage from the site is reviewed by a technician to determine upstream passage. No ASL samples will be collected. The weir will be operational from late-May until mid-August. The weir is located approximately 0.15 miles upstream from Kenai Lake. No spawning is known to occur downstream of the weir. During 2013, 280 Chinook salmon were counted at the Quartz Creek weir.

Russian River Weir

The Russian River weir[8] provides an escapement estimate for the Russian River genetic reporting group to the SSART model. The weir is an engineered structure operated annually by the Alaska Department of Fish and Game near the outlet of Lower Russian Lake. Upstream migrating fish are physically blocked by a closed fish trap gate until the weir attendant begins the daily count. Fish are counted by direct observation as they swim through a fish trap. No ASL samples will be collected. The weir is located approximately 3 miles upstream from the Russian River confluence with the Kenai River. During 2013, 110 Chinook salmon were counted at the Russian River weir.

Chinook salmon are known to spawn between the weir and the confluence. The magnitude of downstream spawning is assessed by a stream survey conducted annually in late-August. The survey count of Chinook salmon spawning downstream of the Russian River weir has ranged from 15% to 53% of the annual weir passage from 2007-2013[9]. Because many of these fish spawn near the confluence with the Kenai River we are uncertain which GSI reporting group they belong to. However, SSART model abundance estimates are minimally affected by their inclusion as Russian River escapement.

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[7] The Slikok Creek weir count varied between 2% (SE=0.4%) and 6% (SE=0.7%) of the sum of the Funny River and Slikok Creek weir counts between 2008 and 2012.

[8] The Russian River weir is described in a separate operational plan (Pawluk, FY13/FY15 Operational Plan, "Sockeye Salmon Escapement Studies at the Russian River, Alaska").

[9] Excluding the 2011-2012 surveys which were considered unreliable.

Harvest estimates and stock composition of the harvest

Downstream of the Soldotna Bridge

The Kenai River downstream of the Soldotna Bridge was closed to Chinook salmon harvest prior to July 1, 2014 by emergency order on February 27, 2014 (2-KS-1-04-14). When the fishery reopens, harvest will be estimated by the Kenai River Creel Survey[1] and stock composition of the harvest will be estimated from tissue samples taken from harvested fish. The creel survey is operated annually by the Alaska Department of Fish and Game.

The creel survey operates 4 days per week (Saturday, Sunday and 2 of the 4 non-Monday weekdays) beginning as soon as the fishery opens until July 31. Harvest sampling opportunity occurs as part of a stratified two-stage roving-access creel survey with approximately 10-12 hours of sampling opportunity occurring during each day. Angler interviews and harvest sampling occur at 6 boat launches in this area. There are several private moorings and a few private launches that are not sampled. Creel survey staff only sample from anglers that have completed fishing for the day.

Given the harvest restrictions in place for the 2014 Kenai River Chinook salmon fishery, the number of tissue samples collected in 2012 and 2013 provide our most likely expectation for sample sizes in 2014, since the fishery was also restricted in those years. During 2012-2013, an average of 50 tissue samples (Table **2**) were genotyped from harvested Chinook salmon sampled by Kenai River Creel Survey staff.

Upstream of the Soldotna Bridge

The Kenai River upstream of the Soldotna Bridge was closed to Chinook salmon harvest in 2014 by emergency order on February 27, 2014 (2-KS-1-04-14). If the fishery upstream of the Soldotna Bridge were to reopen midseason, harvest and the stock composition of the harvest would be estimated as planned for in 2013 (A. Reimer, 2013).

Inriver Abundance Estimates: Considerations of Bias

Complete data required to generate SSART model estimates of abundance have been collected since 2007. Estimates of abundance generated with 2007-2012 data were reported by McKinley and Fleischman (2013) for the early run and by Fleischman and McKinley (2013) for the late run.

As mentioned previously, the SSART model requires an index of relative abundance by time stratum. By employing gillnet CPUE as such an index, it is assumed that catchability of Chinook salmon does not differ across time strata. Recent research has identified a large driver for differential catchability by time strata and stock. Significant migration of Chinook salmon at rm 8.6 occurs outside of the mid-channel ensonified zone (Fleischman & McKinley, 2013; McKinley & Fleischman, 2013), and thus outside of the sampling area of the inriver gillnetting project prior to 2014 (Perschbacher, 2012).[10]

[10] Another possible driver of unequal catchability is fish density, through its effects on net saturation, and through its potential effects on Chinook salmon distance from shore. Density of salmon near rm 8.6 can be an order of magnitude higher in the late run compared to the early run.

Estimates of late-run abundance are especially sensitive to this assumption, because the late run is composed almost exclusively of mainstem spawning fish which are not benchmarked by weir counts. Initial comparisons between sonar counts from the rm 8.6 and rm 13.7 sonar sites indicate that the proportion of fish migrating midriver at rm 8.6 may change over time. Such comparisons will continue in 2014.[11] Depending on the outcome, it may be necessary to devise a different index of relative abundance that incorporates information from the rm-13.7 sonar.

The model also assumes that, within each time stratum, each stock has an equal probability of being captured and sampled. In 2013, experimental netting confirmed that smaller fish migrate closer to the river bank than larger fish (Figure **2**). Stocks with fish that are smaller than average can thus experience reduced probability of capture in the midriver nets.

Violation of this assumption can inject bias into SSART-derived estimates of abundance. The potential for bias was evident in 2013. In simple terms, one can think of SSART-derived estimates as weir counts divided by the estimated proportion p_W of the total run that originates from stocks with weirs, where p_W is estimated from the GSI sample data. In 2013, the major stocks with weirs (Funny River, Upper Killey River) had an unusually large fraction of small fish. Because small fish have a reduced probability of capture, Funny and Killey stocks were probably underrepresented in the GSI samples, p_W may have been underestimated, and total abundance may have been overestimated. Preliminary SSART estimates for 2013 were, in fact, higher than expected.[12]

In the event that the above considerations cannot be satisfactorily addressed, it may be necessary to develop a size-censored version of the analysis, one that includes only large Chinook salmon, which are less prone to migrating out of reach of the sonar and nets.[13] A preliminary version of such an analysis was conducted in preparation for the Upper Cook Inlet Board of Fish meeting in January 2014.[14]

The opportunities for bias[15] described above can be reduced by better equalizing probability of capture across space, time, and fish size. Considerable resources will be devoted to achieving this goal in 2014[1] (also see Inriver run stock composition and index of abundance section above).

Inriver Abundance Estimates: Expected Precision

The precision of the SSART model estimates have improved over time (Table **1**), as the model and input datasets have been improved, although most estimates have failed to satisfy the precision criterion from Objective 1 (both bounds of the 95% credibility intervals are within 25% of the posterior medians).

[11] We will monitor the ratio of large-Chinook net CPUE to rm 13.7 sonar-based abundance estimates. This ratio reflects catchability of the inriver gillnetting project at rm 8.6 because the rm 13.7 sonar site has bank to bank coverage and there is no evidence that DIDSON/ARIS saturates at high fish densities. This ratio will also be affected by holding, spawning, and harvest between rm 8.6 and 13.7, but we anticipate being able to adjust for these factors using radio telemetry and creel data.

[12] These estimates have not been finalized as a result.

[13] A size-structured model is also a possibility, if probability of capture can be more nearly equalized for small and large fish.

[14] http://www.adfg.alaska.gov/static/fishing/chinookproject/PDFs/kenai_king_salmon_faqs_01282014.pdf

[15] Also, the potential for bias is exacerbated during runs with large proportions of small fish, like 2013. If it turns out that 2013 was an anomaly, bias considerations will be less important.

For the 2014 season we expect similar run sizes to 2012 and 2013. The 2012 season was used to estimate our expected precision for 2014 because SSART estimates were not finalized for all sizes of Chinook salmon in 2013. Relative to 2012, the input dataset is expected to change as follows;

- Inclusion of Quartz Creek and Grant Creek escapement estimates.
- Increased GSI samples and radio tag deployments near rm 8.6.
- No GSI samples or radio tag deployments near rm 21.0.
- Harvest sampling downstream of the Soldotna Bridge will be limited to samples collected by Kenai River Creel survey staff.

To estimate the expected precision for 2014, first the 2014 data were simulated by modifying the 2012 data to reflect expected sampling levels in 2014. The simulated 2014 data were added to the actual 6 year SSART dataset (2007-2012). SSART2 v4.6b was then run on the resulting 7 years of data (6 years actual,1 year simulated). Modifications to simulate 2014 sampling levels include;

- The posterior medians for escapement into the Quartz Creek and Grant Creek drainages from SSART v4.6b were used as weir counts in the modified dataset.
- GSI data and radio telemetry final destinations for Chinook salmon captured by the inriver gillnetting crew near rm 8.6 were duplicated in the modified dataset to approximate the increased sample size expected from doubling the sampling effort.
- GSI data and radio telemetry final destinations for Chinook salmon captured by inriver gillnetting crews near rm 21.0 were removed from the modified dataset because this sampling program will be discontinued in 2014.
- GSI data from Chinook harvested downstream of the Soldotna Bridge and not sampled by Kenai River Creel survey staff were removed from the modified dataset because supplementary harvest sampling programs will be discontinued in 2014.

For both early and late runs, simulation results indicate the lower bound of the 95% Bayesian credibility interval should be within 19% of the 2014 posterior median while the upper bound of the 95% Bayesian credibility interval should be within 26% of the 2014 posterior median (Table 1).

Migratory Timing and Distribution

Radio telemetry data collected by this project will refine historic run timing and distribution information used in fisheries management.

Radio Tag Deployments

Up to three hundred and fifty radio tags will be deployed in Chinook salmon of all sizes in 2014. In previous seasons, Chinook salmon less than 550 mm MEF were not tagged because of higher mortality rates experienced by smaller Chinook salmon. To mitigate mortality concerns for smaller Chinook salmon in 2014 two sizes of radio tags will be deployed. Chinook salmon less than or equal to 600 mm MEF will be tagged with ATS model F1835B[16] radio transmitters. Chinook salmon greater than 600 mm MEF will be tagged with Advanced Telemetry Systems

[16] ATS 1835B radio tags are 17 mm diameter, 48 mm long and weight 16 grams.

(ATS, Isanti, MN) model F1845B[17] radio transmitters. Both models of radio tag are equipped with a "mortality code" which emits if a motion activated switch within each tag is not toggled for 18 hours.

At rm 8.6[18], between May 16 and June 30, all Chinook salmon sampled for ASL by the Kenai River Inriver Gillnetting project will receive a radio transmitter. Between July 1 and August 15, captured Chinook salmon may be subsampled before radio tagging to ensure radio tags are available through August 15.

The inriver gillnetting project is substantially redesigned in 2014 and the anticipated number of radio tags deployed under the new design, and the size composition of the radio tagged fish is unknown. For planning purposes we increased the number of Chinook salmon captured by tagging crews near rm 8.6 in 2013 to account for the extra sampling effort that will be employed in 2014. The 2013 run size was used in planning because the 2013 abundance is closest to the 2014 forecast. In the early run, we anticipate radio tagging 95 Chinook salmon, including 20 that are less than 600 mm MEF. In the late run, we anticipate radio tagging 229 Chinook salmon, including 34 that are less than 600 mm MEF. Thus we anticipate radio tagging 54 Chinook salmon less than or equal to 600 mm MEF and 270 Chinook salmon greater than 600mm MEF in 2014. We have 280 1845B radio transmitters and 70 1835B radio transmitters available for this project. In the event our actual tag deployments exceed these expectations our tagging frequency after June 30 will be adjusted so that fish are radio tagged through August 15.

Radio Telemetry

Radio-tagged Chinook salmon will be located passively, by a network of stationary radio receiving stations, and actively, by manually tracking from an outboard skiff or fixed-wing aircraft. Stationary receiving stations allow 24-hour monitoring of radio tagged Chinook salmon at key points along their migration routes, although specific fish locations are not determined. Manual tracking allows each fish to be located precisely with respect to area and time. This detection scheme should provide multiple, redundant locations for each tagged animal along expected migration corridors and detect unusual but noteworthy behavior patterns.

Pulse-coded radio transmitters broadcasting on 14 frequencies (151.264-151.635 MHz, 25 pulse codes per frequency) will be used for this project. During stationary radio tracking the scan time for each frequency will be 2 s with a 7 s timeout. Thus, each frequency will be scanned for 2 s; if a transmission is detected then the receiver pauses for 7 seconds on each antenna to decode the pulse code and signal strength. Total scan time will range from 28 s (14 frequencies * 2 s/frequency) when no signals are detected to 4 m 54 s (14 frequencies * 7 s/frequency * 3 antennas) when each frequency has at least one signal detected. During manual radio tracking the scan time for each frequency will be 2 s. If the equipment operator notices an audible transmission during manual radio tracking the receiver is paused at the operator's discretion until the tag location can be accurately determined. Given an average pulse rate of 45 pulses per minute a 2 s scan time will provide sufficient time for each tag to send two transmissions while the signal is being monitored. Similar scan times have provided satisfactory detection and resolution for both manual and stationary tracking in past years.

[17] ATS 1845B radio tags are 19 mm diameter, 56 mm long and weight 26 grams.

[18] Fish captured with gillnets near rm 12 will not be radio tagged during either run.

A risk associated with pulse-coded transmitters is the possibility of encountering abundant co-located radio transmitters. The manufacturer states that the R4100 receiver is capable of simultaneously decoding up to three pulse patterns on a single frequency, the R4500 receiver is capable of simultaneously decoding up to six pulse patterns on a single frequency, and the R4520 receiver is capable of simultaneously decoding up to 15 pulse patterns on a single frequency. The probability of successfully decoding multiple pulse codes is increased as the timeout is increased. We plan to employ three tactics to ensure collocated fish are successfully detected. First, radio tags will be deployed by pulse code ensuring the temporal separation between tags with the same frequency is maximized at the time of release. Second, R4520 receivers will be utilized at sites with the highest possibility of collocation and R4100 receivers will be deployed at sites where the odds of collocation are low. Lastly, the timeout will be changed to 15 seconds at sites that are exposed to large numbers of collocated fish. In this case, maximum scan time would be 10.5 minutes. We feel this is a reasonable tradeoff because a high incidence of collocation implies holding, which mitigates the need for a quick scan time.

Fixed radio receiving stations will be placed at the following locations (see Figure 1);

Location	Receiver	Purpose
River mile 14 sonar site	4500	Mainstem spawning distribution relative to sonar
Slikok Creek confluence	4500	Tributary use, mainstem migration
Soldotna Bridge	4500	Mainstem migration, coincides with SWHS boundary
Funny River confluence	4500	Tributary use, mainstem migration
Moose River confluence	4100	Mainstem migration, coincides with SWHS boundary
Killey River confluence	4520	Tributary use, mainstem migration, % of Killey migrants above weir
Killey River weir	4520	% of Killey migrants above weir
Skilak Lake outlet	4100	Mainstem migration, coincides with SWHS boundary
Skilak Lake inlet	4100	Mainstem migration
Bean Creek	4100	Mainstem migration, enter upper Tributaries

Each fixed station will be equipped with two or three directional antennas; one antenna pointed upstream, one antenna pointed downstream and one antenna pointed up the tributary when applicable. The direction of fish movement can be discerned by comparing signal strengths between antennas within the chronological data.

Determining radio tag fates

The second primary objective and all of the secondary objectives for this project require that each radio-tagged Chinook salmon be assigned a fate and a spawning destination. Our method is described more fully in (A. M. Reimer, 2013).

Radio-tagged fish will be assigned 1 of 4 fates based on their behavior post tagging: drop-out, regurgitation, censor, or migrant. All of the telemetry data will be consolidated into one graphic per fish before deciding on a fate.

1) Drop-outs: Fish categorized as drop-outs enter salt water immediately after tagging.

2) Regurgitation: Tags that are permanently stationary immediately after deployment, proximate to or downstream of the tagging site, were categorized as regurgitations.

3) Censor: Fish that display post-tagging upstream migration that is insufficient in length, duration, or both and cannot be placed in a spawning area during a spawning period for a period of time sufficient for spawning. Criteria for classifying censored fish are explained in detail below.

4) Migrant: Fish that migrate upstream of the tagging site and enter known spawning areas during known spawning periods for a period of time sufficient for spawning were considered migrants. Chinook salmon that enter a Kenai River tributary will be considered migrants to that tributary. Mainstem Kenai River spawning Chinook salmon will be assigned an approximate spawning river mile based on demonstrated site fidelity.

Censoring Criteria for Fish in the Mainstem Kenai River

Migrating Chinook salmon often hold in the mainstem of the Kenai River for days or weeks prior to resuming upstream migration. However, most of the Kenai River provides suitable spawning substrate, and spawning and migrating fish are indistinguishable while collocated. Often holding behavior is revealed by subsequent upstream migration. When holding behavior is followed by mortality, we will censor fish that fail to meet the following minimum spawning requirements:

1) Harvested fish cannot spawn.

2) Fish that fail to display site fidelity upstream of rm 13 (Honeymoon Cove) cannot spawn.

3) Fish deemed mortalities prior to 1 July cannot spawn.

4) Fish that fail to display 6 days of site fidelity prior to mortality cannot spawn.

5) Fish deemed mortalities within 18 days of release cannot spawn.

Previous authors (T. N. Bendock & Alexandersdottir, 1990; T. N. Bendock & Alexandersdottir, 1991; T. N. Bendock & Alexandersdottir, 1992) have used rm 12 as the downstream limit to Chinook salmon spawning. In 2009, ADF&G staff used drift gillnets to capture mainstem spawning Chinook salmon in the lower Kenai River for genetic baseline sampling, but were unable to locate spawning Chinook salmon downstream of rm 13.0 (Honeymoon Cove).

The earliest returning Kenai River Chinook salmon enter freshwater in May, migrate 44 miles upstream, and congregate at the confluence with the Killey River prior to migrating up the Killey River a maximum of 33 additional miles. Spawning site selection, gamete deposition, and redd defense follow migration. These fish congregate near the Killey River confluence from early June to late July. Because the earliest arriving Kenai River Chinook salmon are still migrating in late June, we consider 1 July a conservative estimate of the earliest spawning date for Kenai River Chinook salmon.

ADF&G staff used drift gillnets to capture mainstem spawning Chinook salmon in various river sections during August and September of 2003, 2006, 2009, and 2011. For all years and sampling events, the majority of the Chinook salmon captured in the middle of August were firm[19], but the majority of the Chinook salmon captured by the end of August were ripe[20]. Based

[19] Chinook salmon failed to express gametes in response to light abdominal pressure.

on these observations, we will use the minimum values for site fidelity and stream life displayed by Kenai River Chinook salmon radio tagged between 2010 and 2013 and spawning in September to approximate the minimum values of fish that spawned earlier in the season. This method should be conservative because stream life is known to decrease for later arriving salmon (Quinn, 2005).

Mortality Criteria

Most of the censoring criteria require assigning a mortality date to radio-tagged Chinook salmon. Two complementary sources of information will be used to determine mortality: 1) rapid, permanent, downstream movement and 2) the radio tag's mortality signal. Permanent downstream movement is a definitive indicator of mortality. Because mortality signals are less definitive they will be considered in aggregate, and fish will be deemed mortalities only after consistent mortality signals are detected. When inconsistent mortality information is available, a mortality date will not be assigned.

Expected Precision, Radio-telemetry

We expect to deploy 324 radio-tags at rm 8.6 in 2014 which is sufficient to exceed the precision criterion specified in Objective 2. This calculation assumes that:

(1) Run sizes at the rm-8.6 tagging site are similar to 2013 and sampling effort doubles.
(1) All fish caught in gillnets at rm-8.6 are radio tagged;
(2) 81% of the gillnet catches at rm-8.6 are mainstem-spawning Chinook salmon. This assumption is based on the 2007-2012 SSART model estimates of stock composition by time strata. This leads to 264 viable tags deployed in mainstem-spawning fish.
(3) 42% of the tags deployed will provide spawning destination data (based on 2010-2012 radio tag data). This further reduces the number of useful radio tags, leaving 111 viable tags.
(4) Finally we assumed based on the 2012-2013 data that at least 80% (i.e. $p = 0.8$) of the mainstem spawning Chinook salmon migrate upstream of rm 13.7.

Given these assumptions, we expect to estimate the proportion of mainstem-spawning Chinook salmon that migrate upstream of rm 13.7 such that the estimate is within 8 percentage points of the true value 95% of the time.

DATA COLLECTION

Laboratory Analysis

Assaying Genotypes

DNA extraction and genotyping will generally follow the methods described in detail in Rogers Olive et al. (2013). Briefly, genomic DNA will be extracted from tissue samples using a DNeasy 96 Tissue Kit by QIAGEN (Valencia, CA). SNP loci to be screened will be the set developed by the Gene Conservation Laboratory and surveyed in Kenai River Chinook populations. Fluidigm 192.24 Dynamic Arrays (http://www.fluidigm.com) will be used to screen 38 SNP markers; this differs from the methods of Rogers Olive et al. (2013) where 96.96 Dynamic Arrays were used. The Dynamic Arrays will be read on a Fluidigm EP1 System or BioMark System after amplification and scored using Fluidigm SNP Genotyping Analysis software. Assays that fail to

[20] Chinook salmon expressed gametes in response to light abdominal pressure.

amplify on the Fluidigm system will be reanalyzed on the Applied Biosystems platform. The plates will be scanned on an Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems' Sequence Detection Software version 2.2.

Genotypes produced on both platforms will be imported and archived in the Gene Conservation Laboratory (GCL) Oracle database, LOKI.

Laboratory Failure Rates and Quality Control

Overall failure rate will be calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. An individual genotype will be considered a failure when a locus for a fish cannot be satisfactorily scored.

Quality control (QC) measures will be used to identify laboratory errors and to determine the reproducibility of genotypes. In this process, 8 of every 96 fish (1 row per 96-well plate) will be re-extracted and reanalyzed for all markers by staff not involved with the original analysis. Laboratory errors found during the QC process will be corrected, and genotypes will be corrected in the database. Inconsistencies not attributable to laboratory error will be recorded, but original genotype scores will be retained in the database.

Radio tracking

The majority of telemetry data will be collected at automated, fixed, data-recording stations. A typical fixed station will consist of a guy-wire stabilized mast with two or three directional antennas, an antennae switch, radio receiver, a data collection computer, a 12-volt deep-cycle battery and a weather-resistant box to house the battery and the receiving and data collection equipment. Antennas will be Yagi-style model P154-4 (Cushcraft, Inc. New Hampshire) tuned to receive the 150-154 MHz frequency band. The antennae switch will be ATS Model 100. Stations will be equipped with either a ATS model 4000 or 4100 receiver driven by an ATS model 5041 data collection computer (DCC), an ATS R4500C receiver/DCC , or a ATS R4520C receiver/DCC. This system will be used to detect unique radio tags and record the radio frequency, pulse code, date, time, antenna on which the signal was detected, and a measure of signal strength.

The general location of fixed, data-recording station sites were chosen to answer research questions. The specific location will be chosen to maximize the odds of detecting radio tagged fish. Detection range is increased by maximizing antenna height so sites will be located on high ground or 20-foot masts will be used. Each fixed station will be equipped with two or three directional antennas. Stations placed at tributary confluences will have one antenna pointed upstream, one antenna pointed downstream and one antenna pointed up the tributary. Stations without a nearby tributary will be similarly situated with only an upstream and downstream antenna.

Telemetry stations will be set up mid-May starting at the most downstream sites. After site installation, the detection range for each site will be tested and mapped with a reference tag. The testing procedure calls for two staff members communicating via walkie-talkie; one at the radio receiving station and one in a boat near the site. The boat is held stationary while a radio transmitter is lowered to the river bottom using a weighted string. The location-specific signal

strength for each antenna is then recorded on a map of the site. This procedure is repeated until the detection area for the site has been accurately mapped and the ability to detect tags on each antenna is satisfactory. Of primary interest is a long reach with bank-to-bank detection on both antennas and ensuring that the pattern of signal strengths on each antenna allows correct determination of the tag location relative to the site.

Data collection computers will be downloaded weekly using a laptop computer and software supplied by the manufacturer. During download sessions each fixed site will undergo routine maintenance. Two records of download and maintenance history will be kept. A site log will be kept at each fixed station and used to record the download/maintenance history at that station over the course of the season (Appendix D1). In addition, a fixed station download form will be used to document all download/maintenance activities at all sites during a given week (Appendix D2).

To complement fixed-station data, mobile telemetry will be regularly employed. The mainstem Kenai River downstream of Skilak Lake will be tracked by boat twice weekly from late-May thorough mid-September. The mainstem Kenai River upstream of Skilak Lake will be tracked by boat once weekly from late-June thorough mid-September. Tributaries to the Kenai River will be tracked by airplane every 10 days from late-June to mid-August.

An ATS R4520 receiver with a Cushcraft® P154-4 Yagi-style antenna will be used in riverboat surveys. A single antenna will be installed on a short mast affixed to the boat console and oriented toward the bow of the boat. The boat will be driven at a moderate rate of speed while the receiver, gain set to 3-4, scans all active frequencies. If the boat driver notices an audible transmission the receiver is paused until the tag location can be determined by maximizing the signal strength of the decoded transmission. To save time, location is determined to within a few hundred yards although presence or absence of Chinook salmon relative to the Slikok Creek, Funny River, Moose River, and Killey River closures is determined definitively. Each successfully decoded transmission triggers the R4520 to record the following information; date, time, frequency, pulse code, GPS coordinates, mortality switch position and signal strength.

An ATS R4520 receiver with dual H-style antennas will be used for airplane surveys from a Cessna 180. The airplane will be flown slowly adjacent to the stream of river of interest while the receiver, gain set to max, scans all active frequencies. If a transmission is heard, the scan will be briefly held on the active frequency while the receiver decodes the transmission. In most cases, the plane continues its flight path without regard for the presence or absence of radio tags and tags are located 2-4 times at disjoint locations along the flight path. In areas with multiple collocated fish the airplane will fly tight circles above the collocated radio tags to allow sufficient time to decode all tags present. Each successfully decoded transmission triggers the R4520 to record the following information; date, time, frequency, pulse code, GPS coordinates, mortality switch position and signal strength. The record with the largest signal strength will be considered the approximate location.

DATA REDUCTION

Data reduction procedures for the cooperative projects are described separately in each project's operation plan. Herein, we describe the additional data reduction procedures that will take place in 2014.

Telemetry data

Raw telemetry data will be downloaded from ATS equipment in a proprietary format and saved with a file name that references the date and time when the download occurred. SAS® software will be used to convert the individual downloads into a seasonal file in comma-separated file format. A data map for the fixed station telemetry file is shown in Appendix E1. The date, time, and direction of fish movement past each fixed station will be discerned by comparing signal strengths between the antennas at each station within the chronological data.

Boat tracking data from telemetry equipment will be supplemented with descriptive location information (river mile and relationship to fishery management areas) collected using Juniper Systems Inc.™ Allegro CE™ field computers running Dataplus Professional® software. Data files are saved in a proprietary format that can be merged with telemetry files and converted into comma-separated ASCII files using SAS® software. Air tracking data is similarly supplemented with descriptive location information recorded by hand. A data map for the manual tracking telemetry file is shown in Appendix E2.

DATA ANALYSIS

SSART model

Quantitative inference about Chinook salmon abundance will be made by fitting a space – time model (Bromaghin et al., 2010) to observed weir counts, harvest estimates, netting CPUE estimates, and genetic stock identification (GSI) data[21]. The "space" dimension of the model consists of the six stock groups that have been found to be genetically differentiable: KB (Killey River / Benjamin Creek), FS (Funny River / Slikok Creek), G (Grant Creek), MJ (mainstem Kenai River upstream and downstream of Skilak Lake / Juneau Creek), QC (Quartz and Crescent Creeks), and R (Russian River).[22] The "time" dimension is stratified into six approximately two-week periods beginning in mid-May and ending in mid-August. Information about relative abundance across time is provided by catch rates from the rm 8.6 netting project. Stock composition information is provided by allele frequencies from fish sampled from the run by time period, and also from fish sampled from the harvest. Information on absolute abundance is provided by direct estimation of a subset of the run, specifically weir counts for five stocks. Total harvest is estimated directly, by creel, guide logbook data and a mail survey. The model, which describes the run size and run timing of fish during a single year, is as follows.

The number of Chinook salmon from stock group *i* that pass by the netting project at river-mile 8.6 during year *y,* time period *t* is:

[21] The current methods differ from those of Bromaghin et al. in the use of GSI allele frequency data, and the inclusion of harvest, and in the adoption of a Bayesian, rather than maximum likelihood, framework.

[22] The GSI mixture model was developed using ten individual stocks. However, the ability to differentiate Killey vs Benjamin, Funny vs Slikok, Mainstem vs Juneau, and Quartz vs Crescent is not sufficient for purposes of the SSART model. Therefore, for purposes of planning, developing, and testing the SSART model, we have collapsed the GSI baseline to 6 stock groups that can be more accurately distinguished from allele frequency data.

$$N_{iyt} = N_{iy}\pi_{iyt} \tag{1}$$

where π_{iyt} are run-timing proportions, which sum to one across time periods t for each stock i, and which approximately follow a normal distribution shape. That is, the *expected* run timing (proportion T_{iyt} of stock i, passing river mile 8.6 at time t) is derived from a bell-shaped (normal pdf) function

$$\mathrm{T}_{iyt} = \frac{e^{-\frac{1}{2}z_{iyt}^2}}{\sum_t e^{-\frac{1}{2}z_{iyt}^2}}, \text{ where} \tag{2}$$

$$z_{iyt} = \left(t - \bar{t}_{iy}\right)/\sigma_{T1A}, \text{and} \tag{3}$$

$$z_{iyt} = \left(t - \bar{t}_{iy}\right)/\sigma_{T1B}, \tag{4}$$

with means $\bar{t}_{iy}$ and standard deviation σ_{T1A} for tributary stocks or σ_{T1B} for mainstem/Juneau.[23]

Run timing means $\bar{t}_{iy}$ vary among years according to a normal distribution with standard deviation σ_{T2}. Actual run timing is corrupted (i.e., abundance by time period deviates from a perfect bell shape) by lognormal multiplicative errors $\exp(\varepsilon_{T3t})$ with standard deviation $\sigma_{T3.}$

$$\tau_{iyt} = \mathrm{T}_{iyt} e^{\varepsilon_{T3t}} \tag{5}$$

$$\pi_{iyt} = \tau_{iyt} / \sum_t \tau_{iyt} \tag{6}$$

The proportion of stock group i in the run during time period t is

$$\theta_{yti} = N_{iyt} / \sum_i N_{iyt} \tag{7}$$

Fish from stock i are exposed to harvest rate h_{iy} in year y[24], resulting in harvest H_{iy} :

$$H_{iy} = N_{iy} h_{iy} \tag{8}$$

The proportion of stock group i in the harvest is

$$\theta_{Hyi} = H_{iy} / H_y \tag{9}$$

where H_y is the total harvest, across all stock groups, in year y.

Observed annual data consist of weir counts, an estimate of harvest, netting CPUE estimates, individual genotypes from fish sampled from the rm-8.6 netting project, and multinomial count data constructed to reproduce stock composition information from GSI sampling of the harvest.

[23] The current version of the model assumes that stocks KB, FS, and QC have the same run timing mean within a year, and that stocks G and R have the same run timing mean within a year.

[24] The current version of the model assumes that harvest rates for stock groups KB, FS, and QC are equal, and that harvest rates for stock groups G and R equal because of similar run timing.

Escapement estimates at the Funny River, Quartz Creek, Killey River, Grant Creek, and Russian River weirs are modeled as:

$$\hat{S}_i = S_i e^{\varepsilon_{Si}} \tag{10}$$

where $S_i = N_i - H_i$ is the number of fish from stock i that "escape" the fishery and have the opportunity to spawn, the ε_{Si} are normal $(0,\sigma^2_{Si})$ and σ_{Si} is arbitrarily set to 0.05 to reflect good precision in the weir-based escapement estimates.

An annual estimate of inriver harvest above river mile 8.6, combined from the creel, mail survey and guide logbook data is modeled as:

$$\hat{H}_y = H_y e^{\varepsilon_{Hy}} \tag{9}$$

where ε_{Hy} is normal $(0,\sigma^2_{Hy})$, and σ_{Hy} is the coefficient of variation of the harvest estimate.

Catch per unit effort in the netting project during time period t in year y is modeled as linearly related to abundance:

$$CPUE_{yt} = q_y N_{yt} e^{\varepsilon_{Nyt}} \tag{10}$$

where q_y is the constant of proportionality between abundance and standardized netting catch specific to year y, and the ε_{Nyt} are normal $(0,\sigma^2_N)$.

Allele counts at multiple (k = 1 to 38) genetic loci are observed for each of the M_{yt} fish sampled from the run during year y and time stratum t. Separately for each year and time stratum, each allele count x for fish m at locus k is modeled as having a binomial($q_{z(m),k}$, 2) distribution[25], where q_{ik} is the frequency of allele k in stock i. The integer quantity $z(m)$, the stock identity index (1 to 6) for fish m, has a categorical prior distribution[26] with proportions θ_{t1}, θ_{t2}, $\theta_{t3,}$ θ_{t4}, θ_{t5}, θ_{t6}.

Multinomial count "data", constructed from a separate analysis of allele frequency data sampled from harvested fish, will inform the SSART model about stock composition of the harvest. Allele counts will be observed for each of the L fish sampled from the harvest. Separately for each stratum (identified by year, below/above Soldotna Bridge, and time period below the bridge), each allele count w for fish l at locus k is modeled as having a binomial($q_{z(l),k}$, 2) distribution, where $z(l)$ is the stock identity index for fish l. Stock composition of the entire harvest is the weighted average of stratum stock proportions.

Auxiliary information about the allele frequencies q_{ik} is available from baseline genetic samples collected on the spawning grounds of each stock (Jim Jasper, ADF&G Anchorage, personal communication). For each stock i, the baseline allele count y at locus k is modeled as having a binomial(q_{ik},n_{ik}) distribution, where n_{ik} is the maximum number of possible instances[27] of allele k in fish sampled from the baseline of stock i.

[25] The specified allele is present on none, one, or both of the homologous chromosomes, thus the possible values of x are 0, 1, or 2.

[26] The categorical distribution is the multivariate analogue of the Bernoulli distribution, or alternatively a multinomial distribution with one trial. If z has a categorical(θ_1, θ_2, θ_3, θ_4, θ_5, θ_6) distribution, it can assume values 1 to 6 with probabilities θ_1, θ_2, θ_3, θ_4, θ_5, θ_6.

[27] Optimally, n is 2 times the number of fish in the baseline sample for that stock, but sometimes it is slightly less due to occasional inability to identify an allele in the laboratory.

OpenBUGS code for the main SSART model can be found in Appendix B1, and for the auxiliary harvest stock composition model in Appendix B3. To speed processing time, the stock compositions of the harvests are estimated in the harvest stock composition model and transferred to the SSART model via a multinomial data vector with the same effective sample size.

Markov Chain Monte Carlo (MCMC) methods are employed using OpenBUGS (Lunn, Thomas, Best, & Spiegelhalter, 2000), a Bayesian software program. Bayesian statistical methods employ probability as a language to quantify uncertainty about model parameters. Knowledge existing about the parameters outside the framework of the experimental design is the "prior" probability distribution. The output of the Bayesian analysis is called the "posterior" probability distribution, which is a synthesis of the prior information and the information in the data.

Bayesian analyses require that prior probability distributions be specified for all unknowns in the model. Informative prior distributions have been constructed for σ_{T1A} and σ_{T2} based on historical Russian River weir counts. Annual abundance N_y is modeled as hierarchical, lognormally distributed among years, with Dirichlet-distributed stock composition. An inverse gamma(100,1) prior distribution, equivalent to a CV of 0.1, is given to σ_N. Sensitivity of the posterior distribution of N_y to the precision of this prior will be investigated in the future. All other root parameters of the model are assigned non-informative priors, designed to have minimal effects on the posterior (see Appendix B1 and Appendix B3).

Migratory Timing and Distribution

Objective 2

The proportion of mainstem-spawning Chinook salmon that migrated upstream of the rm 13.7 sonar site (Objective 2) will be estimated as follows:

$$\hat{p} = \frac{x}{n} \tag{11}$$

where: x = the number of radio-tagged Chinook salmon that passed upstream of rm 13.7 and were ultimately tracked to the mainstem Kenai River; and,

n = the number of radio-tagged Chinook salmon that were ultimately tracked to the mainstem Kenai River.

The variance of the above proportion will be estimated according to Cochran (1977):

$$\text{var}[\hat{p}] = \frac{\hat{p}(1-\hat{p})}{n-1} \tag{12}$$

Temporal Weighting for Chinook Salmon Released from River Mile 8.6

The spawning destinations assigned to Chinook salmon will be used to estimate composition of Chinook salmon subject to the Kenai River sport fishery upstream and downstream of Slikok Creek as well as to determine the locations of various stocks or run timing groups relative to regulatory boundaries throughout their instream migration. However, tagging rates may vary temporally if actual sample sizes exceed expectations and a subsample of Chinook salmon is selected for radio tagging during the late run. If the tagging rate does vary temporally we will split the tagging season into 2 time strata: 1) 16 May to 30 June, 2) 1 July to the end of the

season. A weight (w_i) will be assigned to each time stratum that is inversely proportional to the tagging rate for that stratum:

$$w_i = \frac{c_i}{t_i} \tag{5}$$

where c_i is the number of Chinook salmon caught during time stratum *i*, and t_i is the number of fish tagged during stratum *i*.

Then p_s, the contribution of stock *s* in a specific section of the river can be estimated as follows:

$$\hat{p}_s = \frac{\sum_{i=1}^{T} w_i n_i}{\sum_{i=1}^{T} w_i m_i} \tag{6}$$

where n_i is the number of fish from stock *s* tagged during time stratum *i* that was found in a specific section of the river, m_i is the number of fish tagged during time stratum *i* that was found in a specific section of the river, and *T* is the number of time strata. Assuming independence of the tagging events in different time strata and treating m_i as a constant, the variance of $\hat{p}_s$ will be estimated as follows:

$$\mathrm{var}(\hat{p}_s) = \frac{\sum_{i=1}^{T} w_i^{\,2}\,\mathrm{var}(n_i)}{(\sum_{i=1}^{T} w_i m_i)^2} \tag{7}$$

where $\mathrm{var}(n_i) = m_i \hat{p}_i (1 - \hat{p}_i)$ and $\hat{p}_i = \frac{n_i}{m_i}$.

SCHEDULE AND DELIVERABLES

Task	Time Frame	Responsibility
Operational planning	Spring	Reimer/Antonovich
Procure equipment	Spring	Reimer
Equipment preparation	May 16-May 31	Reimer/Tech III
Capture and GSI sampling	May 16-August 15	ADF&G
Capture and tagging	May 16-July 5	ADF&G
Radio telemetry	May 25-August 31	Reimer/Tech III
Lower Kenai creel	May 16-July 31	ADFG
Funny River weir	early-May to early-August	USFWS
Killey River weir	early-May to early-August	USFWS
Quartz Creek weir	early-May to early-August	USFWS
Grant Creek weir	June to September	Kenai Hydro
Russian River weir	June 10-Sept. 30	ADFG
Genotype Samples	Winter	Gene Conservation Laboratory
Editing data	Winter	Reimer
Data analysis	Winter	Reimer/Antonovich
FDS report	Spring	Reimer/Antonovich

BUDGET SUMMARY

BUDGET SUMMARY

Calendar year 2014

Line	Category	FY14-2851 $K	FY14-2305 $K	FY15-2851 $K	FY15-2305 $K
100	Personnel Services	63.9	0.0	26.0	44.8
200	Travel	0.0	0.0	0.0	0.0
300	Contractual	1.0	44.9	5.4	67.0
400	Commodities	0.0	55.8	1.4	4.0
500	Equipment	0.0	4.8	0.0	0.0
Total		64.9	105.5	32.8	115.8

PROJECT PERSONNEL

Calendar year 2014

PCN	Name	Class	FY14-2851 Months	FY15-2851 Months	FY15-2305 Months
4017	Reimer	FB II	6.0	1.0	5.0
4249	Vacant	FWT III	2.0	3.0	0.0

BUDGET NARRATIVE

Line 100: Personnel

Funds support one Fisheries Biologist II, one Fisheries Technician III and three Fisheries Technician IIs. Fiscal year 2014 funds support technicians during July/August 2013 and May/June 2014. Fiscal year 2015 funds support technicians during July/August 2014 and May/June 2015. Responsibilities are detailed below.

Line 300: Contractual

Funds cover vehicles, cellular phones, and telemetry equipment maintenance. CIP funds will be used for aerial radio tracking and an RSA to Gene Conservation Laboratory.

Line 400: Commodities

Funds cover miscellaneous project expenses. CIP funds will be used for telemetry equipment and radio tags.

RESPONSIBILITIES

Adam Reimer, Fishery Biologist II, PCN 4017, 1/1-12/31

- SSART model: Develop and administer project budget. Author operational plan. Procurement of equipment. Coordinate with project leaders within and outside of Department. Install, maintain and remove telemetry stations. Hire and supervise seasonal staff. Airplane tracking. Assist with boat tracking. Primary author in the writing of the final project reports.
-

Steve Fleischman, Fisheries Scientist I

- Assist with development of SSART statistical model and its implementation in OpenBUGS.

Anton Antonovich, Biometrician III

- Review operational plan, provide sample size determination and estimation procedures, advise project leader regarding statistical procedures.

Andy Barclay, Fishery Biologist III

- Coordinate project components in the Gene Conservation Laboratory including sample transfer; preparing, conducting, and error checking laboratory analysis; and assisting with the preparation of required reports.

Vacant, Fish and Wildlife Technician III

- Maintain remote radio receiving stations. Manual tracking of radio tagged Chinook salmon. Assist with other field duties as required.

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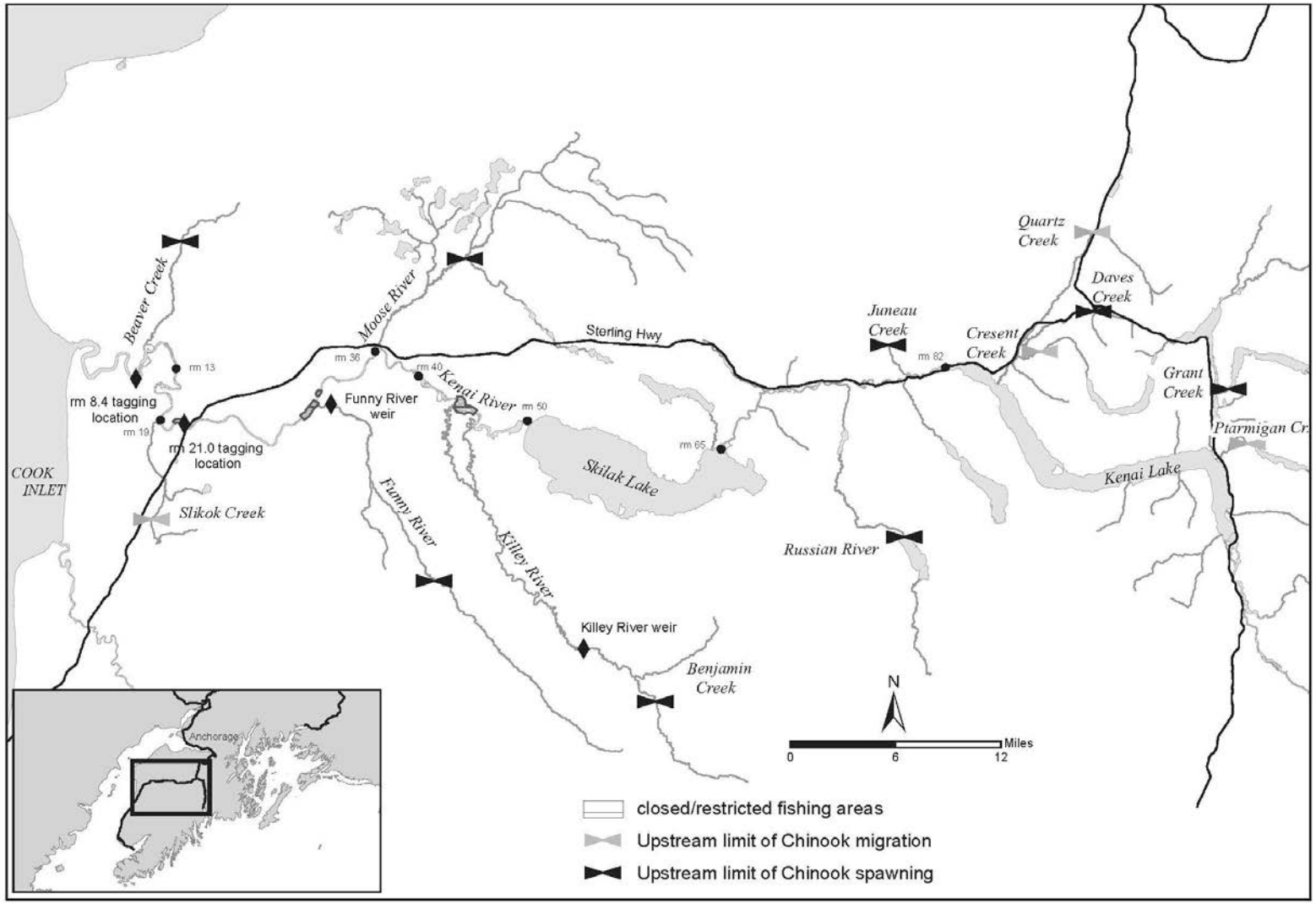
Figure 1.–The Kenai River Drainage[1].



1- The Kenai River upstream of Skilak Lake and all tributaries to the Kenai River are also closed to sport fishing. These areas are not indicated in Figure 1 to reduce clutter.

Figure 2.–Cumulative length distribution for early-run, Kenai River Chinook salmon in 2013.

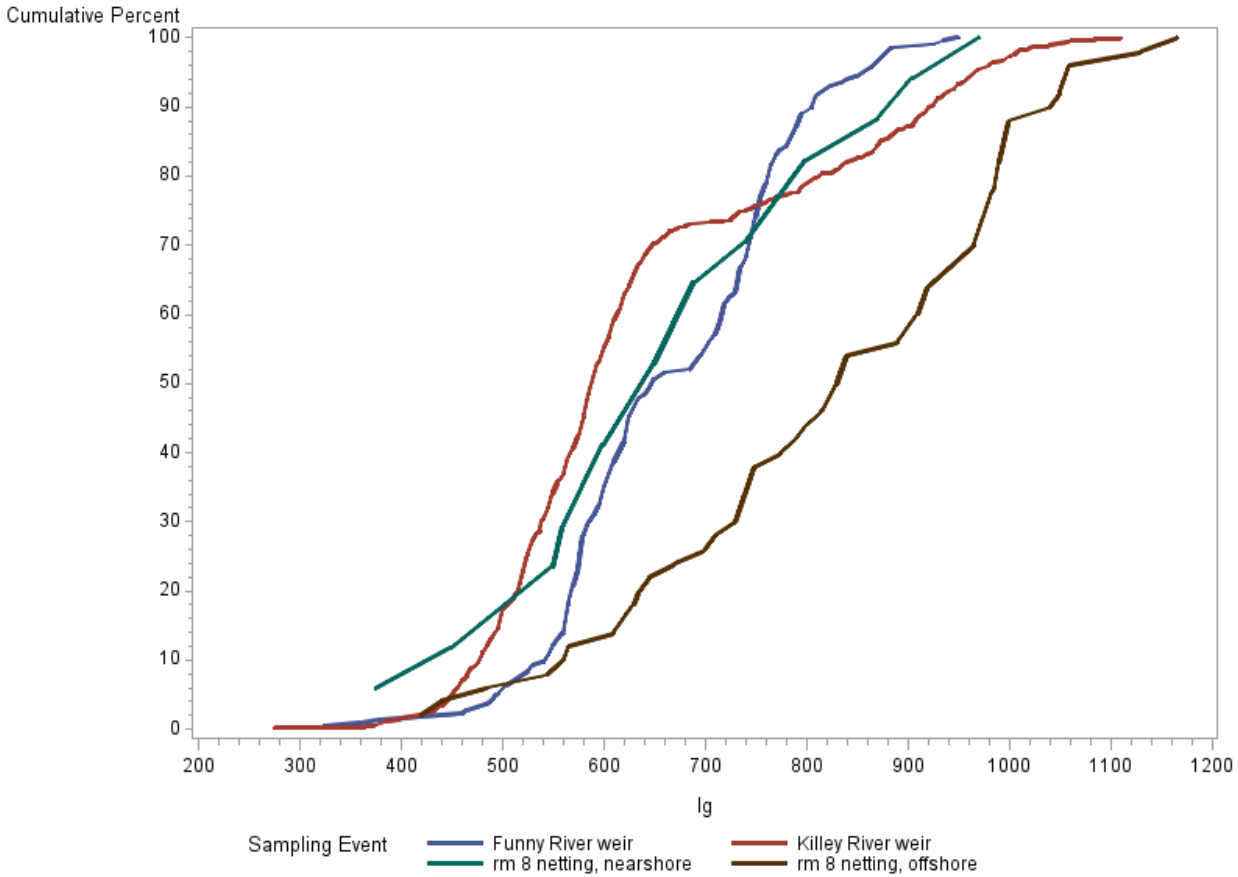


Table 1.–SSART v4.6b model estimates for 2007-2012 with simulated estimates of expected precision for 2014**.**

				95% Baysian credibility interval				
Year	mean	sd	median	lower bound	% below median	upper bound	% above median	samples
Early Run								
SSART2 v4.6b model estimates								
2007	13,010	2,405	12,700	9,186	0.28	18,430	0.45	67,777
2008	8,636	989	8,564	6,896	0.19	10,760	0.26	67,777
2009	10,580	2,263	10,270	7,140	0.30	16,010	0.56	67,777
2010	8,347	1,206	8,268	6,240	0.25	10,900	0.32	67,777
2011	9,267	1,529	9,157	6,612	0.28	12,660	0.38	67,777
2012	6,513	818	6,421	5,156	0.20	8,408	0.31	67,777
Simulated SSART2 v4.6b model estimates run with modified dataset[1]								
2007	13,370	2,271	13,080	9,803	0.25	18,690	0.43	80,971
2008	8,752	998	8,679	7,028	0.19	10,870	0.25	80,971
2009	10,200	1,959	9,957	7,040	0.29	14,760	0.48	80,971
2010	8,608	1,255	8,484	6,545	0.23	11,430	0.35	80,971
2011	9,433	1,525	9,255	6,917	0.25	12,860	0.39	80,971
2012	6,621	721	6,547	5,416	0.17	8,250	0.26	80,971
2014	*6,338*	*587*	*6,296*	*5,310*	*0.16*	*7,619*	*0.21*	*80,971*
Late Run								
SSART2 v4.6b model estimates								
2007	51,060	10,110	49,680	34,850	0.30	73,590	0.48	67,777
2008	47,460	6,463	46,950	36,190	0.23	61,360	0.31	67,777
2009	44,660	10,070	43,250	29,710	0.31	69,360	0.60	67,777
2010	21,330	3,457	21,130	15,210	0.28	28,420	0.35	67,777
2011	27,300	4,895	27,020	18,770	0.31	38,090	0.41	67,777
2012	25,080	3,811	24,610	18,770	0.24	34,020	0.38	67,777
Simulated SSART2 v4.6b model estimates run with modified dataset[1]								
2007	52,800	9,431	51,760	38,010	0.27	74,290	0.44	80,971
2008	47,200	6,352	46,700	36,340	0.22	60,920	0.30	80,971
2009	42,730	8,601	41,710	29,050	0.30	63,390	0.52	80,971
2010	22,300	3,693	21,940	16,150	0.26	30,710	0.40	80,971
2011	27,750	4,796	27,240	19,830	0.27	38,210	0.40	80,971
2012	25,400	3,321	25,060	19,910	0.21	33,020	0.32	80,971
2014	*24,560*	*2,848*	*24,360*	*19,620*	*0.19*	*30,810*	*0.26*	*80,971*

[1] To simulate the precision we expect in 2014 the 6 year SSART dataset was modified by duplicating the 2012 data , modifying the duplicated year to reflect expected sampling levels in 2014, and running SSART2 v4.6b on the resulting 7 years of data. Modifications to simulate 2014 sampling levels include; 1) weir counts for Quartz and Grant Creeks were included using the posterior median of the estimated escapement in 2012 from SSART2 v4.6b, 2) Stock composition data for the inriver run was doubled by duplicating the existing data for fish captured near rm 8.6, 3) Stock composition data for the inriver run was reduced by removing all samples for fish not captured near rm 8.6, 4) Stock composition data for the harvest downstream of rm 21 was reduced by removing all samples for fish not collected by Kenai River Creel survey staff.

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Table 2. –Number of Kenai River Chinook salmon in Gene Conservation Laboratory database by sampling program, 2007-2013.

	Netting		Sport Harvest relative to the Soldotna Bridge			
			Downstream			Upstream
Year	rm 8[1]	rm 21	Creel Survey	Harvest Sampling[2]	Guide Harvest	Harvest sampling
2007	369		386			147
2008	469		378			360
2009	516		368			191
2010	512		286	161		352
2011	645	54	317	23		
2012	392	44	43	43	56	
2013	231	29	56	31		

[1] From 2007-2009 genetic samples were taken from a subsample of the Chinook salmon captured.
[2] 801 samples were collected by the supplementary harvest samplers in 2011, only 23 were processed.

APPENDIX A: GENETIC SAMPLING INSTRUCTIONS

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Appendix A1.–Collection of Axillary Process Tissue Samples for DNA Analysis, ADF&G Gene Conservation Lab, Anchorage.

I. General Information

We will be using tissue samples from the axillary process from individual fish to determine the genetic characteristics and profile of a particular run or stock of fish. This is a non-lethal method of collecting tissue samples from adult fish for genetic analysis. The most important thing to remember in collecting samples is that **only quality tissue samples give quality results** so the fish tissues need to be as "fresh" and cold as possible at all times.

Sample preservative: Ethanol (ETOH) preserves tissues for later DNA extraction without having to store frozen tissues. Avoid extended contact with skin.

II. Supplies included with sampling kit:

1. Dog toenail clipper & scissors - use to cut off the axillary process (fleshy spine)
2. Cryovial- a small (2ml) plastic vial, pre-labeled with caps.
3. Cryovial rack- white plastic rack or neon box holds cryovials while sampling
4. Ethanol (ETOH) – bulk in Nalgene bottles
5. Squirt bottle – use to fill or "top off" each cryovial with ETOH
6. Paper towels – use to blot any excess water or fish slime off fin
7. Printout of sampling instructions
8. Data sheets or Rite-in-rain booklet
9. Gloves – lab gloves for decanting ethanol
10. Laminated "return address" labels

III. General set-up:

1. To insure that the tissues are kept fresh and cold, working fast is necessary. It is important to have your sampling area and supplies set up **before** the fish are caught.
2. Sample kits will come with pre-labeled and numbered cryovials for each individual fish (i.e. 1,2,3, ...). If not, label the empty plastic cryovials with the pre-printed labels in advance, with the adhesive labels provided in the sampling kit. Place the cryovials in the cryovial racks in an order that will allow you to work quickly. We find it easiest to set up ten individuals at a time.
3. Get set up in as comfortable a place as possible. You might use a portable table, piece of plywood, or anything to give you a surface at a good height.
4. Have the caps for the tubes set out along with the sampling tools provided.

IV. Sample procedure:

1. Tissue type: Axillary process samples should be "white" skeletal fleshy lobe just above the pelvic fin (see enclosed diagram). Pelvic or pectoral fin ray may be substituted if needed but **NO adipose tissue**.
2. Prior to sampling, fill the vials half way with ETOH. Fill only the vials that you will use for a particular sampling period.

3. Using dog toenail clippers or scissors, remove the entire axillary process or a portion of the lobe that will fit into the cryovial and place the tissue into the designated cryotube labeled as follows (Fish #1 has it's tissue loaded in cryotube labeled # 1 etc.). If you have trouble getting the tissue into the tubes, cut it into smaller pieces.
4. To avoid any excess water, blood, dirt or fish slime in the vial, wipe the axillary process prior to sampling. Place axillary process tissue into ETOH. The tissue/ethanol ratio should be slightly less than 1:3 to thoroughly soak the tissue in the buffer.
5. Top up tubes with ETOH and screw cap on securely. Invert tube twice to mix ETOH and tissue. **It is important** to wipe your toenail clippers, other sampling tools and area off before sampling the next fish to avoid cross contamination between fish.
6. Discard remaining ethanol from the bulk bottle before shipping. **Tissue samples must remain in 2ml ethanol**, these small quantities do not require HAZMAT paperwork. Store vials containing tissues at room temperature, but away from heat. In the field: keep samples out of direct sun, rain and store capped vials in a dry, relatively cool location. Freezing the tissues collected in ETOH is not required.

V. Data to Record

Most field stations use electronic data recording devices. Otherwise, data forms are included in the sampling kit.

We appreciate your help with the sampling. If you have any questions, please give us a call.

VI. Shipping: No HAZMAT paperwork is required for return shipment of these samples.

Ship samples to:

ADF&G – Genetics Lab
333 Raspberry Road
Anchorage, Alaska 99518
Shipping code:

Lab staff: 1-907-267-2247
Judy Berger: 1-907-267-2175
Bill Templin: 1-907-267-2234

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APPENDIX B: ANALYTICAL METHODS

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Appendix B1.-OpenBUGS code for Bayesian estimation of inriver abundance[28].

```
model{
  RT.mean.trib ~ dnorm(2.0,1.0E-2)I(-1,6)
  RT.mean.i[4] ~ dnorm(4.5,1.0E-2)I(-1,6)
  RT.mean.gr ~ dnorm(4.0,1.0E-2)I(-1,6)
  RT.mean.i[1] <- RT.mean.trib
  RT.mean.i[2] <- RT.mean.trib
  RT.mean.i[3] <- RT.mean.gr
  RT.mean.i[5] <- RT.mean.trib
  RT.mean.i[6] <- RT.mean.gr
  RT.tau1.trib ~ dgamma(7.5,2.4)   #   timing duration  RUSSIAN R WEIR  SIGMA=8.4d on average
  RT.tau1.ms ~ dgamma(0.1,0.1)   #   timing duration  non-informative
  RT.tau2 ~ dgamma(16.5,0.87)  # how consistent is mean timing among years
                                  # RT means have SD=3.4 days based on n=33
  RT.tau3 ~ dgamma(0.1,0.1)  # in a given year, how much can timing deviate from normal
  log.N.tau ~ dgamma(0.1,0.1)
  index.tau ~ dgamma(100,1)  # CV apx 0.1
  RT.sigma1.trib <- 1 / sqrt(RT.tau1.trib)  #run timing duration
  RT.sigma1.ms <- 1 / sqrt(RT.tau1.ms)  #run timing duration
  RT.sigma2 <- 1 / sqrt(RT.tau2)  #annual variation in mean timing
  RT.sigma3 <- 1 / sqrt(RT.tau3)  #run timing process error deviation from normal curve
  index.sigma <- 1 / sqrt(index.tau)
  for(y in 1:Y) { q[y] ~ dbeta(1,1) }
  N.sigma <- 1 / sqrt(log.N.tau)

  log.N.mean ~ dnorm(0,1.0E-12)
  N.median <- exp(log.N.mean)
  D.scale ~ dunif(0,1)
  D.sum <- 1 / (D.scale * D.scale)
  for (i in 1:5) {      theta0p[i] ~ dbeta(0.5,0.5)      }
  theta0[1] <- theta0p[1]
  theta0[2] <- theta0p[2] * (1 - theta0[1])
  theta0[3] <- theta0p[3] * (1 - theta0[1] - theta0[2])
  theta0[4] <- theta0p[4] * (1 - theta0[1] - theta0[2] - theta0[3])
  theta0[5] <- theta0p[5] * (1 - theta0[1] - theta0[2] - theta0[3] - theta0[4])
  theta0[6] <- 1 - theta0[1] - theta0[2] - theta0[3] - theta0[4] - theta0[5]
 for (i in 1:C) {
  gamma[i] <- D.sum * theta0[i]
  for (y in 1:Y) {
     g[y,i] ~ dgamma(gamma[i],0.1)
     theta0.y[y,i] <- g[y,i]/sum(g[y,])
   }
  }
  for(y in 1:Y) {
    log.Ny.mean[y] ~ dnorm(log.N.mean,log.N.tau)   #hierarchical Ny
    Ny.median[y] <- exp(log.Ny.mean[y])
    for(i in 1:C) {
      N.iy[i,y] <- theta0.y[y,i] * Ny.median[y]
      log.Niy[i,y] <- log(N.iy[i,y])
      RT.mean.iy[i,y] ~ dnorm(RT.mean.i[i],RT.tau2)
      }
    }
  for(y in 1:Y) {
```

[28] Prior distributions are specified in green font, sampling distributions of the data (the "likelihood") are specified in blue font.

```
    N.y[y] <- sum(N.iy[,y])
    Ny.msj[y] <- N.iy[4,y]
    Ny.trib[y] <- N.y[y] - Ny.msj[y]
    Ny.early[y] <- sum(N.yt[y,1:3])
    Ny.late[y] <- sum(N.yt[y,4:6])
    Ny.july[y] <- sum(N.yt[y,4:5])
    Ny.trib.late[y] <- Ny.late[y] - sum(N.iyt[4,y,4:6])
    }

  for(y in 1:Y) {
    for(t in 1:T) {
      z[1,y,t] <- (t - RT.mean.iy[1,y]) / RT.sigma1.trib
      z[2,y,t] <- (t - RT.mean.iy[2,y]) / RT.sigma1.trib
      z[3,y,t] <- (t - RT.mean.iy[3,y]) / RT.sigma1.trib
      z[4,y,t] <- (t - RT.mean.iy[4,y]) / RT.sigma1.ms
      z[5,y,t] <- (t - RT.mean.iy[5,y]) / RT.sigma1.trib
      z[6,y,t] <- (t - RT.mean.iy[6,y]) / RT.sigma1.trib
      N.yt[y,t] <- sum(N.iyt[,y,t])
      log.Nqy[y,t] <- log(N.yt[y,t] * q[y])
      log.index[y,t] ~ dnorm(log.Nqy[y,t], index.tau)
      }
    for(i in 1:C) {
      RT.sum[i,y] <- sum(RT[i,y,])
      for(t in 1:T) {
        log.RunTiming[i,y,t] <- log(exp(-.5*z[i,y,t]*z[i,y,t]))  # kernal of normal pdf
        RT[i,y,t] ~ dlnorm(log.RunTiming[i,y,t],RT.tau3)
        pi[i,y,t] <- RT[i,y,t] / RT.sum[i,y]
        N.iyt[i,y,t] <- pi[i,y,t] * N.iy[i,y]
        theta[y,t,i] <- N.iyt[i,y,t] / N.yt[y,t]    # NOTE REVERSAL OF I,J INDICES;
        }
      }
    }

# transition probabilities between rm 21 (row) and rm 8 (col) timestrata
  tp[1,1] <- 1; tp[1,2] <- 0; tp[1,3] <- 0; tp[1,4] <- 0; tp[1,5] <- 0; tp[1,6] <- 0;
                        tp[2,3] <- 0; tp[2,4] <- 0; tp[2,5] <- 0; tp[2,6] <- 0;
                                    tp[3,4] <- 0; tp[3,5] <- 0; tp[3,6] <- 0;
                                                tp[4,5] <- 0; tp[4,6] <- 0;
        tp[2,1:2] ~ ddirich(ones[1:2])
        tp[3,1:3] ~ ddirich(ones[1:3])
        tp[4,1:4] ~ ddirich(ones[1:4])

  for (i in 1:4){
          c8[i,1:6] ~ dmulti(tp[i,1:6], c21[i])
                  for (r in 1:6) { tpc[i,r] <- cut(tp[i,r]) }  # cut feedback on q
        }

  for(i in 1:C) {
    for(h in 1:38) {
      qd[i,h] ~ dbeta(0.5,0.5)
      Yd[i,h] ~ dbin(qd[i,h],nd[i,h])          # BASELINE ALLELE FREQUENCIES
      }
    }

  for(t in 1:T) { for(i in 1:C) {theta1[t,i] <- theta[1,t,i]} }
  for(m in 1:M[1]) {
```

```
    z1[m] ~ dcat(theta1[tstrat1[m],1:C])     # STOCK ID
    for(h in 1:38) {
      Xd1[m,h] ~ dbin(qd[z1[m],h],2)        # ALLELE COUNTS, ONE PER FISH PER LOCUS
      }
    }
  for(t in 1:T) { for(i in 1:C) {theta2[t,i] <- theta[2,t,i]} }
  for(m in 1:M[2]) {
    z2[m] ~ dcat(theta2[tstrat2[m],1:C])
    for(h in 1:38) {
      Xd2[m,h] ~ dbin(qd[z2[m],h],2)
      }
    }
  for(t in 1:T) { for(i in 1:C) {theta3[t,i] <- theta[3,t,i]} }
  for(m in 1:M[3]) {
    z3[m] ~ dcat(theta3[tstrat3[m],1:C])
    for(h in 1:38) {
      Xd3[m,h] ~ dbin(qd[z3[m],h],2)
      }
    }
  for(t in 1:T) { for(i in 1:C) {theta4[t,i] <- theta[4,t,i]} }
  for(m in 1:M[4]) {
    z4[m] ~ dcat(theta4[tstrat4[m],1:C])
    for(h in 1:38) {
      Xd4[m,h] ~ dbin(qd[z4[m],h],2)
      }
    }

for(t in 1:T) { for(i in 1:C) {theta5[t,i] <- theta[5,t,i]} }

  for(m in 1:645) {
    z5[m] ~ dcat(theta5[tstrat5[m],1:C])
    for(h in 1:38) {
      Xd5[m,h] ~ dbin(qd[z5[m],h],2)
      }
    }
  for(m in 646:699) {
          tstrat5[m]~dcat(tpc[tstrat5_21[m],1:6])
          tstrat5_21[m]~dcat(quarters[])
    z5[m] ~ dcat(theta5[tstrat5[m],1:C])
    for(h in 1:38) {
      Xd5[m,h] ~ dbin(qd[z5[m],h],2)
      }
    }

for(t in 1:T) { for(i in 1:C) {theta6[t,i] <- theta[6,t,i]} }

  for(m in 1:392) {
    z6[m] ~ dcat(theta6[tstrat6[m],1:C])
    for(h in 1:38) {
      Xd6[m,h] ~ dbin(qd[z6[m],h],2)
      }
    }
  for(m in 393:436) {
          tstrat6[m]~dcat(tpc[tstrat6_21[m],1:6])
          tstrat6_21[m]~dcat(quarters[])
    z6[m] ~ dcat(theta6[tstrat6[m],1:C])
```

```
    for(h in 1:38) {
      Xd6[m,h] ~ dbin(qd[z6[m],h],2)
      }
    }

for(y in 1:Y) {
    HRm.y[y] ~ dbeta(0.5,0.5)
    HRgr.y[y] ~ dbeta(0.5,0.5)
    HRt.y[y] ~ dbeta(0.5,0.5)
    HR.iy[1,y] <- HRt.y[y]
    HR.iy[2,y] <- HRt.y[y]
    HR.iy[3,y] <- HRgr.y[y]
    HR.iy[4,y] <- HRm.y[y]
    HR.iy[5,y] <- HRt.y[y]
    HR.iy[6,y] <- HRgr.y[y]
    for(i in 1:C) {
      H.iy[i,y] <- N.iy[i,y] * HR.iy[i,y]
      theta.H[y,i] <- H.iy[i,y] / H.y[y]
      S.iy[i,y] <- N.iy[i,y] - H.iy[i,y]
      log.Siy[i,y] <- log(S.iy[i,y])
      log.Syi.hat[y,i] ~ dnorm(log.Siy[i,y],tau.logSiy[i,y])
      tau.logSiy[i,y] <- 1 / log(cv.Syi[y,i] * cv.Syi[y,i] + 1)
      }
    }

for(y in 1:Y) {
    log.H.hat[y] ~ dnorm(log.H[y],tau.logH[y])
    tau.logH[y] <- 1 / log(cv.H[y] * cv.H[y] + 1)
    x[y,1:C] ~ dmulti(theta.H[y,1:C],n.H[y])
    H.y[y] <- sum(H.iy[,y])
    n.H[y] <- sum(x[y,])
    log.H[y] <- log(H.y[y])
    }

rho.Benj ~ dbeta(0.5,0.5)
B.scale ~ dunif(0,1)
B <- 1 / (B.scale * B.scale)
B1 <- rho.Benj * B
B2 <- B - B1
tau.logSB <- 1 / log(0.05 * 0.05 + 1)
for(y in 1:Y) {
    rho.y[y] ~ dbeta(B1,B2)
    b[y] ~ dbin(rho.y[y],bk[y])                    # BENJAMIN RADIO DATA
    S.Benj[y] <- rho.y[y] * S.iy[1,y]
    log.SB[y] <- log(S.Benj[y])
    log.SB.hat[y] ~ dnorm(log.SB[y],tau.logSB)    # BENJAMIN WEIR DATA
    }
}
```

Appendix B2.-Annotated dataset for Bayesian estimation of inriver abundance**.**

```
list(C=6, Y=6, T=6, ones=c(1,1,1,1,1,1), quarters=c(0.25,0.25,0.25,0.25),
M=c(369,469,516,512,699,436),

log.SB.hat=c(NA,NA,NA,NA,NA,7.39),
bk=c(0,0,0,50,60,51),
b=c(0,0,0,19,28,21),

#from SWHS recalc
log.H.hat=c(9.35,9.40,8.99,8.97,8.86,6.05),
cv.H=c(0.066,0.060,0.059,0.059,0.077,0.251),

#from Harvest GSi theta v2.5a
x=structure(.Data=c(21,7,2,103,2,1,…),.Dim=c(6,6)),

#describes timestrata during capture relative to timestrata when passing rm 21
c8=structure(.Data=c(7,0,0,0,0,0, 23,20,0,0,0,0, 4,71,22,0,0,0, 0,6,16,7,0,0),.Dim=c(4,6)),
c21=c(7,43,97,29),

log.Syi.hat=structure(.Data=c(NA,7.66,NA,NA,NA,4.48,…),.Dim=c(6,6)),

cv.Syi=structure(.Data=c(0.1,0.1,0.1,0.1,0.1,0.1,…),.Dim=c(6,6)),

log.index=structure(.Data=c(-1.41, 0.21, 0.09, 1.06, 1.85, 0.14,…),.Dim=c(6,6)),

z4=c(NA,NA,NA,1,1,NA,NA,1,NA,1,NA,NA,NA,NA,1,1,2,NA,1,1,NA,NA,NA,1,1,1,NA,NA,NA,1,1,1,…),
z5=c(NA,1,1,NA,1,1,NA,NA,NA,NA,1,1,NA,2,NA,NA,1,NA,2,NA,NA,NA,NA,NA,2,NA,NA,2,1,NA,1,…),
z6=c(1,1,1,1,NA,1,1,NA,1,NA,NA,1,NA,NA,2,1,NA,NA,2,NA,1,1,1,NA,NA,1,1,1,NA,1,1,NA,1,NA,1,…),

Yd=structure(.Data=c(668,240,735,685,589,105,…),.Dim=c(6,38)),
nd=structure(.Data=c(914,908,902,906,906,906,…),.Dim=c(6,38)),

tstrat1=c(1,…,2,…,3,…,4,…,5,…,6,…),
Xd1=structure(.Data=c(2,1,2,2,2,0,0,2,0,2,2,2,2,0,0,0,0,0,2,1,1,2,2,0,0,1,1,0,0,…),.Dim=c(369,38)),

…

tstrat6=c(1,…,2,…,3,…,4,…,5,…,6,…,NA,…),
tstrat6_21=c(NA,…,2,…,3,…,4,…),
Xd6=structure(.Data=c(1,1,2,1,0,0,1,2,0,1,2,1,1,0,0,1,0,0,2,0,0,1,2,0,0,2,2,0,0,…),.Dim=c(436,38)))
)
```

Appendix B3.-OpenBUGS code for Bayesian estimation of harvest stock composition [29].

```
model{
#-------------------------------------------------------------------
  RT.mean.trib ~ dnorm(2.0,2.7)I(0,5) #from BK, FS, and QC radios dates in fishery
  RT.mean.i[4] ~ dnorm(4.5,1.0E-2)I(0,5)
  RT.mean.gr ~ dnorm(3.0,1.0E-2)I(0,5)
  RT.mean.i[1] <- RT.mean.trib
  RT.mean.i[2] <- RT.mean.trib
  RT.mean.i[3] <- RT.mean.gr
  RT.mean.i[5] <- RT.mean.trib
  RT.mean.i[6] <- RT.mean.gr

  RTm.mean.trib ~ dnorm(0.8,12.6)I(0,2) #from BK, FS, and QC radios dates in fishery
  RTm.mean.i[4] ~ dnorm(2.0,1.0E-2)I(0,2)
  RTm.mean.gr ~ dnorm(1.3,1.0E-2)I(0,2)
  RTm.mean.i[1] <- RTm.mean.trib
  RTm.mean.i[2] <- RTm.mean.trib
  RTm.mean.i[3] <- RTm.mean.gr
  RTm.mean.i[5] <- RTm.mean.trib
  RTm.mean.i[6] <- RTm.mean.gr

  RT.tau1 ~ dgamma(7.5,2.3)   #   timing duration  from rr weir
  RT.tau2 ~ dgamma(16.5,0.86)
  RTm.tau1 ~ dgamma(7.5,0.6)   #   timing duration  from rr weir
  RTm.tau2 ~ dgamma(16.5,0.22)
  RT.tau3 ~ dgamma(0.1,0.1)  # in a given year, how much can timing deviate from normal
  log.HL.tau ~ dgamma(0.1,0.1) # Variability of log.HLi accross years;
  log.HM.tau ~ dgamma(0.1,0.1) # Variability of log.HMi accross years;

  RT.sigma1 <- 1 / sqrt(RT.tau1)
  RTm.sigma1 <- 1 / sqrt(RTm.tau1)
  RT.sigma2 <- 1 / sqrt(RT.tau2)
  RTm.sigma2 <- 1 / sqrt(RTm.tau2)
  RT.sigma3 <- 1 / sqrt(RT.tau3)  #run timing process error deviation from normal curve
  HL.sigma <- 1 / sqrt(log.HL.tau)
  HM.sigma <- 1 / sqrt(log.HM.tau)

  for(i in 1:C) {
    log.HLi.mean[i] ~ dnorm(0,1.0E-12)I(0,)
    log.HMi.mean[i] ~ dnorm(0,1.0E-12)I(0,)
    for(y in 1:Y) {
      log.HLiy[i,y] ~ dnorm(log.HLi.mean[i],log.HL.tau)I(1,)
                RT.mean.iy[i,y] ~ dnorm(RT.mean.i[i],RT.tau2)
                log.HMiy[i,y] ~ dnorm(log.HMi.mean[i],log.HM.tau)I(1,)
                RTm.mean.iy[i,y] ~ dnorm(RTm.mean.i[i],RTm.tau2)
      }
    }

 for(y in 1:Y) {
    for(i in 1:C) {
      HL.iy[i,y] <- exp(log.HLiy[i,y])
      RT.sum[i,y] <- sum(RT[i,y,])
                HM.iy[i,y] <- exp(log.HMiy[i,y])
```

[29] Prior distributions are specified in green font, sampling distributions of the data (the "likelihood") are specified in blue font.

```
      RTm.sum[i,y] <- sum(RTm[i,y,])
      for(t in 1:T.L) {
                              z[i,y,t] <- (t - RT.mean.iy[i,y]) / RT.sigma1
        log.RunTiming[i,y,t] <- log(exp(- z[i,y,t]*z[i,y,t]))  # kernal of normal pdf
        RT[i,y,t] ~ dlnorm(log.RunTiming[i,y,t],RT.tau3)
        pi[i,y,t] <- RT[i,y,t] / RT.sum[i,y]
        HL.iyt[i,y,t] <- pi[i,y,t] * HL.iy[i,y]
        theta.Lk[y,t,i] <- HL.iyt[i,y,t] / HL.yt[y,t]    # NOTE REVERSAL OF I,J INDICES;
      }
      for(t in 1:T.M) {
                              zm[i,y,t] <- (t - RTm.mean.iy[i,y]) / RTm.sigma1
        log.RunTimingM[i,y,t] <- log(exp(- .5*zm[i,y,t]*zm[i,y,t]))  # kernal of normal pdf
        RTm[i,y,t] ~ dlnorm(log.RunTiming[i,y,t],RT.tau3)
        piM[i,y,t] <- RTm[i,y,t] / RTm.sum[i,y]
        HM.iyt[i,y,t] <- piM[i,y,t] * HM.iy[i,y]
        theta.Mk[y,t,i] <- HM.iyt[i,y,t] / HM.yt[y,t]    # NOTE REVERSAL OF I,J INDICES;
      }
    }
    for(t in 1:T.L) {
      HL.yt[y,t] <- sum(HL.iyt[,y,t])
    }
    for(t in 1:T.M) {
      HM.yt[y,t] <- sum(HM.iyt[,y,t])
    }
  }
#-------------------------------------------------------------------------------------------------------------
  for(y in 1:Y) {
    for(t in 1:T.L) {
      log.HLyt[y,t] <- log(HL.yt[y,t])
      tau.HLyt[y,t] <- 1 / cv.HLyt[y,t] / cv.HLyt[y,t]
      log.HLyt.hat[y,t] ~ dnorm(log.HLyt[y,t], tau.HLyt[y,t])
    }
          for(t in 1:T.M) {
      log.HMyt[y,t] <- log(HM.yt[y,t])
      tau.HMyt[y,t] <- 1 / cv.HMyt[y,t] / cv.HMyt[y,t]
      log.HMyt.hat[y,t] ~ dnorm(log.HMyt[y,t], tau.HMyt[y,t])
    }
    for(i in 1:C) {
      H.iy[i,y] <- HL.iy[i,y] + HM.iy[i,y]
      theta.H[i,y] <- H.iy[i,y] / H.y[y]
      theta.L[i,y] <- HL.iy[i,y] / HL.y[y]
      theta.M[i,y] <- HM.iy[i,y] / HM.y[y]
    }
  }

  for(y in 1:Y) {
    HL.y[y] <- sum(HL.yt[y,])
          HM.y[y] <- sum(HM.yt[y,])
    H.y[y] <- HL.y[y] + HM.y[y]
  }

  for(i in 1:C) {
    for(h in 1:A) {
      qd[i,h] ~ dbeta(0.5,0.5)
      Yd[i,h] ~ dbin(qd[i,h],nd[i,h])          # BASELINE ALLELE FREQUENCIES
      }
```

```
  }
#_____________________________________________________________
 for(i in 1:C) {                              # YEAR 2007 (i.e. y=1)
   for(t in 1:T.L) {
      theta.Lk.1[t,i] <- theta.Lk[1,t,i]
   }
         for(t in 1:T.M) {
      theta.Mk.1[t,i] <- theta.Mk[1,t,i]
   }
 }
 for(m2 in 1:M2[1]) {
  z2.1[m2] ~ dcat(theta.Lk.1[tstrat.L.1[m2],1:C])          # SPORT LOWER STOCK ID
  for(h in 1:A) {
   Xd2.1[m2,h] ~ dbin(qd[z2.1[m2],h],2)                 # SPORT L ALLELE COUNTS
  }
 }
 for(m3 in 1:M3[1]) {
  z3.1[m3] ~ dcat(theta.Mk.1[tstrat.M.1[m3],1:C])          # SPORT MIDDLE STOCK ID
  for(h in 1:A) {
   Xd3.1[m3,h] ~ dbin(qd[z3.1[m3],h],2)                 # SPORT M ALLELE COUNTS
  }
 }

#_____________________________________________________________
 for(i in 1:C) {                                 # YEAR 2008 (i.e. y=2)
   for(t in 1:T.L) {
      theta.Lk.2[t,i] <- theta.Lk[2,t,i]
   }
         for(t in 1:T.M) {
      theta.Mk.2[t,i] <- theta.Mk[2,t,i]
   }

 }
 for(m2 in 1:M2[2]) {
  z2.2[m2] ~ dcat(theta.Lk.2[tstrat.L.2[m2],1:C])          # SPORT LOWER STOCK ID
  for(h in 1:A) {
   Xd2.2[m2,h] ~ dbin(qd[z2.2[m2],h],2)                 # SPORT L ALLELE COUNTS
  }
 }
 for(m3 in 1:M3[2]) {
  z3.2[m3] ~ dcat(theta.Mk.2[tstrat.M.2[m3],1:C])          # SPORT MIDDLE STOCK ID
  for(h in 1:A) {
   Xd3.2[m3,h] ~ dbin(qd[z3.2[m3],h],2)                 # SPORT M ALLELE COUNTS
  }
 }

#_____________________________________________________________
 for(i in 1:C) {                                 # YEAR 2009 (i.e. y=3)
   for(t in 1:T.L) {
      theta.Lk.3[t,i] <- theta.Lk[3,t,i]
   }
         for(t in 1:T.M) {
      theta.Mk.3[t,i] <- theta.Mk[3,t,i]
   }
 }
 for(m2 in 1:M2[3]) {
```

```
   z2.3[m2] ~ dcat(theta.Lk.3[tstrat.L.3[m2],1:C])          # SPORT LOWER STOCK ID
   for(h in 1:A) {
    Xd2.3[m2,h] ~ dbin(qd[z2.3[m2],h],2)                  # SPORT L ALLELE COUNTS
   }
  }
  for(m3 in 1:M3[3]) {
   z3.3[m3] ~ dcat(theta.Mk.3[tstrat.M.3[m3],1:C])          # SPORT MIDDLE STOCK ID
   for(h in 1:A) {
    Xd3.3[m3,h] ~ dbin(qd[z3.3[m3],h],2)                  # SPORT M ALLELE COUNTS
   }
  }

#_____________________________________________________________
for(i in 1:C) {                                          # YEAR 2010 (i.e. y=4)
    for(t in 1:T.L) {
       theta.Lk.4[t,i] <- theta.Lk[4,t,i]
    }
          for(t in 1:T.M) {
       theta.Mk.4[t,i] <- theta.Mk[4,t,i]
    }

  }
  for(m2 in 1:M2[4]) {
   z2.4[m2] ~ dcat(theta.Lk.4[tstrat.L.4[m2],1:C])          # SPORT LOWER STOCK ID
   for(h in 1:A) {
    Xd2.4[m2,h] ~ dbin(qd[z2.4[m2],h],2)                  # SPORT L ALLELE COUNTS
   }
  }
  for(m3 in 1:M3[4]) {
   z3.4[m3] ~ dcat(theta.Mk.4[tstrat.M.4[m3],1:C])          # SPORT MIDDLE STOCK ID
   for(h in 1:A) {
    Xd3.4[m3,h] ~ dbin(qd[z3.4[m3],h],2)                  # SPORT M ALLELE COUNTS
   }
  }

#_____________________________________________________________
for(i in 1:C) {                                          # YEAR 2011 (i.e. y=5)
    for(t in 1:T.L) {
       theta.Lk.5[t,i] <- theta.Lk[5,t,i]
    }

  }
  for(m2 in 1:M2[5]) {
   z2.5[m2] ~ dcat(theta.Lk.5[tstrat.L.5[m2],1:C])          # SPORT LOWER STOCK ID
   for(h in 1:A) {
    Xd2.5[m2,h] ~ dbin(qd[z2.5[m2],h],2)                  # SPORT L ALLELE COUNTS
   }
  }
#_____________________________________________________________
for(i in 1:C) {                                          # YEAR 2012 (i.e. y=6)
    for(t in 1:T.L) {
       theta.Lk.6[t,i] <- theta.Lk[6,t,i]
    }

  }
  for(m2 in 1:M2[6]) {
```

```
    z2.6[m2] ~ dcat(theta.Lk.6[tstrat.L.6[m2],1:C])          # SPORT LOWER STOCK ID
    for(h in 1:A) {
      Xd2.6[m2,h] ~ dbin(qd[z2.6[m2],h],2)                  # SPORT L ALLELE COUNTS
    }
  }
}
```

Appendix B4.-Annotated dataset for Bayesian estimation of harvest stock composition**.**

```
list(C=6, Y=6, T.L=5, T.M=2, A=38, M2=c(386,379,368,443,340,142), M3=c(147,359,191,356,0,0),

log.HLyt.hat=structure(.Data=c(3.00, 6.87, 7.34, 7.69, 8.58,…),.Dim=c(6,5)),

cv.HLyt=structure(.Data=c(0.44, 0.18, 0.27, 0.14, 0.10,…),.Dim=c(6,5)),

log.HMyt.hat=structure(.Data=c(6.65, 6.46, 6.15, 6.64,…),.Dim=c(6,2)),

cv.HMyt=structure(.Data=c(0.12, 0.08, 0.09, 0.07, 0.16,…),.Dim=c(6,2)),

Yd=structure(.Data=c(668,240,735,685,589,105,182,756,…),.Dim=c(6,38)),
nd=structure(.Data=c(914,908,902,906,906,906,912,906,…),.Dim=c(6,38)),

tstrat.L.1=c(1,…,2,…,3,…,4,…,5,…),
Xd2.1=structure(.Data=c(1,1,1,2,0,1,1,2,0,2,2,2,2,0,0,0,0,… ),.Dim=c(386,38)),

tstrat.M.1=c(1,…,2,…),
Xd3.1=structure(.Data=c(2,0,2,1,1,0,0,2,0,2,2,2,0,0,0,1,0,… ),.Dim=c(147,38)),

…

tstrat.L.6=c(1,…,2,…,3,…,4,…),
Xd2.6=structure(.Data=c(2,1,1,1,0,0,0,2,0,2,2,2,1,0,0,1,0,),.Dim=c(142,38))
)
```

APPENDIX D: SAMPLING FORMS

Appendix D1.–Fixed station site log**.**

Kenai River Chinook Salmon Fixed Station Site Log

Site Code: _____ Site Name: _____

Date	Time	Rec. /DCC	Batt. Volts	# of blocks	Comments

DCC capacity is 32,024 blocks, R4500 capactiy is 98,304 blocks (stationary)

Appendix D2.–Fixed station download form.

Kenai River Chinook Salmon Fixed Station Download Form

Name: _____ Week of:_____

name	Date	Rec/ DCC	Batt. voltage	blocks	filename	Comments
Chinook **S**onar						
Slikok **C**reek						
Soldotna **B**ridge						
Funny **R**iver						
Moose **R**iver						
Middle **K**illey						
Skilak **D**unes						
Skilak **I**nlet						
Bean **C**reek						
EXample	5/20/07	5/e	12.0/6.0	20630	EXA05202007	

Kenai River Chinook Salmon Fixed Station Download Form

Name: _____ Week of:_____

name	Date	Rec/ DCC	Batt. voltage	blocks	filename	Comments
Chinook **S**onar						
Slikok **C**reek						
Soldotna **B**ridge						
Funny **R**iver						
Moose **R**iver						
Middle **K**illey						
Skilak **D**unes						
Skilak **I**nlet						
Bean **C**reek						
EXample	5/20/07	5/e	12.0/6.0	20630	EXA05202007	

APPENDIX E: DATA MAPS

Appendix E1.–Fixed station telemetry data map.

Data Map for files:
kkstation10.dta

Data Field Name	Start Column	End Column	Comma Column	Codes/ Comments
Date code	1	8	9	format YYYYMMDD
Hour	10	11	12	24-hour clock
Minute	13	14	15	
Antenna number	16	16	17	1-3
Frequency	18	23	24	KHz, six digit number; 151205-151464
Pulse code	25	27	28	
Mortality signal	29	29	30	Y or blank
(Blank)	31	34	35	
Signal strength	36	38	39	measure of signal strength
Station name	40	42	43	Character code
Latitude	40	50	51	DDD MM.MMMM
Longitude	52	62	63	DDD MM.MMMM
Rivermile	64	67	68	

Appendix E2.–Manual tracking telemetry data map.

Data Field Name	Start Column	End Column	Comma Column	Codes/ Comments
Date code	1	8	9	format YYYYMMDD
Survey method	10	14	15	Boat, Plane or Foot
Survey start rivermile	16	19	20	Downstream extent of survey
Survey end rivermile	21	24	25	Upstream extent of survey
Time located	26	29	30	hhmm, 24-hour clock
Frequency	28	33	34	KHz, six digit number; Tracking freq is reported 151204-151464
Pulse code	25	27	28	
Latitude	29	39	40	DDD MM.MMMM
Longitude	41	51	52	DDD MM.MMMM
Signal strength	53	55	56	
Rivermile	57	60	61	
Closed area	62	62	63	1=Slikok Creek, 2=Centenial, 3=Funny River, 4=Morgan's Hole, 5=Moose River, 6=Killey River, 7=Upper Kenai
Drainage	64	78	79	
Mortality	80	80		Y or blank