Regional Operational Plan SF.2A.2013.14

Kenai River Chinook Salmon Abundance and Migratory Timing

by

Adam Reimer

June 2013

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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Adam Reimer

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

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Division of Sport Fish

June 2013

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TABLE OF CONTENTS

TABLE OF CONTENTS (Continued)

LIST OF FIGURES

LIST OF TABLES

LIST OF APPENDICES

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. These estimates of abundance will be used, in conjunction with sonar based estimates of abundance to develop escapement goals for Kenai River Chinook salmon. 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. 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 et al. 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. Accurate enumeration of run size has proven difficult because of uncertainty surrounding the inriver run estimate. The 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 and 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 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 and 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. These estimates of run size are model estimates because of uncertainty surrounding the inriver run component which is the subject of considerable research.

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 (Bendock and Alexandersdottir 1992; Burger et al. 1983) although some tributaries (Russian River and Grant Creek) have demonstrated later return timing. Tributaries of the Kenai River (Figure 11) 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 (Bendock and Alexandersdottir 1992; Burger et al. 1983). 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 (Bendock and Alexandersdottir 1992; Burger et al. 1983; Hammarstrom

et al. 1985). The entire Kenai River mainstem upstream of the intertidal area (rm12) is suitable spawning habitat for Chinook salmon (Burger et al. 1983).

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 being addressed by a related project (Tim McKinley, Alaska Sustainable Salmon Fund Project Completion Report, AKSSF # 45143 (700)).

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 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. Sonar estimates of inriver passage provide the basis for estimating spawning escapement and implementing management plans. Implementation of these management plans has been contentious and attracts much public scrutiny. Restrictions were imposed in each year from 1989 through 1992 to ensure spawning escapement goals were met. Since 1993, the 1997, 1998, 2000, 2002, 2010, 2011 and 2012 early runs, and the 1998, 2011 and 2012 late runs were restricted to meet escapement goals.

Daily and seasonal estimates of Chinook salmon abundance at the Kenai River mouth 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 2002 to 2006, sockeye salmon passage estimates generated by the river mile 19 sockeye sonar project ranged from 614,946 to 1,499,692 (Westerman and Willette 2010) while late-run Chinook salmon passage estimates generated by the Chinook sonar project ranged from 37,743 to 56,205 (Miller et al. 2010). 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. Currently, mixture-model estimates based on DIDSON/ARIS-measured fish lengths are considered the best long-term solution for assessing Kenai River Chinook salmon abundance.

Post-season assessments of Kenai River Chinook salmon abundance, independent of the hydroacoustic estimates, have been produced for 2007-2012 using the Stock Specific Abundance and Run Timing (SSART) model, which is based on genetic stock identification data and weir counts of one or more genetically identifiable stocks. The most recent estimates are shown in Table 1 and have been compared to sonar estimates for both the early and late runs (McKinley and Fleischman 2013, Fleischman and McKinley 2013). This operational plan describes abundance estimation using the SSART model in 2013.

MIGRATORY DISTRIBUTION AND TIMING

Radio tags will be 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 beyond our modeling efforts.

The Chinook salmon sonar site has traditionally been located at rivermile 8.5 in an attempt to locate the counter downstream of removals due to harvest and/or spawning. However, the site is tidally influenced and enumerates a variable fraction of the passing fish depending on tide stage. Consequently, ADF&G is exploring an upstream site during the 2013 season. Radio tags deployed during this study will help estimate the fraction of mainstem spawning Chinook salmon downstream of the new sonar site (Kenai River mile 13.7) to evaluate escapement based on the run past the new site.

Kenai River sport fishing regulations are complex and highly refined, as appropriate for such a popular sport fishery. A major source of management uncertainty involves implementing stock specific fishing regulations during mixed stock sport fisheries. For example, the overlap in the run timing of tributary- and mainstem-spawning Chinook salmon within the Kenai River makes restrictions or liberalization directed at one stock difficult. Radio tags deployed during this study will help update spatial and temporal distribution information.

OBJECTIVES

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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 modes.
2. Estimate the proportion of mainstem-spawning Chinook salmon that migrated upstream of Kenai river mile 13.7 such that the estimate is within 11 percentage points of the true value 95% of the time.

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. Collect genetic samples from Kenai River Chinook salmon sport-harvested downstream of the Soldotna Bridge from May 16 to July 31, 2013.
3. Collect genetic samples from Kenai River Chinook salmon sport-harvested upstream of the Soldotna Bridge from early-June to July 31, 2013.
4. Report the cumulative temporal distribution of tributary-bound Chinook salmon migrating upstream of the following locations: the Slikok Creek confluence, the Soldotna Bridge, the Funny River confluence, and the Moose River confluence.
5. Report the cumulative temporal distribution of radio tagged Chinook salmon entering the Funny River.

6. Report the cumulative temporal distribution of radio tagged Chinook salmon entering the Killey River.
7. Create a large scale habitat map for Slikok Creek downstream of Arc Loop Road.

METHODS

STUDY DESIGN

Inriver Abundance

The Stock Specific Abundance and Run Timing model (SSART) was developed by the USFWS (Bromaghin et al. 2010) and later modified by ADF&G[1]. The model creates a space-time matrix of relative abundance where the genetic reporting groups (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 component and 2-week strata represent the time component. This space component is estimated from two data sources: genetic stock identification (GSI) estimates of inriver gillnetting samples and radio telemetry final destinations. The time component is estimated using the CPUE of an inriver gillnetting program located near rm 8.5. 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 2013 season we will have known escapements for 5 of the 6 reporting groups (the exception being mainstem Kenai River-Juneau Creek). 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, stock-specific estimates of abundance, harvest rate, and harvest by time period are readily available.

Unlike traditional mark-recapture experiments, which assume marked fish behavior is unaffected by marking, SSART model estimates mainly utilize GSI stock composition estimates. GSI estimates are produced using tissue samples, and are not reliant on fish behavior after sampling. Handling effect is a large source of potential bias, and unbiased estimates are important for this project, given that its primary purpose is to evaluate potential bias in the DIDSON/ARIS estimates. However, GSI estimates of stock composition can be supplemented with radio telemetry final destinations within the SSART model. The information is complimentary because radio telemetry data improves the precision of unbiased GSI estimates. Radio telemetry final destinations are available for use as a secondary estimate of stock composition by the SSART model in 2010-2012.

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.

Inriver run stock composition and index of abundance

The temporal index of abundance used for the SSART model is taken from the offshore sampling boat associated with the Kenai River Chinook Salmon Inriver Gillnetting Study. Stock composition of the inriver run is estimated from GSI and radio telemetry data collected from three areas; the nearshore and offshore sampling boats associated with the Kenai River Chinook

[1] 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.

Salmon Inriver Gillnetting Study and supplementary inriver gillnetting that occurs near Kenai rm 21.

Kenai River Chinook Salmon Inriver Gillnetting Study – "Offshore"

The Kenai River Inriver Gillnetting Study[2] has fished a standardized location defined by the rivermile 8.5 Chinook salmon sonar site's ensonified zone since 2002. During 2013, two boats will be associated with this project. The boat tasked with gillnetting the ensonified zone, will be referred to as the offshore boat. The offshore boat provides CPUE estimates as a temporal index of abundance and stock composition estimates for the Chinook salmon run to the SSART model.

Sampling occurs for 6.5 hours per day, May 16 to August 10, near the Kenai River Chinook salmon sonar. ASL samples are taken from every fish sampled prior to July 1 and every other fish sampled per drift after July 1. Radio tags are deployed on a subset of those sampled (see Radio Tag Deployments section below). Genetics samples are taken from every fish captured. Every Chinook salmon captured will receive a hole punch in the upper caudal fin.

The project uses two mesh sizes to reduce the size selectivity of the sample. Both mesh sizes are undersized for the majority of Kenai River Chinook salmon which reduces damage to gill filaments during capture. Gillnets are deployed systematically with respect to bank and mesh size to ensure that fish of all sizes, throughout the sampling area have reasonable possibility of capture.

From 2009-2012 an annual average of 586 Chinook salmon (range 475-726) have been handled by Kenai River Inriver Gillnetting Study staff (Table 2). In 2012, 392 Chinook salmon were genotyped and radio tags were deployed on 225.

Kenai River Chinook Salmon Inriver Gillnetting Study – "Nearshore"

Recent analysis suggest that approximately 35% of Kenai River Chinook salmon pass the rm 8.5 Chinook salmon sonar outside of the ensonified zone, primarily between each transducer and the shoreline (McKinley and Fleischman 2013). These fish are not subject to capture by the offshore netting boat, which strives to keep the drifting nets positioned in water that passes through the ensonified zone. In 2013, ADF&G staff will deploy a second "nearshore" boat, tasked with fishing between the ensonified area and the shoreline. The nearshore netting crew's methods will likely be modified inseason, since deploying the net in this area may require differing practices than described above. Still, the nearshore crew will mimic the offshore crew's methods when practical, except for fishing a reduced schedule of 2-3 days per week. We anticipate a modest increase in the number of fish sampled for stock composition information (GSI samples and radio tags)[3].

Rivermile 21 Inriver Gillnetting

During the 2011 and 2012 seasons, a pilot study was conducted to test the feasibility of deploying radio tags near Kenai rivermile 21. In 2011, 49 radio transmitters were deployed, one day per week, from 2 June to 13 July. Of the transmitters deployed at this location, final

[2] The Kenai River Inriver Gillnetting Study and the Kenai River Creel Survey are described in another operational plan (McKinley FY13/FY14 Operational Plan, Kenai River Creel Survey, Inriver Gillnetting and Age Composition Study).

[3] If 35% of the Chinook salmon passing upstream do not migrate thru the ensonified zone, the fish available to capture by the nearshore boat would be about 53% (0.35/0.65) of those available to the offshore boat. Further, the nearshore boat will only fish 2-3 days per week. Therefore, based on space and time considerations alone, we would expect the nearshore boat to sample 15-20% as many fish as the offshore boat. The actual catch may differ because the nearshore boat may catch fish with higher or lower efficiency than the offshore boat.

spawning destination could be determined for 39 (80%), compared to 38% of transmitters deployed at rm 8.5. In 2012, 38 radio transmitters were deployed, one day per week, from 7 June to 4 July. Of the transmitters deployed at this location, final spawning destination could be determined for 32 (84%), compared to 55% of transmitters deployed at rm 8.5. In both years, the sampling design called for a fixed number of tag deployments per day; it took about 3 hours to deploy 6-8 tags. No major problems were encountered with respect to staff safety or gillnet durability, and catch rates were high. In both years, fish tagged in July migrated exclusively to mainstem spawning destinations.

The increased proportion of successful migrants at the rm 21 tagging location was due to improved survival, probably because tagged fish were better acclimated to fresh water, and less potential for harvest, because the fish were captured upstream of the major sport fishery. Radio tag deployments in this area have the greatest potential to improve our stock composition estimates in the early run, when multiple tributary stocks are migrating through the area. A disadvantage of deploying radio tags in this area is uncertainty surrounding which timestrata individuals marked at rm 21 represent.[4] Historical telemetry-based data on migration timing between rm 8.5 and rm 21 is incorporated into the SSART model to estimate entry timing of fish sampled at rm 21. Both GSI and radio tag stock composition information is utilized.

In 2013, Chinook salmon will be captured between Kenai rivermile 20.2 and 21.0, one day per week from late-May to late-June (Figure 2). The start date may be delayed if the water level in the area is too low to deploy gillnets from a motorized boat. Sampling at rm 21 will end in June because negligible tributary-spawning Chinook salmon pass this area in July. The geographic boundaries encompass a low use area of the Kenai River and will allow Chinook salmon to be captured and tagged without disturbing sport anglers.

Gillnet capture probabilities depend on fish size. Gillnets of two mesh sizes (5.0" and 7.5" stretched) will be used to reduce the overall size selectivity of our sampling. Each mesh size would be fished alternately for 1-hour periods and the mesh size used first will alternate daily.

All wild Chinook salmon that are captured will be sampled for ASL information and a genetic sample. In 2011 and 2012, a fixed number of radio tags were deployed each day requiring about 3 hours on the water. In 2013, staff will work one, 7.5 hour day per week and collect GSI samples and deploy radio tags on all captured Chinook salmon of appropriate size and vitality.

Total abundance by reporting group

Killey River Weir

The Killey River weir is a resistance board weir that was operated by the United States Fish and Wildlife Service (USFWS) for the first season in 2012. This weir provides an escapement estimate for part of the Benjamin Creek/Killey River genetic reporting group for the SSART model. The weir will be operational from early-June until mid-August. Upstream migrating fish are allowed to swim feely through the fish pass 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 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

[4] In the model, entry time is defined as time of migration past rm 9, which cannot be observed for fish that have already arrived at rm 21.

Killey River fish that migrated upstream of the weir. During 2012, the USFWS observed 1471 Chinook salmon at the Killey River weir, although some time periods were missed due to equipment error and/or high water. Of the 51 radio tagged Chinook salmon that entered the Killey River drainage in 2012, 21 continued upstream of the Killey River weir.

Funny River Weir

The Funny River weir is a resistance board weir operated by the United States Fish and Wildlife Service since 2006. This weir provides an escapement estimate for the Funny River part of the Funny River-Slikok Creek genetic reporting group for the SSART model. Upstream migrating fish are allowed to swim feely through the fish pass 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 is located approximately 0.75 miles upstream from the Funny River confluence with the Kenai River. Little to no spawning is known to occur downstream of the weir.

Slikok Creek weir

No weir will be operated on Slikok Creek in 2013. 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.

Grant Creek Weir

The Grant Creek weir will be operated by the McMillen, LLC on behalf of the Grant Lake Hydro Project (FERC # 13212) for the first season in 2013. The weir will provide an escapement estimate for the Grant Creek genetic reporting group for the SSART model. The weir will be operational from break-up to freeze-up. Upstream migrating fish will be passed manually after some handling/tagging. The weir's location is not yet determined, but will be located as close to Grant Lake as possible, minimizing the probability that fish will spawn downstream of the weir.

Quartz Creek Weir

The Quartz Creek weir is a resistance board weir that will be operated by the United States Fish and Wildlife Service for the first season in 2013. This weir will provide an escapement estimate for the Quartz Creek/Crescent Creek genetic reporting group for the SSART model. The weir will be operational from late-May till mid-August. Upstream migrating fish will be allowed to swim freely through the fish pass where they are recorded by a motion-activated digital video recording device. The video footage from the site will be reviewed by a technician to determine upstream passage. The weir will be located approximately 0.15 miles upstream from Kenai Lake. Little to no spawning is known to occur downstream of the weir.

Russian River Weir

The Russian River weir[5] is an engineered structure operated annually by the Alaska Department of Fish and Game near the outlet of Lower Russian Lake. This weir provides an escapement estimate for the Russian River genetic reporting group for the SSART model. 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. The weir is

[5] 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").

located approximately 3 miles upstream from the Russian River confluence with the Kenai River.

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 2007-2010 (the 2011 and 2012 surveys were considered unreliable). 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.

Harvest estimates

Downstream of the Soldotna Bridge

Harvest downstream of the Soldotna Bridge is estimated by the Kenai River Chinook Salmon Creel Survey[2] and included in the SSART model directly. Additional information about the Kenai River Chinook Salmon Creel Survey is included in the Harvest Stock Composition section below.

Upstream of the Soldotna Bridge

To estimate harvest upstream of the Soldotna Bridge we use the product of the ratio of harvest upstream of the Soldotna Bridge to total harvest from the guide logbooks and total SWHS harvest estimate. This represents a change from past SSART estimates, where the SWHS estimates for the area upstream of the Soldotna Bridge were used.

During 2011, low water precluded boat access to the Kenai River upstream of the Soldotna Bridge until mid-June. Harvest sampling staff were amongst the first to access the area, by jet boat, and were sampling before propellor-driven fishing boats had accessed the area. Staff sampled only 4 fish over 11 days prior to the trophy fishing restriction that began on June 29 and continued through the end of the season. Trophy fishing (catch and release for fish between 20 inches and 55 inches total length) virtually eliminated angling harvest and effort upstream of the Soldotna Bridge because harvest opportunity remained available downstream and anglers focused their effort in that area. Boats that remained had little opportunity for legal harvest because there are very few Chinook salmon less than 20, or greater than 55, inches total length in the Kenai River drainage.[6]

Given these observations, it is probable that very few Chinook salmon were harvested upstream of the Soldotna Bridge in 2011, especially during the late run. However, SWHS estimates for 2011 were 521 (se=111) for the early run and 894 (se=161) for the late run, which is far more harvest than is feasible under the circumstances described above. SWHS staff were unable to discern anything unusual in the individual responses they received. We hypothesize that some lower river anglers misreport their geographic location causing a positive bias in the Chinook salmon harvest estimate upstream of the Soldotna Bridge. We suspect that this bias may extend to years other than just 2011.

The SWHS serves the Department well by providing harvest estimates for a variety of species and areas that would not be cost effective to estimate otherwise. However, it may be at a

[6] As an example, only 1.25% of fish sampled by the onsite creel survey were less 20 in or greater than 55 in in 2011.

structural disadvantage when attempting to estimate Chinook salmon harvest upstream of the Soldotna Bridge. The Kenai River fishery is characterized by a large number of guided anglers and a large number of non-resident anglers (both guided and non-guided). Many of these anglers are passive participants in the decision of when and where to fish. Chinook salmon angling effort downstream of the Soldotna Bridge exceeds Chinook salmon angling effort upstream of the Soldotna Bridge by up to an order of magnitude (Table 3).

Guide logbook data were used to obtain an alternative estimate of middle river harvest. Professional fishing guides have been required to complete logbooks that detail their catch by river section since 2006. This mandatory program is a census of guided harvest. Additionally, it is filled out by the guide, as opposed to the angler; and it is filled out at the end of the fishing day, as opposed to months after the end of the fishing season. This information should be largely immune from the geographic misreporting bias we hypothesize above. Guide logbook reports indicate a lower fraction of their total harvest occurred upstream of the Soldotna Bridge (Table 3). These logbook fractions will be used to apportion the total SWHS harvest estimate into harvest below and above the Soldotna Bridge for the purposes of the SSART model.

A potential weakness of this approach is that guides and unguided anglers may disperse themselves differently with respect of river section, and the ratio of Kenai River harvest upstream of the Soldotna Bridge to total harvest for guides may not be representative of unguided anglers. Since we have no data to inform the ratio for unguided anglers we can only attempt to determine if using the guided ratio as a proxy introduces bias. Indeed, unguided anglers may be less likely to disperse upstream relative to guides. Between 2006 and 2010 Kenai River creel technicians stratified their boat counts relative to Poachers Cove (rm=17.4). This boundary is just downstream of the hydrological and physical boundary that distinguished the Kenai River above and below the Soldotna Bridge[7]. Upstream the river is characterized by fast water, large rocks and fewer well-defined fishing holes. Downstream the water is slower, safer and features numerous large fishing areas. Guides were more likely to fish upstream of Poacher's Cove than unguided anglers during most years and runs. Conversely, our hypothesis suggests unguided anglers may be less likely to replicate this error due to an increased familiarity with the Kenai River. However, between 1996 and 2000 a plurality of unguided anglers participating in the early-run Kenai River Chinook salmon fishery were non-residents (McKinley et al. 2002). These observations suggest our use of the guided logbook data to geographically reapportion the SWHS harvest of unguided anglers may not introduce substantial bias.

Harvest Stock Composition

Stock composition of the harvest downstream of the Soldotna Bridge is estimated from GSI data collected from harvest fish sampled by three projects; the Kenai River Chinook Salmon Creel Survey, supplementary harvest sampling that occurs downstream of the Soldotna Bridge, and a voluntary guide sampling program. Stock composition of the harvest upstream of the Soldotna Bridge is estimated from GSI data collected by harvest samplers.

Kenai River Chinook Salmon Creel Survey

The Kenai River Creel Survey[2] is operated annually by the Alaska Department of Fish and Game to estimate harvest between the Soldotna Bridge and Cook Inlet and to sample the harvest of

[7] The Soldotna Bridge is located at Kenai river mile 21. Thus, the Kenai River downstream of the Soldotna Bridge contains a small area that hydrologically similar to the Kenai River upstream of the Soldotna Bridge.

Chinook salmon in the same area for GSI. The creel survey provides an estimate of sport harvest downstream of the Soldotna Bridge as well as the stock composition of that harvest to the SSART model.

The creel survey operates 4 days per week from May 16 to July 31 (Saturday, Sunday and 2 of the 4 non-Monday weekdays). 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 (Figure 2). There are several private moorings and a couple of private launches that are not sampled. Creel survey staff only sample from anglers that have completed fishing for the day. From 2007-2012 an average of 296 tissue samples (Table 2) were genotyped from harvested Chinook salmon by Kenai River Creel Survey staff.

Lower Kenai River Chinook Salmon Harvest Sampling

Additional harvest sampling in the lower Kenai River improves upon the stock composition estimates of the sport harvest downstream of the Soldotna Bridge because the Kenai River Chinook Salmon Creel Survey samples only a small fraction of the harvest in the study area.

Sampling of the Chinook salmon harvest downstream of the Soldotna Bridge will be supplemented by a single Fisheries Technician II working two 10-hour shifts per week[8] from May 15 to July 31. The start and stop times may vary during the season dependent on previous sampling trends; varying the time of day for sampling is not likely to bias estimates of stock composition of the harvest. The sampling dates and locations were selected to ensure that the creel survey and the supplementary harvest sampler are never assigned to the same place at the same time. Other than constraints designed to avoid creel survey staff, and occasional opportunistic sampling of special events that would otherwise go unsampled, all sampling days, times and locations were chosen to maximize the number of fish sampled. The supplementary Chinook salmon harvest sampling schedule is shown in Appendix C1. A portion of the axillary process will be excised from sampled fish and sent to the ADF&G Gene Conservation Lab in Anchorage for analysis. Lower Kenai River Harvest sampling staff collected 161, 801, and 43 tissue samples (Table 2) in 2010-2012 respectively.

Voluntary Guide Sampling

It is difficult to attain an adequate number of tissue samples during the early run using a random sampling design due to low harvest and logistical constraints that concentrate our sampling at Pillar's Boat Launch (Figure 2). Guided anglers harvest a large majority of the fish during the early run (Perschbacher 2012). In 2012, we increased our sample sizes during the early run by partnering with 20 professional fishing guides who collected genetic samples from Chinook salmon harvested by their clients. A total of 56 fish were sampled and genotyped in 2012 (Table 2). Because the sample design for this data collection effort was not randomized, there is potential for bias. However, the stock composition estimated from these samples was similar to the stock composition estimated using the Lower Kenai River Creel and Lower Kenai River Harvest Sampler samples in 2012. Additionally, the total number of fish sampled by all sampling programs prior to June 16, 2012 (134) represents a large fraction (41%) of the estimated harvest during the same time period.

[8] From 2010-2012 harvest sampling was scheduled to occur 4 days per week however samples were not always collected, due to fishery restrictions, or processed, due to administrative decisions.

This program will be repeated in 2013, with a similar number of guides. Guides who frequent the early run, fish primarily below the Soldotna Bridge, and access the fishery thru areas excluded from our sampling programs will be asked to participate in the program. Each participating guide will be given a sampling kit consisting of a vial box, vials, and a field notebook and asked to collect one axillary fin clip per harvested fish. The field notebook will be used to associate vial numbers with the date and location (above or below the Soldotna Bridge) of harvest. To prevent double sampling, harvest sampling and creel survey staff technicians will be given a list of participating guides and will verify their clients' fish have not been previously sampled if encountered. An additional protection is afforded by censoring duplicate genotypes before the data is analyzed.

Middle Kenai River Chinook Salmon Harvest Sampling

Chinook salmon harvest sampling upstream of Soldotna Bridge was conducted as part of a larger project[9] operated by the Alaska Department of Fish and Game from 2007-2010. Since 2010, a reduced harvest sampling effort has been planned, and realized harvest sampling upstream of the Soldotna Bridge has been minimal because of fishery restrictions. Harvest sampling in the middle Kenai River provides stock composition information about harvest upstream of the Soldotna Bridge for the SSART model.

A roving harvest sampling survey will be conducted from early-June through July 31 on the Kenai River Chinook salmon sport fishery between the Soldotna Bridge (rm 21.0) and the Moose River (rm 36.3). Although the fishery is open prior to June, anglers do not access the area because of navigational hazards imposed by low water levels. Harvest sampling of the fishery will begin as soon as the water level in the area is sufficient for motorized boat travel. The majority of the harvest above the Soldotna Bridge occurs between Soldotna Bridge and Moose River. Harvest was low enough in the section between Moose River and Skilak Lake that sampling one day per week in 2007 produced only eight samples. Due to our inability to sample such a small and diffuse harvest, no sampling was conducted in the Moose River to Skilak Lake section in 2008-2012, and no sampling is planned for 2013.

Many anglers fishing this section of river access the fishery via private docks, as there are relatively few public access locations. Anglers will be contacted while fishing or exiting the fishery by ADF&G technicians operating an outboard-powered skiff. Sampling will be conducted Tuesday through Saturday, from approximately 1000 to 1600 hours. The start and stop times may vary during the season dependent on previous sampling trends; varying the time of day for sampling is not likely to bias estimates of stock composition of the harvest. Sampling effort will be distributed as evenly as possible within this reach. Harvested Chinook salmon will be sampled for age, sex, length, and maturity (coloration); location of capture will also be recorded. A portion of the axillary process will be excised from sampled fish and sent to the ADF&G Gene Conservation Lab in Anchorage for analysis. From 2007-2010 an average of 263 tissue samples (Table 2) were collected from harvested Chinook salmon by Middle Kenai River Harvest Sampling Study staff. This program did not operate during 2011 or 2012 due to fishery closures.

[9] Tim McKinley, Alaska Sustainable Salmon Fund Project Completion Report, AKSSF # 45143 (700)

2007-2012 Inriver Abundance Estimates and Expected Precision for 2013

All of the information necessary to generate SSART model estimates of abundance has been collected since the 2007 field season and estimates of abundance have been generated for the 2007-2012 runs. Early SSART model estimates were imprecise, with coefficient of variation (CV) values of 19-35%. However, the model and input datasets have been improved annually, resulting in increasingly precise estimates. The most recent SSART estimates have coefficient of variation (CV) values of 12-23% (Table 1).

For the 2013 season we expect similar run sizes to 2010 and 2012, although the 2012 season is the most applicable comparison because we collected additional data (Killey River weir and rm 21 netting) in 2012 that was not available in 2010. Precision improvements will be due to improvements in the following areas:

- Quartz Creek and Grant Creek escapement estimates
- Increased tag deployments from the rm-21 netting boat: We collected stock identification data (GSI samples and radio tag final fates) from 49 and 38 Chinook salmon at the rm-21 sampling area in 2011 and 2012, respectively. In 2013, we will double our sampling effort and confine tagging to May and June.
- Increased tag deployments from the rm-8.5 nearshore boat: This project is new in 2013, so we have limited knowledge to predict the number of extra tags deployed.

Precision of SSART estimates may decrease because of:

- Reduced staff time dedicated to harvest sampling downstream of the Soldotna Bridge.
- No stock composition data collected near rm 21 in July.

We simulated the expected precision for 2013 by rerunning the SSART model on contrived datasets. For all simulations the data were censored to account for the reduced harvest sampling and lack of July stock composition data from rm-21 we anticipate in 2013. Escapement estimates for the Quartz Creek and Grant Creek drainages were simulated for all years by using the mean of the escapement posteriors as data for the purpose of the simulation. This simulation is optimistic because it assumes the weir count will be congruent with all of the other data collected. Simulation results indicate CV values decrease by 1-4 percentage points with the addition of the Quartz Creek and Grant Creek weirs (Table 1).

The effects of increased stock identification data were simulated by replicating portions of past years stock identification data. Additional stock identification data from rivermile 8.5 was simulated for all years by assuming a 25% increase in the volume of stock identification data collected. Simulation results indicate CV values decrease by 1-3 percentage points more than would be expected by just the addition of extra weirs (Table 1). Additional stock identification data from rivermile 21 was only simulated for 2011 and 2012 by doubling the volume of stock composition data collected in May and June. Simulation results indicate CV values decrease by 0-1 percentage points more than would be expected by the addition of extra weirs (Table 1). Both simulations are optimistic because they underestimate the variability introduced by distinct additional individuals. While the simulations suggest additional stock identification data from rm 8.5 is more valuable than that from rm 21, catch rates for the nearshore boat at rm 8.5 cannot be predicted accurately and we have simulated a best case scenario. Therefore, additional stock composition data will be collected from both sites because of the reliability of additional sampling near rm 21.

Migratory Timing

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 greater than 550 mm MEF in 2013. Chinook salmon less than 550 mm MEF will not be tagged because of a high mortality rate experienced by smaller Chinook salmon in 2010. In practice, this restriction should be inconsequential as historically a very small fraction of Kenai River Chinook salmon are less than 550 mm MEF (McKinley and Fleischman 2010a; McKinley and Fleischman 2010b).

All appropriately sized Chinook salmon captured by the Kenai River Inriver Gillnetting project between May 16 and June 30 will be radio tagged. During the late run, only a subsample of the appropriately sized Chinook salmon captured by the Kenai River Inriver Gillnetting project will be radio tagged. The offshore boat will radio tag every other appropriately sized Chinook salmon sampled between July 1 and August 10. During the late run the offshore tagging crew samples every other fish they capture during each set, meaning the actual tagging rate is maximized when only one Chinook is captured per set and minimized when multiple Chinook are captured on each set. In 2012, this resulted in 141 Chinook salmon radio tagged out of 345 that were captured (1/2.45). The nearshore boat will radio tag every third appropriately sized Chinook salmon captured between July 1 and August 10 in an attempt to tag at approximately the same rate.

Based on the preseason forecast we believe the run size in 2013 should be similar to the runs of 2010, when 273 would have been deployed[10] by the offshore inriver gillnetting boat, and 2012, when 225 radio tags were deployed by the offshore inriver gillnetting boat. We anticipate the nearshore gillnetting crew could deploy 35-42[11] radio tags in 2013. Doubling effort at rm 21 could result in another 66-78 radio tags being deployed in Chinook salmon greater than 550 mm MEF. Between all three tag deployment programs we anticipate having the opportunity to deploy between 326 and 393 radio tags in 2013. If the high side of this range is realized, we will reduce the tagging frequency during the late run such that the total number of tags deployed is less than 350.

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.

[10] Radio tags were not deployed in July during 2010, but we have estimated the sample size based on 2010 catch rates and the 2013 deployment schedule.

[11] Average of 2010 and 225 tagging by offshore crew, expand by the expected percent of Chinook salmon migrating in the offshore zone (0.35/0.65) and adjust for a 2 day per week schedule (2/7). 2010: 273*(0.35/0.65)*(2/7) = 42, 2012: 225*(0.35/0.65)*(2/7) = 35.

Pulse-coded radio transmitters broadcasting on 17 frequencies (151.203-151.630 MHz, 6-25 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 noted 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 5 m 57 s (17 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 a signal is detected during manual radio tracking the receiver is paused at the operator's discretion until the tag location can be accurately determined. Total scan time will be 28 s (14 frequencies * 2 s/frequency) when no signals are detected. 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. Similar scan times have provided satisfactory detection and resolution in past years.

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 12 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 (Figure 1, Figure 2);

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. 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. The direction of fish movement can be discerned by comparing signal strengths among antennas within the chronological data.

Estimated Precision

We expect to deploy a minimum of 260 radio-tags at rivermile 8.5 in 2013 which is sufficient to exceed the precision criterion specified in Objective 2. This calculation assumes that:

(1) Run sizes and sampling effort at the rm-8.5 tagging site are similar to 2010 and 2012.
(1) All fish caught in gillnets at rm-8.5 during the early run (16 May – 30 June) and every other fish sampled during the late run (1 July – 10 August) are radio tagged;
(2) 81% of the gillnet catches at rm-8.5 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 212 viable tags deployed in mainstem-spawning fish. While mainstem-spawning fish that returned in June will be over represented in this sample, the majority of mainstem-spawning fish return in July (89% or greater in 2007-2012) and the spawning distribution within the mainstem is similar for early-returning and late-returning mainstem spawners.
(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 89 viable tags.
(4) Finally we assumed that at least 50% (i.e. $p = 0.5$) of the mainstem spawning Chinook salmon would migrate upstream of rm 14.

Given these assumptions, we expect to estimate the proportion of mainstem-spawning Chinook salmon that migrate upstream of rm 14 such that the estimate is within 11 percentage points of the true value 95% of the time.

Slikok Creek Habitat Survey

The annual run of Chinook salmon to Slikok Creek has been assessed by a foot survey index count in 1990-2004, and 2006. Additionally, in 2005, genetic tissue samples were collected from Chinook salmon captured during less comprehensive foot surveys. Maximum, single-day counts of live and dead fish ranged from 47 fish to 313 fish from 1990-2006. Recent weir counts (2008-2012) ranged from 27-70. Direct comparison between older index counts and recent weir counts are confounded by the recent removal of migratory restrictions (beaver dams, culverts), recent actions to reduce straying of hatchery stocked Chinook salmon of Crooked Creek origin, and annual variation in early run Kenai River Chinook salmon run strength. Regardless, the 2008-2012 run sizes have resulted in concern about the long-term sustainability of Chinook salmon in Slikok Creek.

The sustainability of Chinook salmon in Slikok Creek is influenced by spawning or rearing habitat. During 2013, a baseline physical habitat survey will be conducted on Slikok Creek to investigate stream channel dimension, fish cover, and urban development from its confluence with the Kenai River to upstream of Arc Loop Road. The upstream extent of the survey will be determined by logistical constraints. A majority of the Slikok Creek riparian area upstream of

Arc Loop Road is State of Alaska, Kenai Peninsula Borough, or Kenai National Wildlife Refuge land and remains undeveloped.

The habitat mapping survey will incorporate a mixture of qualitative assessment and physical measurements to create a record of the form of the river, based on observation. This large scale habitat mapping method takes minimal time and effort to cover long stretches of river, at the expense of microhabitat observations. This level of detail is appropriate because it allows field observation and physical measurement over most of the drainage, yet collects data into a geographic information system (GIS) map for comparison to past and future conditions. Approximately 5 days will be required with 2 people to conduct the habitat survey during mean low flow water conditions, tentatively September 10-14. A similar survey, planned for the 2012 season, was never completed because of flood conditions during the proposed survey period.

DATA COLLECTION

Data collection procedures for the cooperative projects are described separately in each project's operation plan. Herein, we describe the data collection procedures for independent projects that will take place in 2013.

Biological Sampling

Harvest sampling crews

All Chinook salmon encountered by the Lower Kenai River harvest sampler or Middle Kenai River harvest sampler will be sampled for the following;

- Three scales from an area approximately 1 inch above the lateral line between the anterior insertion of the anal fin and the posterior insertion of the dorsal fin.
- A thumbnail sized piece of tissue from either axillary process. Samples will be placed in numbered 2ml plastic vial (Nalgene, VWR Cat. # 66008-710) and with 95% alcohol (Sigma Cat. # R 8382) such that the liquid/tissue ratio is approximately 3:1. For further details see Appendix A1. Genetic samples will be stored at the Soldotna office until the end of the season when they will be transferred to the ADF&G Gene Conservation Laboratory archive.

Data will be recorded using Juniper Systems Inc.™ Allegro CE™ field computers. Information collected for each sampled fish encountered by the harvest sampling crews will include the date, time of day, sampling location, genetic vial number, scale card number, mid-eye to fork-of-tail length, estimated sex based on external characteristics, skin color (red, pink, chrome), and rivermile harvested (to the nearest 10^{th} mile).

All Chinook salmon encountered will be sampled. This practice differs from the creel survey which only interviews anglers who have completed their trip. Harvest Chinook salmon could be sampled by up to three programs; the creel, harvest samplers and/or voluntary guide samplers. Unfortunately, some anglers object to a physical mark on their Chinook salmon. Three steps will be taken to prevent resampling. First, anglers encountered by the ADF&G staff will be asked if their fish have already been sampled. Second, both auxiliary processes will be inspected during sampling to determine if either one has been previously removed. Third, the genetics lab will verify each sample has a unique genotype as a quality control procedure.

Rivermile 21 gillnetting crew

All Chinook salmon captured by the rm 21 gillnetting crew will be sampled for scales and tissue as described above except the tissue sample will be taken from the dorsal fin. Data will be recorded using a Juniper Systems Inc.™ Allegro CE™ field computer. Information collected for each Chinook salmon captured by the rm 21 gillnetting crew will include the date, time of day, rivermile captured, genetic vial number, scale card number, frequency and pulse code of the radio tag inserted, mid-eye to fork-of-tail length, estimated sex based on external characteristics, skin color (red, pink, chrome) and recapture status.

Chinook salmon captured at rm 21 could have been previously sampled by gillnetting crews at either rm 8.5 or rm 21. The gillnetting crew at rm 8.5 mark sampled Chinook salmon with an upper caudal hole punch. The crew at rm 21 will use a lower caudal hole punch to distinguish recaptures. All Chinook salmon will be sampled unless they have been previously caught, sampled and tagged. All Chinook salmon will also be tagged unless they are less that 550 mm MEF or they have been previously caught, sampled and tagged by crews at either rm 8.5 or rm 21.

Laboratory Analysis

DNA will be extracted from tissue using DNeasy 96 tissue kits (QIAGEN Inc., Valencia, CA). SNP loci to be screened will be the set developed by the Gene Conservation Laboratory and surveyed in Kenai River Chinook populations. SNP assays were developed at the ADF&G laboratory (Smith et al. 2005) and at the Northwest Fisheries Science Center, National Marine Fisheries Service (Dr. L. Park, unpublished). Genotyping will be conducted using Fluidigm® 96.96 Dynamic Arrays (http://www.fluidigm.com). The Fluidigm® 96.96 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 96 inlets to accept the sample DNA from each individual fish and on the other are 96 inlets to accept the assays for each SNP marker. Once in the wells, the components are pressurized into the chip using the IFC Controller HX (Fluidigm). The 96 samples and 96 assays are then systematically combined into 9,216 parallel reactions. Each reaction is a mixture of 4µl of assay mix (1x DA Assay Loading Buffer (Fluidigm), 10x TaqMan® SNP Genotyping Assay (Applied Biosystems), and 2.5x ROX (Invitrogen)) and 5ml of sample mix (1x TaqMan® Universal Buffer (Applied Biosystems), 0.05x AmpliTaq® Gold DNA Polymerase (Applied Biosystems), 1x GT Sample Loading Reagent (Fluidigm) and 60-400ng/ul DNA) combined in a 7.2nL chamber. Thermal cycling was performed on an Eppendorf IFC Thermal Cycler as follows: 70°C for 30 min for "Hot-Mix" step, initial denaturation of 10 min at 96°C followed by 40 cycles of 96° for 15 s and 60° for 1 min. The Dynamic Arrays will be read on a Fluidigm® EP1™ System after amplification and scored using Fluidigm® SNP Genotyping Analysis software.

Radio tracking

Radio tags will be tuned per the manufacturer's specifications before use. Tuning consists of placing each tag underwater in the Kenai River and determining the median frequency in the transmitter's frequency range. If the average (across pulse codes) of the median frequencies differs from the printed frequency the average will be used during 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 an ATS Model 100 switch. 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 use a 20-foot mast.

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 approximately weekly using a laptop computer and software supplied by the manufacturer. During download sessions each fixed site will undergo periodic 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 will be tracked by boat twice weekly from late-May thorough mid-August. 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 scans all active frequencies. If a tag is detected, the scan will be held on the active frequency while the receiver decodes the pulse code of each transmission. 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.

An ATS R4520 receiver with dual H-style antennas will be used for airplane surveys. The airplane will be flown slowly while the receiver scans all active frequencies. If a tag is detected,

the scan will be held on the active frequency while the receiver decodes the pulse code of each transmission. 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.

Because some of the management questions regarding Kenai River Chinook salmon require precise location information we plan to determine the location of fish relative to the Soldotna Bridge and the Slikok Creek, Funny River, Moose River, and Killey River sanctuary closures precisely using triangulation and manipulation of the receiver gain.

Slikok Creek Habitat Survey

Surveys will involve walking Slikok Creek (approximately 5.0 rm) and identifying mesohabitats: riffles, glides, pools, backwaters, large woody debris (LWD), overhanging vegetation, undercut banks, and anthropomorphic disturbances (such as culverts, agriculture, roads, residential and commercial development). Habitats will be documented by noting their location and extent, and measuring their physical attributes including stream width, depth, pieces of LWD, and the extent of manmade disturbances along stream channel.

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 2013.

Harvest sampling and rm 21 netting data

Harvest sampling and rm 21 netting data will be collected using Juniper Systems Inc.™ Allegro CE™ field computers running Dataplus Professional® software. Datafiles are saved in a proprietary format that can be converted into comma-separated ASCII files using SAS® software. A data map for harvest sampling data is shown in Appendix E1. A data map for rm 21 netting data is shown in Appendix E4.

Slikok Creek Habitat Survey

A habitat map will be produced by incorporating the field observations and measurements into ArcGIS.

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 E2.

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. Datafiles 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 E3.

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[12]. 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).[13] 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 8.5 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 8.5 during year *y*, time period *t* is:

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

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 (abundance for stock i at time t, upon passing river mile 8.5) is proportional to a bell-shaped (normal pdf) function T_{iyt}:

$$\mathrm{T}_{iyt} = e^{-z_{iyt}^2} \tag{2}$$

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

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

with means $\bar{t}_{iy}$ and standard deviation σ_{T1A} for tributary stocks or σ_{T1B} for mainstem/Juneau.[14]

[12] 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.

[13] 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.

[14] The current version of the model assumes that stocks KB, FS, and QC have the same mean.

Run timing means $\bar{t}_{iy}$ vary among years as 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(ε_{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[15], 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-8.5 netting project, and multinomial count data constructed to reproduce stock composition information from GSI sampling of the harvest.

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 8.5, combined from the creel and mail survey, 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:

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

[15] In one version of the current model, harvest rates for stock groups KB, FS, and QC are equal because of similar run timing.

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[16], 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[17] 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} was 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[18] of allele k in fish sampled from the baseline of stock i.

OpenBUGS code for the main SSART model can be found in Appendix B1, and for the auxiliary harvest stock composition model in Appendix B2. 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 with the same effective sample size.

Markov Chain Monte Carlo (MCMC) methods were employed using WinBUGS (Lunn et al. 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 was hierarchical, lognormally distributed among years, with Dirichlet-distributed stock composition. An inverse gamma(100,1) prior distribution, equivalent to a CV of 0.1, was 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 were assigned non-informative priors, designed to have minimal effects on the posterior (see Appendix B1 and Appendix B2).

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[16] 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.

[17] 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, $\theta_{3,}$ θ_4, θ_5, θ_6) distribution, it can assume values 1 to 6 with probabilities θ_1, θ_2, $\theta_{3,}$ θ_4, θ_5, θ_6.

[18] 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.

Equal Catchability Assumption

Because escapement is known for most the major tributary stocks groups, and tributary stocks primarily return during the early run, the SSART model is heavily reliant on catch rates from the rm 8.5 netting project to estimate abundance during the late run. The concern is that net saturation and distribution of fish across the river may change over the season causing catchability q_y (Equation 10) to trend over time. If the q_y increases or decreases between runs, than the SSART model estimate of abundance for the late run will be biased in the same direction. In past years we have had limited information available to evaluate the magnitude of this bias. However, beginning in 2013, ADF&G is planning a second sonar site at Kenai rm 14. The rm-14 site will have bank to bank coverage, and there is no evidence that DIDSON/ARIS saturates at high fish densities. The ratio of net cpue to rm-14 abundance estimates reflects catchability and we would expect a trend over time if it changes. This ratio will also be affected by holding, spawning, and harvest between miles 9 and 14, but we anticipate being able to adjust for these factors using radio telemetry and creel data. This assessment relies on sonar data, which threatens the perceived independence of the SSART estimate. However, the reliance on sonar data is extraneous to absolute abundance. Instead, sonar data is used to test assumptions or provide information about the relative abundance through time.

A second approach to evaluate the assumption of equal probability of capture over time is to use sport CPUE as the temporal index of abundance. This comparison is not possible during years with fishery closures, and is likely a less reliable index. However agreement of SSART estimates generated using each index of abundance would be consistent with a finding that probability of capture does not change over time.

Migratory Timing

The proportion of mainstem-spawning Chinook salmon that migrated upstream of the rm 14 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 14 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):

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

The cumulative distribution of migratory timing past the specific locations identified in the project tasks (# 4 - 6) will be summarized by determining the date and time each radio tagged fish swam past the fixed telemetry site. 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. The date, time, and direction of fish movement will be discerned by comparing signal strengths among antennas within the chronological data.

Slikok Creek Habitat Survey

The ArcGIS map produced by this survey (task 7) can be used to identify the longitudinal distribution and total length/area and proportional length/area of each mesohabitat within the study area. The habitat map will then be compared to historic aerial imagery[19] to document and quantify development, stream channel, and physical habitat changes. Historic comparisons will be completed on an ad-hoc basis depending on staff availability and/or cooperation from other agencies or non-profits.

SCHEDULE AND DELIVERABLES

The objectives of this project will be completed during and following the 2013 field season.

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 10	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
Lower Kenai harvest samp.	May 16-July 31	Eskelin/Tech II
Middle Kenai harvest samp.	June 1-July 31	Eskelin/Tech II
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
Slikok Creek Habitat Survey	mid-August	Perschbacher
Genotype Samples	Winter	Gene Conservation Laboratory
Editing data	Winter	Reimer
Data analysis	Winter	Reimer/Antonovich
FDS report	Spring	Reimer/Antonovich

[19] Arial imagery exists for this drainage in 1950, 1996-1998, 2003, 2007, and 2009-2011.

BUDGET SUMMARY

BUDGET SUMMARY

Line	Category	FY13 11222851 ($K)	FY14 11222851 ($K)	FY13 11282305 ($K)	FY14 11282305 ($K)
100	Personnel Services	24.3	71.1	78.5	78.3
200	Travel	0.6	0.0	0.0	0.0
300	Contractual	4.0	10.8	54.3	64.1
400	Commodities	3.6	2.7	85.0	75.9
500	Equipment	0.0	0.0	0.0	0.0
Total		32.5	84.6	217.8	218.3

PROJECT PERSONNEL

PCN	Name	Budget	Level	FY 13 Months	FY 14 Months
4017	A. Reimer	11222851	FB II	3.0	3.0
4017	A. Reimer	11282305	FB II	9.0	9.0
4213	Vacant	11222851	FWT III	2.0	4.0
4306	Vacant	11222851	FWT II	1.5	2.5
4301	Vacant	11222851	FWT II	1.0	2.0

BUDGET NARRATIVE

Line 100: Personnel

Funds support one Fisheries Biologist II, one Fisheries Technician III and two Fisheries Technician II. Fiscal year 2013 funds support technicians during May/June 2013. Fiscal year 2014 funds support technicians during July 2013 and May/June 2014. 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. Primary author in the writing of the final project reports.
- Radio telemetry: Install, maintain and remove telemetry stations. Hire and supervise seasonal staff. Airplane tracking. Assist with boat tracking.

Steve Fleischman, Fisheries Scientist I

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

Tony Eskelin, Fisheries Biologist II

- Lower and Middle River Sport Harvest: Procurement of equipment. Hire and supervise seasonal staff. Assist with collection of field data.

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, PCN 7112

- 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.

Jeff Perschbacher, Fisheries Biologist I

- Slikok Creek habitat assessment.

Vacant, Fish and Wildlife Technician III, PCN 4249, 5/1-8/31

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

Vacant, Fish and Wildlife Technician II, PCN 4306, 5/16-7/31

- Conduct roving harvest sampling survey of popular access site below Soldotna Bridge.

Vacant, Fish and Wildlife Technician II, PCN 4301, 6/1-7/31

- Conduct roving harvest sampling survey between Soldotna Bridge and Moose River.

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FIGURES AND TABLES

Figure 1.–Tributaries to the Kenai River which support populations of Chinook Salmon.

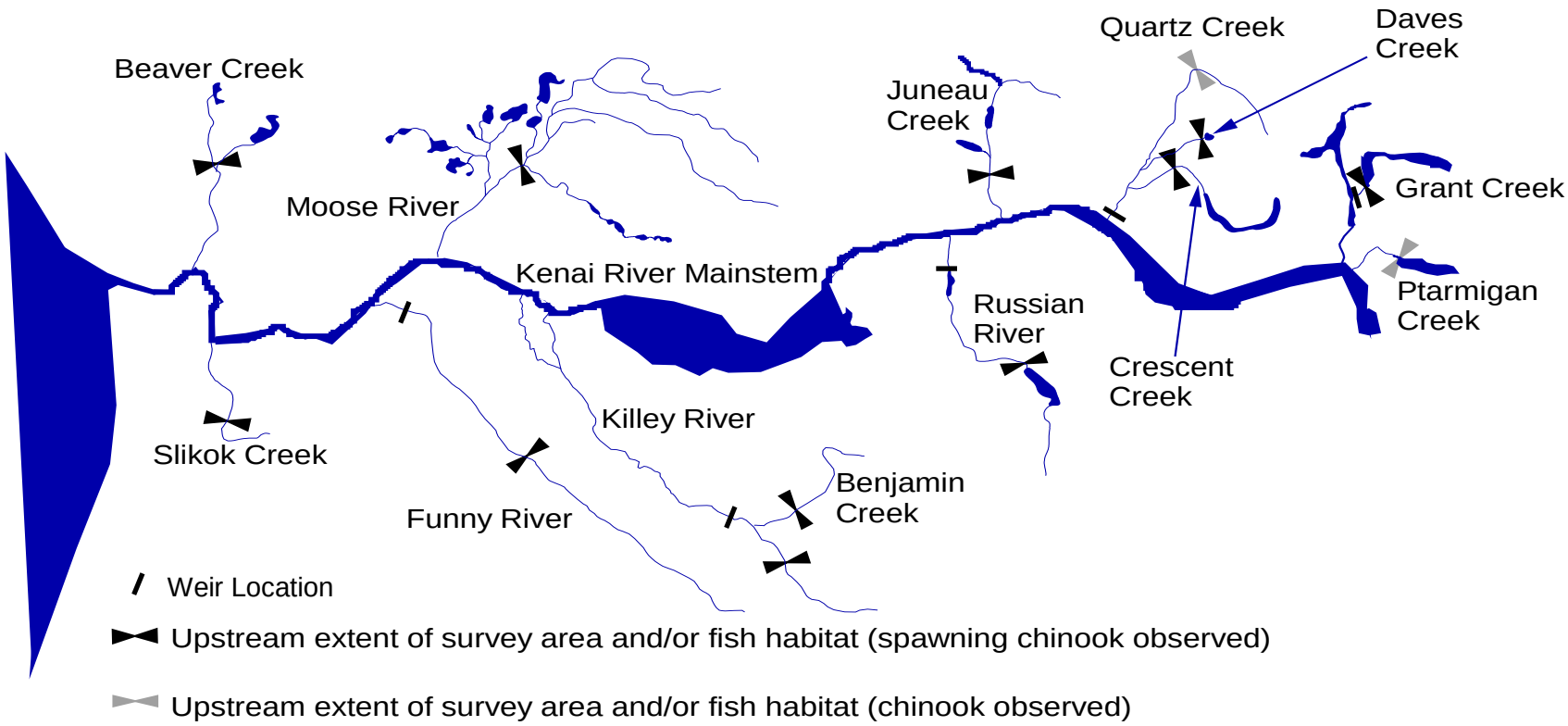

Figure 2.–Kenai River Study Area.

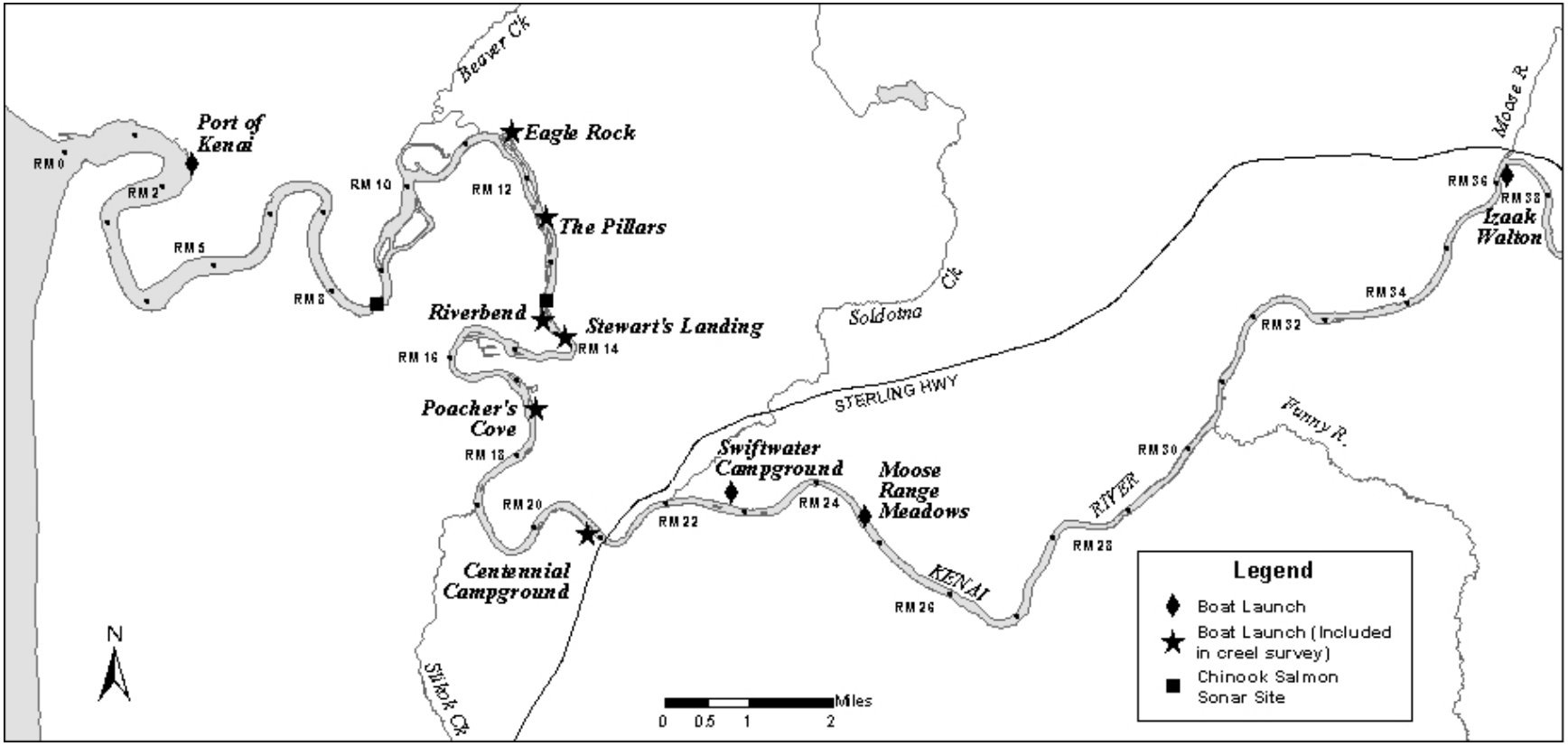

Table 1.–SSART v4.3 model estimates for 2007-2012 and expected precision for 2013.

Early Run								Late Run							
Year	mean	sd	CV	2.5 percentile	median	97.5 percentile	samples	Year	mean	sd	CV	2.5 percentile	median	97.5 percentile	samples
Actual Data															
2007	13010	2405	18.5%	9186	12700	18430	67777	2007	51060	10110	19.8%	34850	49680	73590	67777
2008	8636	989	11.5%	6896	8564	10760	67777	2008	47460	6463	13.6%	36190	46950	61360	67777
2009	10580	2263	21.4%	7140	10270	16010	67777	2009	44660	10070	22.5%	29710	43250	69360	67777
2010	8347	1206	14.4%	6240	8268	10900	67777	2010	21330	3457	16.2%	15210	21130	28420	67777
2011	9267	1529	16.5%	6612	9157	12660	67777	2011	27300	4895	17.9%	18770	27020	38090	67777
2012	6513	818	12.6%	5156	6421	8408	67777	2012	25080	3811	15.2%	18770	24610	34020	67777
Actual Data + simulated Quartz C. & Grant C. - 50% decrease harvest sampling below Soldotna Bridge - no July rm21 catches															
2007	12300	1866	15.2%	9209	12110	16500	90001	2007	48000	7853	16.4%	35100	47280	65410	90001
2008	8513	908	10.7%	6855	8472	10410	90001	2008	46050	5834	12.7%	35100	45840	58200	90001
2009	9886	1727	17.5%	7108	9694	13770	90001	2009	41270	7492	18.2%	29470	40480	57940	90001
2010	8347	1134	13.6%	6478	8242	10850	90001	2010	21740	3271	15.0%	16440	21460	28980	90001
2011	8746	1321	15.1%	6535	8602	11810	90001	2011	25870	4265	16.5%	18830	25400	36070	90001
2012	6071	606	10.0%	5012	6026	7398	90001	2012	23540	2805	11.9%	18540	23360	29570	90001
Actual Data + sim. QC & GC - 50% less H samp. below Soldotna Bridge - no July rm21 + 100% increase in rm21 netting (May/June)															
2007	12090	1777	14.7%	8911	11990	15810	54161	2007	47080	7465	15.9%	33400	46860	62340	54161
2008	8403	911	10.8%	6762	8346	10310	54161	2008	45420	6222	13.7%	34620	45040	58740	54161
2009	9761	1901	19.5%	7047	9473	14730	54161	2009	40730	8596	21.1%	29070	39400	63730	54161
2010	8260	1044	12.6%	6504	8151	10580	54161	2010	21250	2979	14.0%	15890	21040	27450	54161
2011	*8122*	*1178*	*14.5%*	*6122*	*8010*	*10740*	*54161*	*2011*	*23720*	*3776*	*15.9%*	*17360*	*23350*	*31960*	*54161*
2012	*6094*	*626*	*10.3%*	*5015*	*6041*	*7458*	*54161*	*2012*	*23560*	*2902*	*12.3%*	*18700*	*23250*	*29930*	*54161*

-continued-

Table 1.–Page 2 of 2.

Actual Data + sim. QC & GC - 50% less H samp. below Soldotna Bridge - no July rm21 + 25% increase in rm8 netting

2007	11810	1543	13.1%	9313	11570	15420	21493	2007	46030	6410	13.9%	35790	45020	60810	21493
2008	8283	820.6	9.9%	6824	8229	10030	21493	2008	45420	5257	11.6%	36680	44940	56530	21493
2009	10040	1469	14.6%	7487	9920	13440	21493	2009	42460	6525	15.4%	31200	42190	59110	21493
2010	8011	1026	12.8%	6211	7955	10160	21493	2010	20130	2947	14.6%	14890	19980	26240	21493
2011	8659	1170	13.5%	6579	8564	11260	21493	2011	25580	3796	14.8%	18760	25190	34040	21493
2012	6068	589.9	9.7%	5045	6028	7383	21493	2012	23280	2694	11.6%	18410	23100	28890	21493

Table 2.–Number of Kenai River Chinook salmon in Gene Conservation Laboratory database by sampling program, 2007-2012.

	Netting		Sport Harvest			
			Cook Inlet to Soldotna Bridge			Soldotna Bridge to Skilak Lake
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	
07-12 Ave.	484	49	296	76	56	263
10-12 Ave.	516	49	215	76	56	352

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 run based on an administrative decision.

Table 3.–Ratio of Kenai River Chinook salmon upstream of the Soldotna Bridge to total harvest, Statewide Harvest Survey and Guide Logbook program.

		Cook Inlet to Soldotna Bridge		Soldotna Bridge to Skilak Lake		Total		upstream
Year	Run	est.	SE	est.	SE	est.	SE	/ total
SWHS (guided harvest only)								
2006	Early	2,365	262	893	161	3,258	307	0.27
2007	Early	1,701	192	505	152	2,206	245	0.23
2008	Early	1,574	171	452	100	2,026	198	0.22
2009	Early	491	110	262	66	753	128	0.35
2010	Early	425	84	356	76	781	113	0.46
2011	Early	928	144	368	94	1,296	172	0.28
2006	Late	4,706	366	1,295	165	6,001	401	0.22
2007	Late	5,029	416	1,091	160	6,120	446	0.18
2008	Late	4,449	331	772	111	5,221	349	0.15
2009	Late	2,914	254	784	142	3,698	291	0.21
2010	Late	2,993	287	837	141	3,830	320	0.22
2011	Late	3,758	360	514	122	4,272	380	0.12
Guide Logbook data								
2006	Early	2,053		383		2,436		0.16
2007	Early	1,504		360		1,864		0.19
2008	Early	1,645		231		1,876		0.12
2009	Early	500		61		561		0.11
2010	Early	503		228		731		0.31
2011	Early	503		25		528		0.05
2006	Late	5,978		168		6,146		0.03
2007	Late	5,001		239		5,240		0.05
2008	Late	4,693		310		5,003		0.06
2009	Late	3,108		285		3,393		0.08
2010	Late	2,177		566		2,743		0.21
2011	Late	3,076		16		3,092		0.01

APPENDIX A: GENETIC SAMPLING INSTRUCTIONS

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**.

-continued-

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

APPENDIX B: ANALYTICAL METHODS

Appendix B1.–OpenBUGS code for Bayesian estimation of inriver abundance[20].

```
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])
```

-continued-

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

```
  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.N.mean[y] ~ dnorm(0,1.0E-12)
    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) {
    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
```

-continued-

```
    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(- 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
       }
```

-continued-

```
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])
```

-continued-

```
  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])
```

-continued-

```
    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)
#     Bt[y] ~ dgamma(0.1,0.1)
#     B1t[y] <- Bt[y]  * HRt.y[y]
#     B2t[y] <- Bt[y]  - B1t[y]
#     HR.iy[1,y] ~ dbeta(B1t[y],B2t[y])I(0,0.99)
#     HR.iy[2,y] ~ dbeta(B1t[y],B2t[y])I(0,0.99)
#     HR.iy[4,y] ~ dbeta(B1t[y],B2t[y])I(0,0.99)
    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])
```

-continued-

```
  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.–OpenBUGS code for harvest stock composition [21].

```
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
```

-continued-

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

```
  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])
      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(- 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]
```

-continued-

```
        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,])
```

-continued-

```
    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 LOWER STOCK ID
  for(h in 1:A) {
   Xd3.1[m3,h] ~ dbin(qd[z3.1[m3],h],2)                # SPORT M ALLELE COUNTS
  }
 }

#_____________________________________________________________
```

-continued-

```
 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 LOWER 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) {
```

-continued-

```
  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 LOWER 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 LOWER STOCK ID
  for(h in 1:A) {
   Xd3.4[m3,h] ~ dbin(qd[z3.4[m3],h],2)               # SPORT M ALLELE COUNTS
  }
 }
```

-continued-

```
#_____________________________________________________________
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 C: SCHEDULES

Appendix C1.–Supplementary Chinook salmon harvest sampling schedule.

Monday	Tuesday	Wednesday	Thursday	Friday	Saturday
20-May	**21-May**	**22-May**	**23-May**	**24-May**	**25-May**
			10:00 Pillars *20:00 end*	*8:00 Pillars* *18:30 end*	
27-May	**28-May**	**29-May**	**30-May**	**31-May**	**1-Jun**
		8:00 Pillars *19:00 end*	*9:00 Pillars* *19:30 end*		
3-Jun	**4-Jun**	**5-Jun**	**6-Jun**	**7-Jun**	**8-Jun**
		8:00 Pillars *13:00 River bend* *19:30 end*		*10:00 River bend* *15:00 Pillars* *21:00 end*	
10-Jun	**11-Jun**	**12-Jun**	**13-Jun**	**14-Jun**	**15-Jun**
	7:00 Pillars *13:00 Centennial* *18:30 end*	*8:00 River bend* *11:00 Poachers* *19:00 end*			
17-Jun	**18-Jun**	**19-Jun**	**20-Jun**	**21-Jun**	**22-Jun**
	7:00 Pillars *12:00 Poachers* *20:00 end*			*8:00 Centennial* *12:00 River bend* *19:30 end*	
24-Jun	**25-Jun**	**26-Jun**	**27-Jun**	**28-Jun**	**29-Jun**
	9:00 Poachers *13:00 Pillars* *20:00 end*				*8:00 Pillars* *11:00 River bend* *19:30 end*
1-Jul	**2-Jul**	**3-Jul**	**4-Jul**	**5-Jul**	**6-Jul**
		8:00 River bend *16:00 Centennial* *19:30 end*	*10:00 Pillars* *16:00 River bend* *21:00 end*		
8-Jul	**9-Jul**	**10-Jul**	**11-Jul**	**12-Jul**	**13-Jul**
		8:00 Pillars *13:00 Centennial* *19:00 end*		*9:00 Poachers* *13:00 River bend* *20:30 end*	
15-Jul	**16-Jul**	**17-Jul**	**18-Jul**	**19-Jul**	**20-Jul**
	8:00 Pillars *12:00 Poachers* *19:00 end*	*8:00 Centennial* *14:00 River bend* *19:30 end*			
22-Jul	**23-Jul**	**24-Jul**	**25-Jul**	**26-Jul**	**27-Jul**
	7:00 Pillars *12:00 Poachers* *18:30 end*			*8:00 River bend* *13:00 Pillars* *19:00 end*	
29-Jul	**30-Jul**	**31-Jul**			
12:00 Pillars *22:30 end*		*8:00 River bend* *12:00 Pillars* *16:00 Centennial* *18:00 end*			

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	

APPENDIX E: DATA MAPS

Appendix E1.–Harvest sampling data map.

Data Field Name	Start Column	End Column	Comma Column	Codes/ Comments
Date Sampled	1	8	9	
Year	1	4		Two digit year
Month	5	6		
Day	7	8		
Time Sampled	10	13	14	Military time
Sampling Location	15	16	17	01=Centennial, 03=Riverbend, 05=Eagle Rock, 06=Pillar's, 07=Poacher's Cove (not sampled; 02=River Quest, 04=Stewart's)
Collector	18	19	20	Initials of sampler
Species	21	23	24	410 = chinook
Sex	25	25	26	M or F
MEF length	27	30	31	MEFL, millimeters
Scale Card-Fish #	32	36	37	columns 32-33=scale card number, columns 35-36=fish number
Age	38	39	40	column 38=freshwater age, column 39=marine age
Age error	41	41	42	R=regen, M=missing, I=inverted, A=absorbed
GSI collection	43	50	51	
GSI vial number	52	54	56	
Radio frequency	57	62	63	KHz, six digit number
Pulse code	64	65	66	
Rivermile caught	67	70	71	Primarily overlaps creel although some middle river, one dipnet

Appendix E2.–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 E3.–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

Appendix E4.–River mile 21 gillnetting data map.

Files are in revised tagging data file format (modification to projectnum, weighttype and fate fields).				
Data Field Name	Start Column	End Column	Comma Column	Codes/ Comments
Crew number	1	2	3	
Date code	4	11	12	YYYYMMDD
Week of year	13	14	15	1-54
Day type	16	16	17	1=weekday, 2=weekend
Species	18	20	21	Sport fish species codes
SWHS survey area	22	23	24	P0 (zero not O)=Kenai Penninsula freshwaters
SWHS site	25	28	29	0001=Kenai River (Cook Inlet to Soldotna Bridge)
SWHS sublocation	30	31	32	00=null value
Radio tag frequency	33	38	39	KHz
Radio tag pulse code	41	42	43	two digit #
Drift #	45	46	47	unique daily
Rivermile pulled	48	49		02-20
1/10 Rivermile pulled	50	50	51	0-9
Bank pulled	52	54	55	N=north bank, S=south bank, M-mid channel
Length type	56	57	58	FL=fork length, EF=MEFL
Skin Color	59	60	61	C=chrome, B=blushed, R=red
Fishery type	62	63	64	TE=test fishery
Gear code	65	66	67	01=gillnet
Mesh size (inches)	68	68	69	5 (5.0 inch mesh) or 7(7.5 inch mesh)
Mesh size (eighths of an inch)	70	70	71	0 (5.0 inch mesh) or 4 (7.5 inch mesh)
Drift Start Time (Hour)	73	74	75	Two digit military hours
Drift Start Time (Minutes)	77	78	79	Two digit minutes
Drift Start Time (Seconds)	81	82	83	Two digit seconds
Drift Stop Time (Hour)	85	86	87	Two digit military hours
Drift Stop Time (Minutes)	89	90	91	Two digit minutes
Drift Stop Time (Seconds)	93	94	95	Two digit seconds
Scale card #	98	98	99	1-9
Fish #	101	102	103	1-10, card#-fish#, unique daily
Age structure	104	105	106	SC=scales

-continued-

Appendix E4.–Page 2 of 2.

Data Field Name	Start Column	End Column	Comma Column	Codes/ Comments
Tag type	107	108	109	
Handling time	110	117	118	
Maturity index	120	120	121	0=not checked, 2=firm, 3=spawning, 4=spent
Sex	122	122	123	M or F (blank is not certain)
Length	124	127	128	mm
Recap	129	129	130	Y=recap, blank=not a recap
Tag number	131	136	137	
Age	138	139	140	column 138=freshwater age, column 139=marine age
Age error	141	141	142	R=regen, M=missing, I=inverted, A=absorbed, D=dirty
Injury code	143	143	144	1=healthy, 2=bleeding gills, 3=cut/scrape, 4=lethargic, 5=other
Sample	145	145	146	Y=sampled, blank=not sampled
Tag Lost	147	147	148	Y=tag lost, blank=tag not lost
Fin clip	150	151	152	3=adipose, 8=dorsal 9=upper caudal, 10=lower caudal, 99 U&L caudal
Tag color	154	154	155	
Number caught	156	157	158	1-99
Genetic vial number	159	162	end	