Regional Information Report 5J12-24

Western Alaska Salmon Stock Identification Program Technical Document 17: Chum Reporting Groups Exploratory Methods

by

Christopher Habicht,

William D. Templin,

Nicholas A. DeCovich,

and

James R. Jasper

November 2012

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

Symbols and Abbreviations

The following symbols and abbreviations, and others approved for the Système International d'Unités (SI), are used without definition in the following reports by the Divisions of Sport Fish and of Commercial Fisheries: Fishery Manuscripts, Fishery Data Series Reports, Fishery Management Reports, Special Publications and the Division of Commercial Fisheries Regional Reports. All others, including deviations from definitions listed below, are noted in the text at first mention, as well as in the titles or footnotes of tables, and in figure or figure captions.

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

REGIONAL INFORMATION REPORT 5J12-24

WESTERN SALMON STOCK IDENTIFICATION PROGRAM TECHNICAL DOCUMENT 17: CHUM REPORTING GROUPS EXPLORATORY METHODS

by
Christopher Habicht, William D. Templin, Nicholas A. DeCovich, and James R. Jasper
Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory, Anchorage

Alaska Department of Fish and Game
Division of Sport Fish, Research and Technical Services
333 Raspberry Road, Anchorage, Alaska, 99518-1565

November 2012

The Regional Information Report Series was established in 1987 and was redefined in 2006 to meet the Division of Commercial Fisheries regional need for publishing and archiving information such as project operational plans, area management plans, budgetary information, staff comments and opinions to Board of Fisheries proposals, interim or preliminary data and grant agency reports, special meeting or minor workshop results and other regional information not generally reported elsewhere. Reports in this series may contain raw data and preliminary results. Reports in this series receive varying degrees of regional, biometric and editorial review; information in this series may be subsequently finalized and published in a different department reporting series or in the formal literature. Please contact the author or the Division of Commercial Fisheries if in doubt of the level of review or preliminary nature of the data reported. Regional Information Reports are available through the Alaska State Library and on the Internet at http://www.adfg.alaska.gov/sf/publications/.

Christopher Habicht, William D. Templin, Nicholas A. DeCovich, and James R. Jasper
Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory
333 Raspberry Road, Anchorage, Alaska, 99518-1565 USA

This document should be cited as:
Habicht, C., W. D. Templin, N. A. DeCovich, and J. R. Jasper. 2012. Western Salmon Stock Identification Program Technical Document 17: Chum reporting groups exploratory methods. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J12-24, Anchorage.

TABLE OF CONTENTS

LIST OF FIGURES

ABSTRACT

Uncertainty about the magnitude, frequency, location, and timing of nonlocal harvest of sockeye and chum salmon in Western Alaska fisheries was the impetus for the Western Alaska Salmon Stock Identification Program (WASSIP). The project was designed to use genetic data in mixed stock analysis to reduce this uncertainty. Reporting groups refer to the groups of populations to which fishery mixtures were allocated during mixed stock analyses. A meeting of the WASSIP Advisory Panel and the Gene Conservation Laboratory was called due to a lack of concurrence regarding the *ad hoc* committee's recommendation that Coastal Western Alaska (CWAK) be maintained as a single reporting group for WASSIP fishery mixtures (after their review of simulated test results) rather than as 4 reporting groups (documented in earlier WASSIP reports of this series). Three approaches were recommended by the Technical Committee, two of which were adjustments to statistical analysis methods based on previous work by other scientists, nicknamed the Anderson Approach and the Koljonen Approach by the the Gene Conservation Laboratory. The last suggested approach which evaluates the effects of a modest increase in marker numbers on resolution is still being investigated. The Anderson Approach did not follow expectations for better performance compared to the original methods. The Koljonen Approach provided minor differences in composition estimates compared to the original methods. All methods produced much higher correct proportional allocation of populations in CWAK back to the single CWAK reporting group than to their respective subregional group. Neither the Anderson nor the Koljonen approaches provided results that would indicate that the CWAK reporting group should be separated into 4 reporting groups for WASSIP mixture analyses.

Key words: Western Alaska Salmon Stock Identification Program, WASSIP, chum salmon, mixed stock analysis, MSA, reporting groups

INTRODUCTION

A joint Advisory Panel (AP)/Technical Committee (TC) meeting was held in Anchorage on November 14, 2011, to resolve the designation of reporting groups for chum salmon. The meeting was necessary because there was a lack of concurrence among AP members regarding the *ad hoc* committee's recommendation that Coastal Western Alaska (CWAK) should be maintained as a single reporting group for the Western Alaska Salmon Stock Identification Program (WASSIP) fishery mixtures, rather than as 4 reporting groups (Habicht et al. 2012). The *ad hoc* committee was established at the September 2011 meeting to examine the feasibility of further dividing the CWAK reporting group into 4 reporting groups for chum salmon.

One of the concerns among some AP members was that the department had not investigated all reasonable methods that might lead to the ability to divide the CWAK reporting group. At the November meeting, the AP asked the TC if there were any other methods that could be implemented that might lead to further resolution within CWAK. Dr. Waples (TC member) suggested 3 approaches that could be explored that might lead to, or provide insights into, better resolution within CWAK. These approaches were included as part of a motion that was approved at the November meeting as follows:

1. For simulations involving power analysis, implement the algorithm proposed by Anderson et al. (2008), which does not require dropping part of the baseline samples to avoid problems with lack of proper cross validation.
2. For mixture analyses, implement the method proposed by Koljonen et al. (2005), which they found performed better than standard methods (SPAM, Bayes).
3. To give a rough idea of how much additional resolution can be expected from modest increases in numbers of markers, create baseline datasets for a subset of key populations for which data are already available for 3 different marker types: allozymes, SNPs, and microsatellites. Using the combined sets of allele frequencies, simulate mixtures from

the problem areas and see whether these modest increases in marker number and type substantially improve resolution.

The first 2 approaches might guide the statistical analysis methods for WASSIP mixtures and were therefore time sensitive within the WASSIP timeline. These will be referred to as the *Anderson Approach* and the *Koljonen Approach* in the remainder of this document. The last approach was designed to provide insights into future methods that might yield the desired resolution within CWAK. The Gene Conservation Laboratory is working on all 3 approaches, but this document describes the methods and results from the first 2 approaches. Results from the last approach will be presented at a later date when these analyses are complete.

ANDERSON APPROACH

Anderson et al. (2008) introduced an algorithm whereby every individual is pulled out of the baseline, one at a time, and allocated to reporting groups (*leave-one-out*). In their paper, they published a program (ONCOR) that applies the algorithm. The reason why this method may prove to be more appropriate for determining the viability of reporting groups for WASSIP is that this method does not depopulate the baseline as much as the proof tests used in Habicht et al. (2012). In proof tests, all the individuals in the test mixture (for our proof tests, we used 400-fish mixtures) are excluded from the baseline. In contrast, the *leave-one-out* method excludes only the single fish that is being tested. Therefore, our proof tests may yield excessively conservative performance measures.

KOLJONEN APPROACH

Koljonen et al. (2005) compared 4 methods for mixed-stock analysis (MSA):

1) Classical individual assignment (IA);
2) Proportional assignment using conditional maximum likelihood (CML);
3) Proportional assignment using a Bayesian method (BAYES); and
4) Bayesian individual assignment method (BIA).

The main point of the Koljonen et al. (2005) paper was that proportional assignment (CML or BAYES) performs better than classical IA. The authors also found that the BIA method outpaces the BAYES method slightly. The authors used a flat prior for the Bayesian analyses (as suggested in the BAYES publication; Pella and Masuda 2001). Since the TC has recommended that we use an informed prior based on stock compositions of associated strata (Appendix C in Jasper et al. 2012), we used an informed prior based on the CML (SPAM prior) for the proof tests as a surrogate for the associated-strata priors that we plan to use for the WASSIP mixtures. We know from past experience that informed priors provide less biased BAYES results than flat priors, especially where there is little genetic differentiation among reporting groups. We are not advocating using this SPAM prior method (based on the same mixture) for WASSIP samples as per Pella and Masuda (2001), but we needed a surrogate just for these tests.

After reviewing Koljonen et al. (2005), we checked in with Dr. Waples to verify that this was the document to which he was referring in the resolution and that our plans for examining the individual assignment methods (BAYES) were in alignment with his suggestion. Dr. Waples confirmed that this was the right document and suggested using the *posterior probability distribution for each individual* from the BAYES output to conduct a test similar to the one described in Koljonen et al. (2005). Dr. Waples further suggested that we contact Michele Masuda or Jerry Pella confirm the methods.

We examined the methods described in Koljonen et al. (2005) for using the Bayesian individual assignment method and determined that it was similar to the method used in cBAYES, (program in Neaves et al. 2005 and implemented in Beacham et al. 2009), and we will refer to it as the *roll-up* method. In this method, individuals are assigned to a single population at each iteration and the best estimate is derived from the sum of these assignments divided by the number of iterations times the mixture size, or:

$$\hat{p}_i^{roll-up} = \frac{\sum_{k=1}^{K} M_i^{(k)}}{KM}.$$

Where $M_i^{(k)}$is the number of individuals in the mixture that are assigned to stock i at the k^{th} iteration, M is the size of the mixture, and K is the number of iterations. This is similar, but not quite identical, to a Rao-Blackwellized estimator (Robert and Casella 2004). The Rao-Blackwell Method also incorporates the prior into the estimate and has the form:

$$\hat{p}_i^{RB} = \frac{\sum_{k=1}^{K}\left(M_i^{(k)} + \alpha_i\right)}{K\left(M + \sum_{i'=1}^{C} \alpha_{i'}\right)}.$$

By incorporating the prior, this estimate has well characterized properties which allow for the calculation of credibility intervals, among other statistics.

We contacted Michele Masuda and asked her to review our proposed analysis methods. She agreed that these methods would use individual assignment information to come up with stock composition estimates, but was not convinced that the results would be more accurate or precise. She suspected that the slightly better results for the BAYES roll-up composition estimates over the BAYES mixture model estimates, in Table 4 of Koljonen et al. (2005), were somewhat of an artifact. The true composition was 100%, and proportional assignment is biased at the boundaries. If they had reported the mode instead of the mean of the posterior distribution, the results for the 2 methods would likely have been closer. The roll-up composition estimates were also good because the assignments were good. She said that one would actually not expect the roll-up composition estimates to be very good in situations where stocks are genetically similar. The misclassifications between similar stocks will lead to biased composition estimates. It has been shown that bias can be reduced if fractions of individuals are assigned (proportional assignment) instead of classifying whole individuals to stocks. She mentioned that there is a body of published work indicating that using assignments of whole individuals to estimate stock proportions tends to be more biased than proportionate assignments due to misclassification of individuals (Pella and Milner 1987; Koljonen et al. 2005; Manel et al. 2005). Proportional assignment which assigns fractions of fish to stocks allows for direct estimation of stock proportions and evaluation of precision. Due to time constraints, she was unable to evaluate the Rao-Blackwell estimator above. Despite these concerns, we moved ahead with these analyses to determine if there were any improvements in correct allocations to the reporting groups within the CWAK area by using individual assignment methods.

METHODS

Anderson Approach

We used ONCOR, a Windows-based program available at http://www.montana.edu/kalinowski to implement the *leave-one-out* simulations using 9 (CWAK as a single reporting group) and 12 (CWAK divided into 4 reporting groups) reporting groups. This program handles only diploid markers, so we excluded the 2 MHC and 3 mtDNA loci from the analysis. The output from this analysis produces stock proportion point estimates for each population by reporting group for both the 9 and 12 reporting group analyses.

Koljonen Approach

The 15 test mixtures assembled and reported in Habicht et al. (2012), were re-analyzed in BAYES using the original methods, except that the toggle to export individual assignments at each iteration was turned on. Three independent Markov Chain Monte Carlo chains of 40,000 iterations each were completed with different starting values and information from first half of the iterations were discarded to remove influence of initial start values. We defined the starting values for the first chain such that the first third of the baseline populations summed to 0.9 and the remaining populations summed to 0.1. Each chain had a different third of baseline populations sum to 0.9. We assessed the within- and among-chain convergence of these estimates using the Raftery-Lewis and Gelman-Rubin diagnostics, respectively. If the Gelman-Rubin diagnostic for any stock group estimate was greater than 1.2 and the Raftery-Lewis diagnostic suggested each chain had not converged to stable estimates, we reanalyzed the mixture with 80,000-iteration chains following the same protocol. Iterations were thinned to 1 in 100. Output from these assignments was subjected to 2 estimation methods: 1) Rao-Blackwellization, and 2) the roll-up estimator. Point estimates from the Rao-Blackwellization were plotted onto the same plots as presented in Habicht et al. (2012) for visual comparison of performance. The maximum difference in stock composition between the Rao-Blackwellization results and the roll-up results for all 15 test mixtures for all reporting groups was calculated.

RESULTS

Anderson Approach

ONCOR point estimates by population plotted for each reporting group for both the 9 and 12 reporting group analyses are shown in Figures 1 and 2, respectively. Correct proportional allocation of populations in CWAK back to the CWAK reporting group (9-reporting group analysis) was much higher than correct proportional allocations of these populations to their respective subregional group (12- reporting group analysis).

Koljonen Approach

Gelman-Rubin diagnostic for all stock group estimates was less than 1.2 and the Raftery-Lewis diagnostic suggested each chain had converged to stable estimates. Point estimate proportions for each reporting group derived from Rao-Blackwellization for each hypothetical mixture were plotted onto the same plots as presented in Habicht et al. (2012) for visual comparison of performance are shown in Figures 3–9.

The maximum difference in stock composition between the Rao-Blackwell results and the roll-up results for all 15 test mixtures for all reporting groups was 0.0015. This difference was so small that it would be visually indiscernible from the Rao-Blackwell results if plotted in Figures 3-9.

DISCUSSION

Neither the Anderson nor the Koljonen approaches provided results that would indicate that the CWAK reporting group should be separated into 4 reporting groups for WASSIP mixture analyses. The Anderson approach resulted in lower assignment back to the correct reporting group than the original BAYES proportional assignment method. The Koljonen approach provided virtually identical results to the original BAYES proportional assignment method.

ANDERSON APPROACH

The Anderson et al. (2008) *leave-one-out* approach was expected to produce better performing proof tests than the BAYES proof tests originally used to define reporting groups. This improvement was anticipated to come from less depletion of the baseline due to the extraction of mixture individuals from the baseline used in the proof tests. The proof tests removed 400 fish from the baseline, whereas the *leave-one-out* approach removes only 1 fish from the baseline.

The results did not follow expectations for better performance. In the proof tests, all 9 reporting groups (CWAK as a single reporting group) exceeded 90% correct allocation (September presentation), whereas in the *leave-one-out* approach, many populations within reporting groups fell well below this 90% level (Figure 1). Although the overall level dropped for all reporting groups, the order of relative performance remained similar (i.e. Asia and East of Kodiak performed well, and South Peninsula performed least well in both analyses). In the 12 reporting group analysis (CWAK divided into 4 reporting groups), the 4 CWAK reporting groups had the lowest correct assignments (Figure 2).

There are a couple of possible reasons why the *leave-one-out* tests performed worse than the original BAYES proof tests: 1) no mixture information is used when assigning stock proportion to individuals, and 2) individuals with incomplete genotypes were excluded from the analysis. By definition, the *leave-one-out* approach cannot use information from the rest of the mixture to inform allocation of the individual (the mixture is made up of 1 fish). This information from other fish in the mixture may be particularly informative when the mixture is made up of individuals from a single reporting group, as is true in the proof tests. Only a small number of individuals with incomplete genotypes were excluded from the *leave-one-out* analysis, but included in the original analysis (<5%), so this effect was likely small.

KOLJONEN APPROACH

The Koljonen et al. (2005) roll-up method was anticipated to provide better estimates for the less distinguishable reporting groups (such as the 4 reporting groups within CWAK) based on previous work with Atlantic salmon. Those results were based on proof tests where the known mixture was made up of a single reporting group. One of the limitations to the roll-up method is that it does not provide any measure of variation (i.e. no standard deviation or error or no confidence or credibility intervals). This limitation may be why Koljonen et al. (2005) did not use the roll-up when estimating stock compositions from unknown mixtures, instead using the proportional assignment method. By using the Rao-Blackwell method on the individual assignments we were able to derive statistics that included both a point estimate and a credibility interval. However, since all 3 methods (individual assignment with the Rao-Blackwell, individual assignment with the roll-up, and proportional assignment) yielded almost identical point estimates, there is no reason to move to the individual assignment with Rao-Blackwell method. These results follow Michael Masuda's expectations that this method was unlikely to yield better estimates (see Introduction).

ACKNOWLEDGEMENTS

The Technical Document series served as a record of communication between the Alaska Department of Fish and Game Commercial Fisheries Division and the Western Alaska Salmon Stock Identification Program (WASSIP) Technical Committee during the implementation of the program. The authors would like to thank the WASSIP Technical Committee and Advisory Panel for their constructive input on each of the documents throughout the project. The authors would also like to thank Erica Chenoweth who coordinated and prepared the Technical Document series for publication and Publication Specialists Amy Carroll and Joanne MacClellan for implementing the series into Regional Information Reports.

REFERENCES CITED

Anderson, E. C., R. S. Waples and S. T. Kalinowski. 2008. An improved method for predicting the accuracy of genetic stock identification. Canadian Journal of Fisheries and Aquatic Sciences 65:1475–1486.

Beacham, T. D., J. R. Candy, C. Wallace, S. Urawa, S. Sato, N. V. Varnavskaya, K. D. Le and Michael Wetklo. 2009. Microsatellite stock identification of chum salmon on a Pacific Rim basis. North American Journal of Fisheries Management 29:1757–1776.

Debevec, E. M., R. B. Gates, M. Masuda, J. Pella, J. Reynolds, and L. W. Seeb. 2000. SPAM (Version 3.2): Statistics Program for Analyzing Mixtures. Journal of Heredity 91:509–510.

Habicht, C., W. D. Templin, N. DeCovich, and J. R. Jasper. 2012. Western Alaska Salmon Stock Identification Program Technical Document 15: Chum salmon reporting group evaluations using simulated fishery mixtures. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J12-22, Anchorage.

Jasper, J., S. Turner, and C. Habicht. 2012. Western Alaska Salmon Stock Identification Program Technical Document 13: Selection of a prior for mixed stock analysis. Alaska Department of Fish and Game, Regional Information Report 5J12-20, Anchorage.

Koljonen, M-L, J. J. Pella, and M. Masuda. 2005. Classical individual assignments versus mixture modeling to estimate stock proportions in Atlantic salmon (*Salmo salar*) catches from DNA microsatellite data. Canadian Journal of Fisheries and Aquatic Sciences 62:2143–2158.

Manel, S., O. E. Gaggiotti, and R. S. Waples. 2005. Assignment methods: matching biological questions with appropriate techniques. Trends in Ecology and Evolution, 20:136–142.

Neaves, P. I., C .G. Wallace, J. R. Candy, and T. D. Beacham. 2005. CBayes: Computer program for mixed stock analysis of allelic data. Version v5.01. Free program distributed by the authors over the internet from http://www.pac.dfo-mpo.gc.ca/sci/mgl/Cbayes_e.htm (Accessed October 12, 2012).

Pella, J. and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fishery Bulletin 99:151–167.

Pella, J. J. and G. B. Milner. 1987. Use of genetic marks in stock composition analysis. Pages 247–276 [*In*] F. Utter and N. Ryman, editors. Population genetics and fisheries management. University of Washington Press, Seattle, WA.

Robert C. P. and G. Casella. 2004. Monty Carlo Statistical Methods, 2nd Edition. Springer New York.

QUESTIONS FOR TECHNICAL COMMITTEE

1) Do these explorations provide confidence that the department should continue to analyze the WASSIP mixtures using the original methods (proportional assignment BAYES with an informative prior)?
2) Do these explorations support using CWAK as a single reporting group for WASSIP mixtures?

RESPONSES FROM TECHNICAL COMMITTEE

Excerpt of an email from Dr. Robin Waples to Bill Templin, with cc to AP and TC members dated 1/11/12, with affirmation by Dr. Bruce Weir

… You, Chris, and others have done a lot of work in a short time. I would have been surprised if these alternative methods had produced radically different results, but I am a bit surprised that there is essentially no improvement in resolution. Still, you have accomplished an important objective, which is demonstrating that the methods used in your analyses are truly state of the art. Although the existence of these other methods was noted during the course of this project, it was only in the last few months when the limitations to resolution for chum salmon in CWAK became evident that they seemed worth pursuing. Given the considerable disappointment by many in the resolution attainable with the current baseline and methods, it seemed important to evaluate any reasonable alternative that might produce a more useful result. You have now done that, so the Advisory Panel has a firmer foundation for making decisions about future options. The third analysis still might prove informative, but in any case it could not be implemented within the time frame for this project, so it is not as time sensitive. For the record, I would answer 'yes' to both the questions posed to the TC at the end of the document.

I am a bit curious about the results for the Anderson et al. method, but don't have time to work on that at the moment. The suggested explanation could be correct, but when I get time I will try to discuss this with Eric and see if he has any ideas. I would not, however, suggest holding up your project for those discussions.

FIGURES

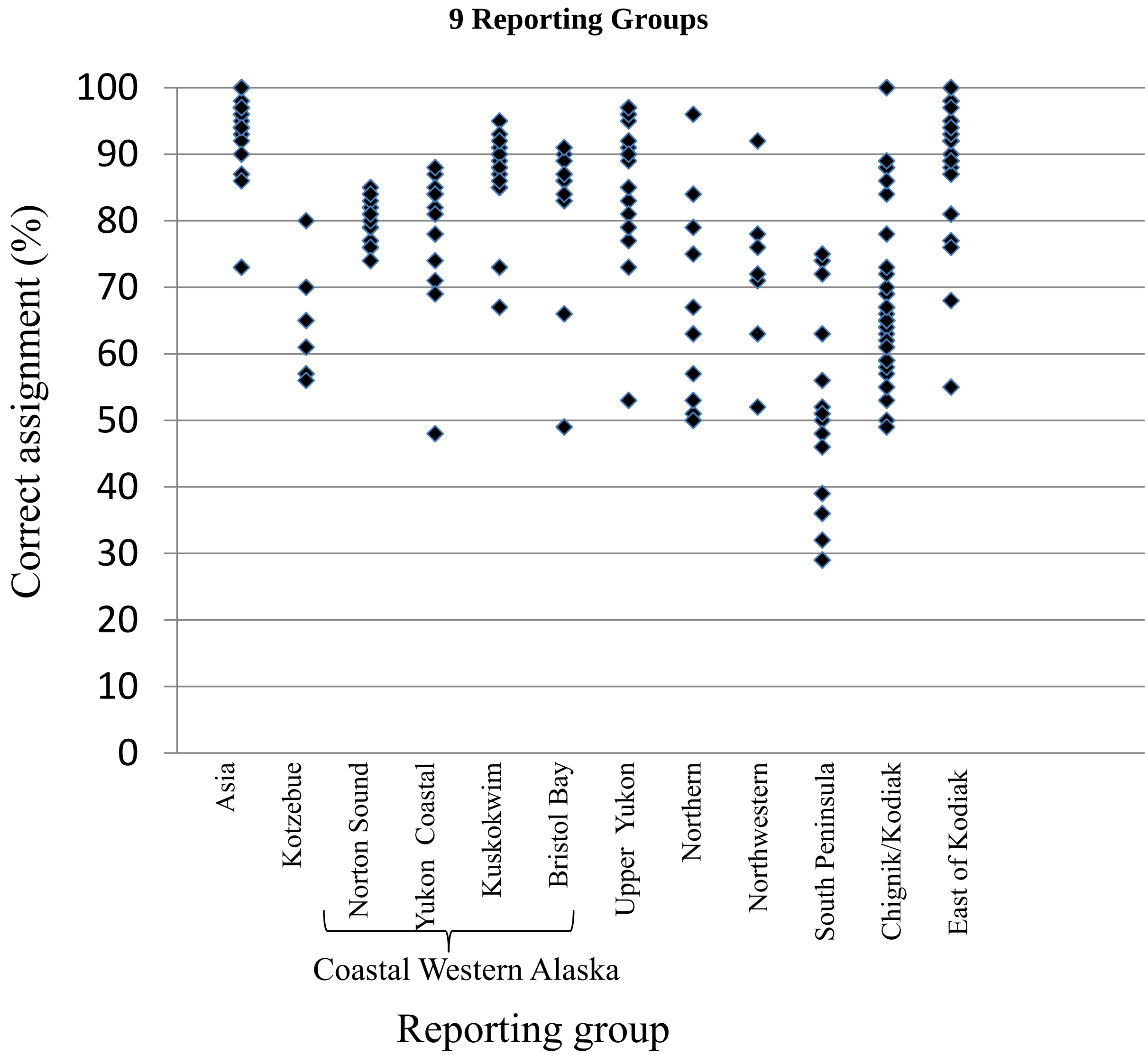

Figure 1.–Percent of correctly assigned individuals to 9 reporting groups using the *leave-one-out* method from Anderson et al. (2008). These 9 reporting groups include a single Coastal Western Alaska reporting group composed of Norton, Yukon Coastal, Kuskokwim, and Bristol Bay. Each diamond represents the average correct assignment for each population within each reporting group.

12 Reporting Groups

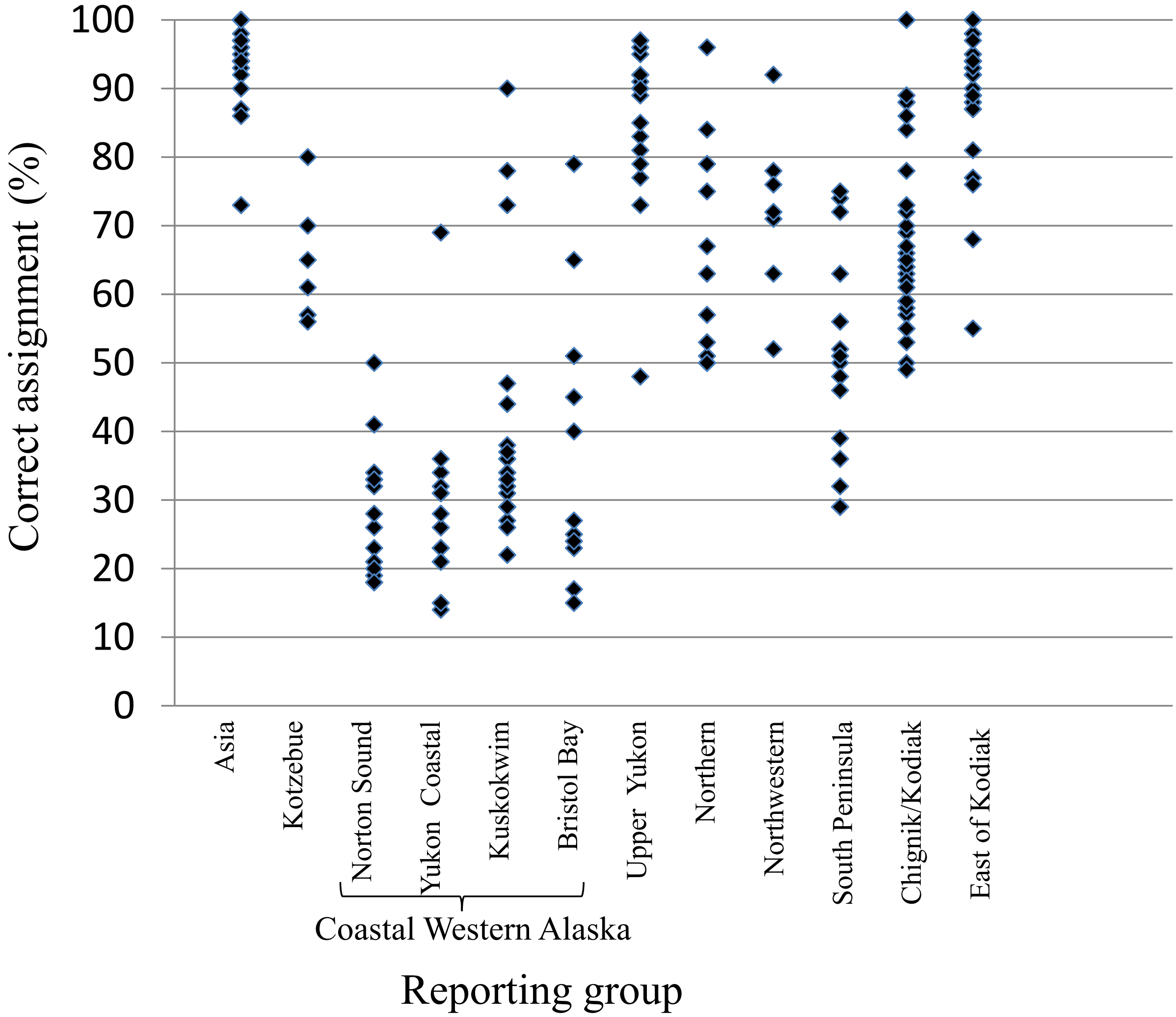

Figure 2.–Percent of correctly assignments of individuals to 12 reporting groups using the *leave-one-out* method from Anderson et al. (2008). These 12 reporting groups include the separation of Coastal Western Alaska into 4 reporting groups. Each diamond represents the average correct assignment for each population within each reporting group.

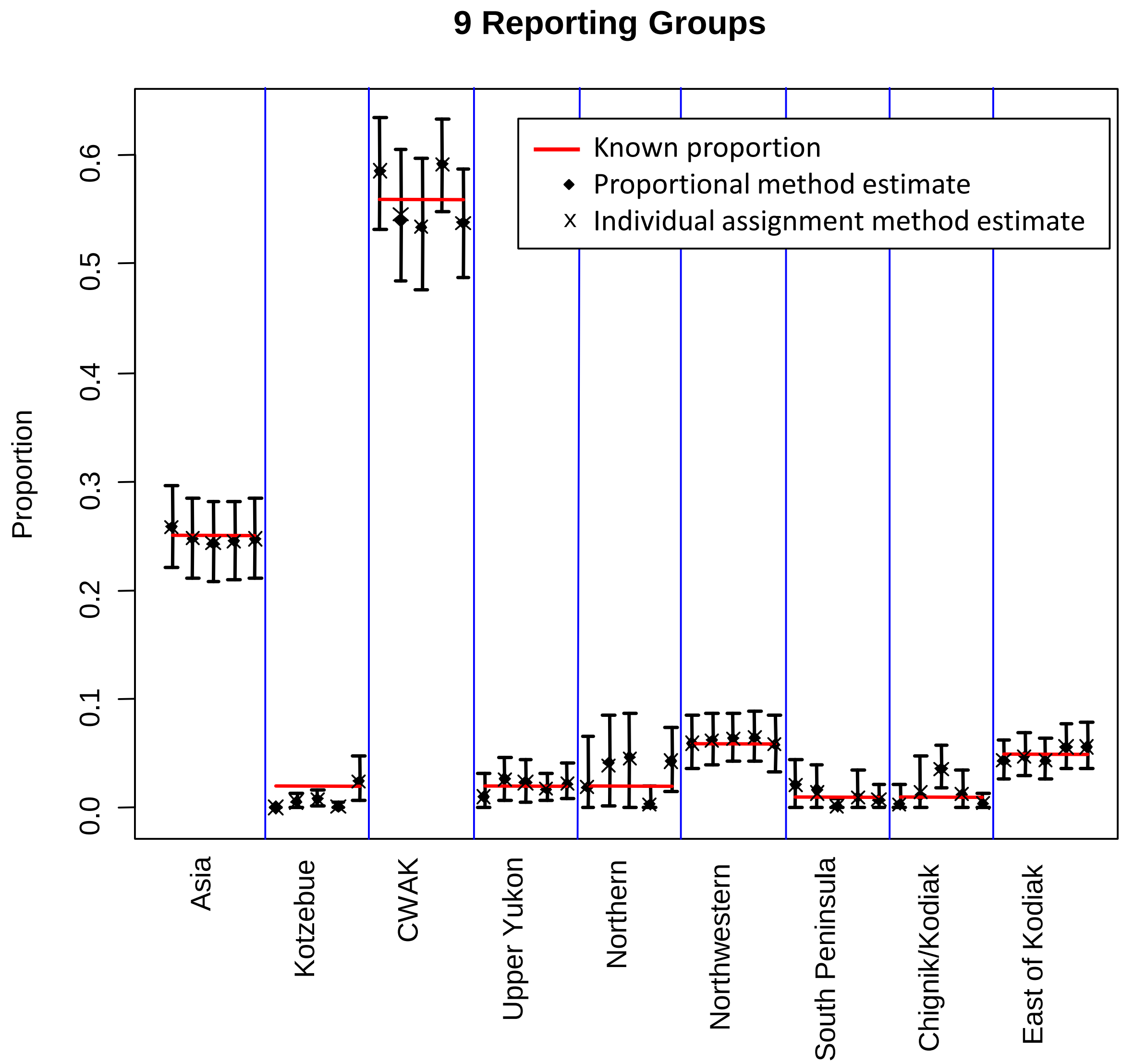

Figure 3.–BAYES estimates for 5 replicate samples for the fishery-based proof test *South Pen June (b) as run* (Habicht et al. 2012, Figure 3) for 9 reporting groups where Coastal Western Alaska (CWAK) is a single reporting group.

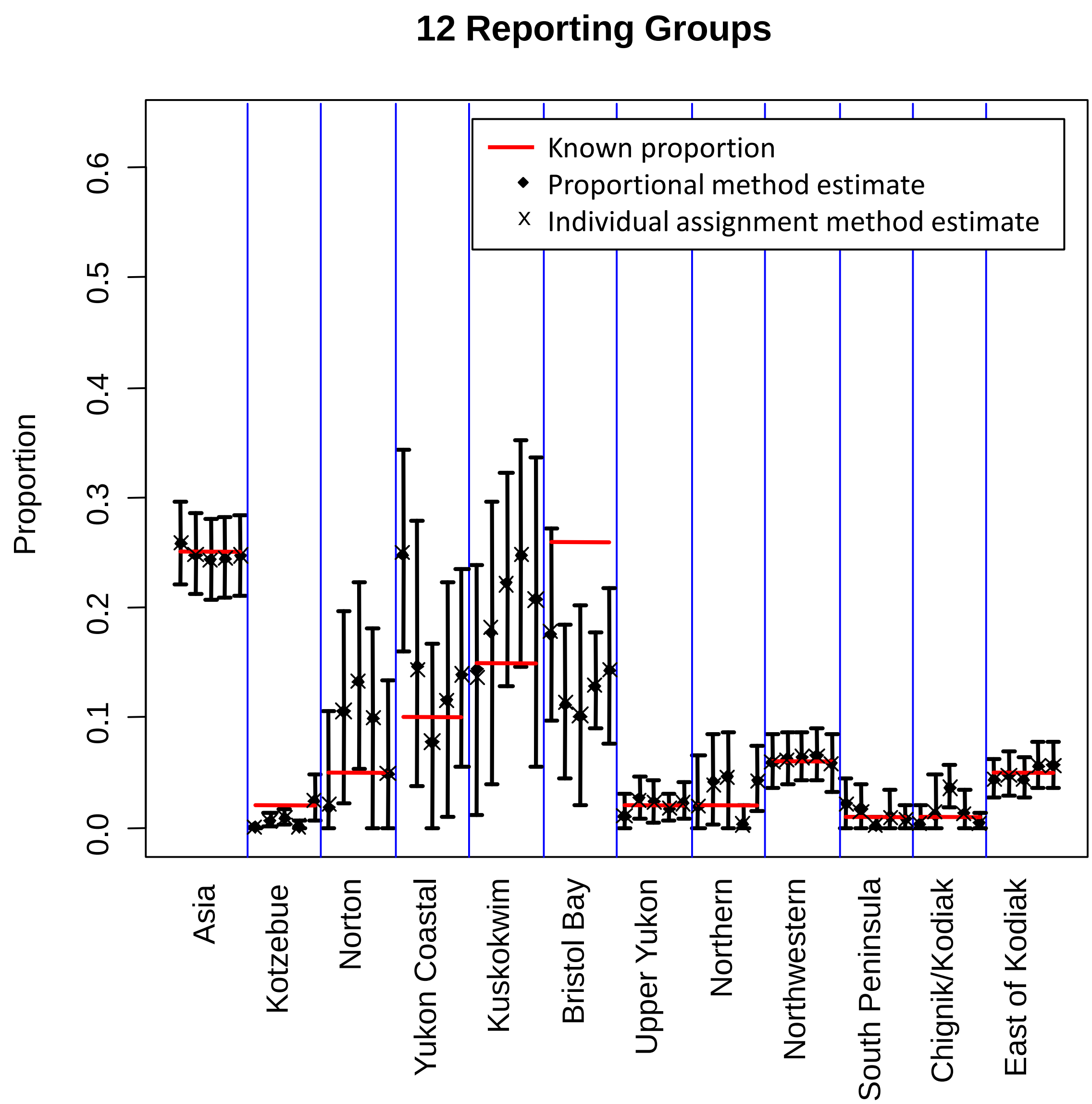

Figure 4.–BAYES estimates for 5 replicate samples for the fishery-based proof test *South Pen June (b) as run* (Habicht et al. 2012, Figure 4) for 12 reporting groups where Coastal Western Alaska (CWAK) is divided into 4 reporting groups

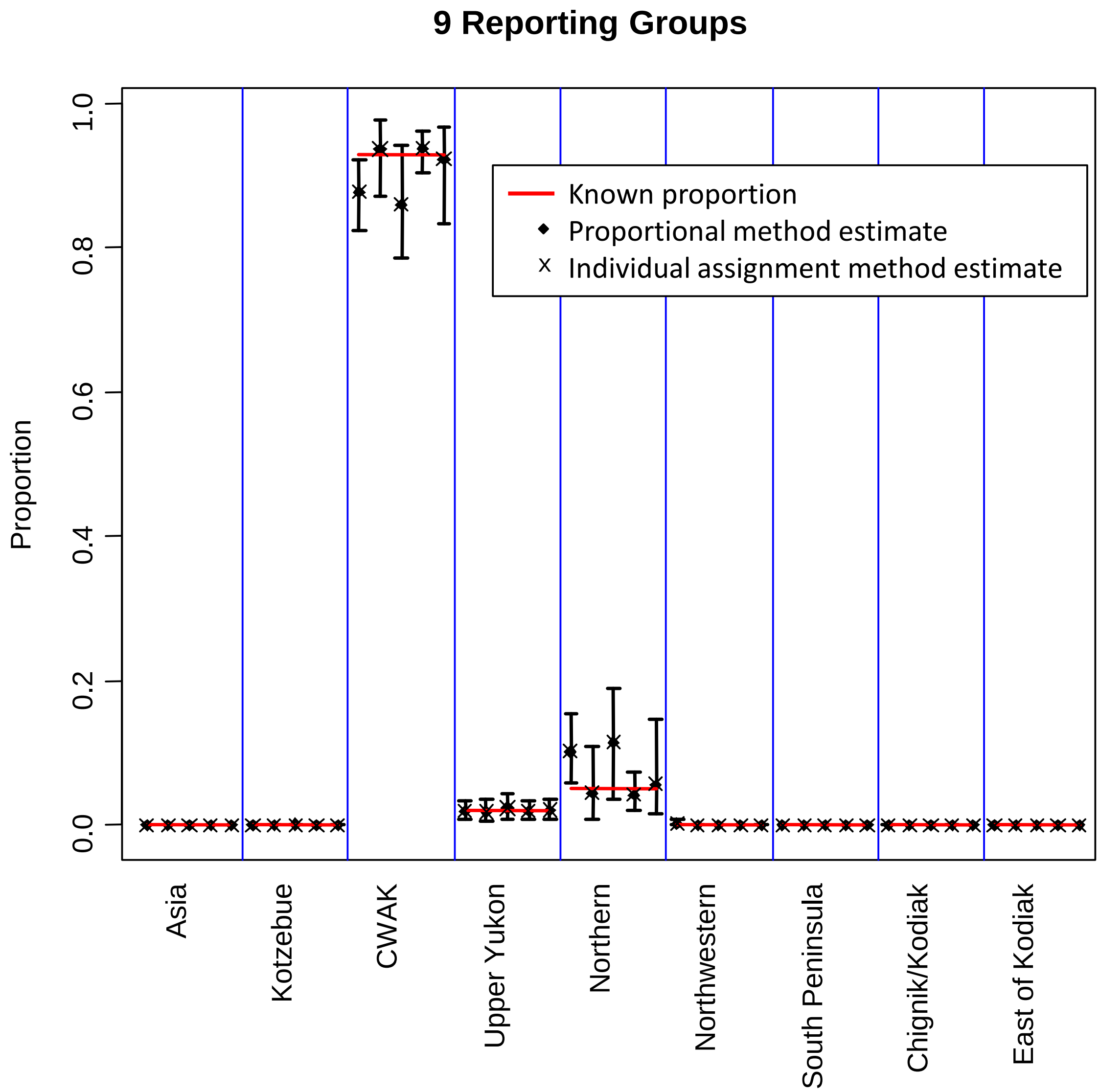

Figure 5.–BAYES estimates for 5 replicate samples for the fishery-based proof test *Bristol Bay* (Habicht et al. 2012, Figure 5) for 9 reporting groups where Coastal Western Alaska (CWAK) is a single reporting group.

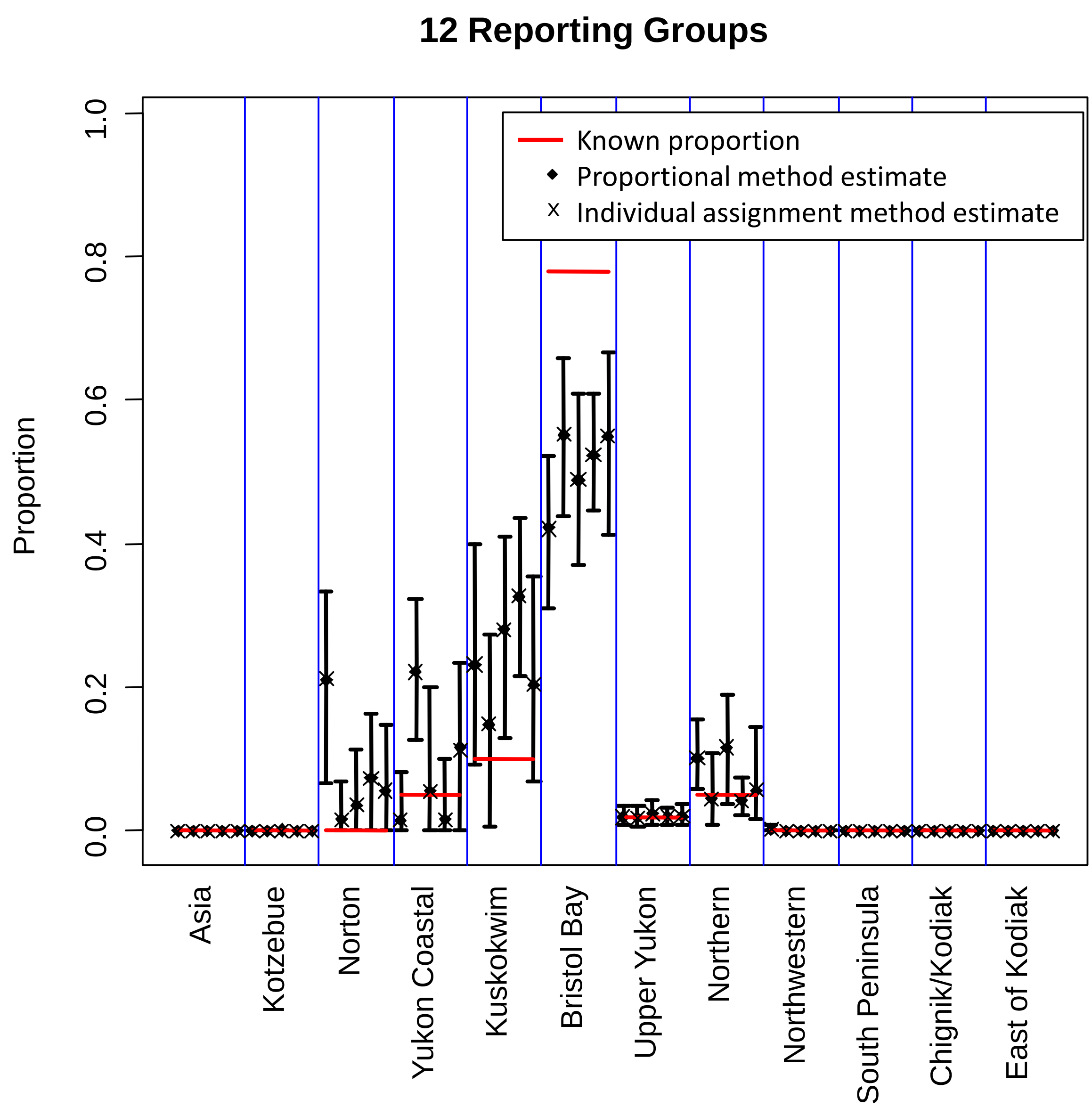

Figure 6.–BAYES estimates for 5 replicate samples for the fishery-based proof test *Bristol Bay* (Habicht et al. 2012, Figure 6) for 12 reporting groups where Coastal Western Alaska (CWAK) is divided into 4 reporting groups..

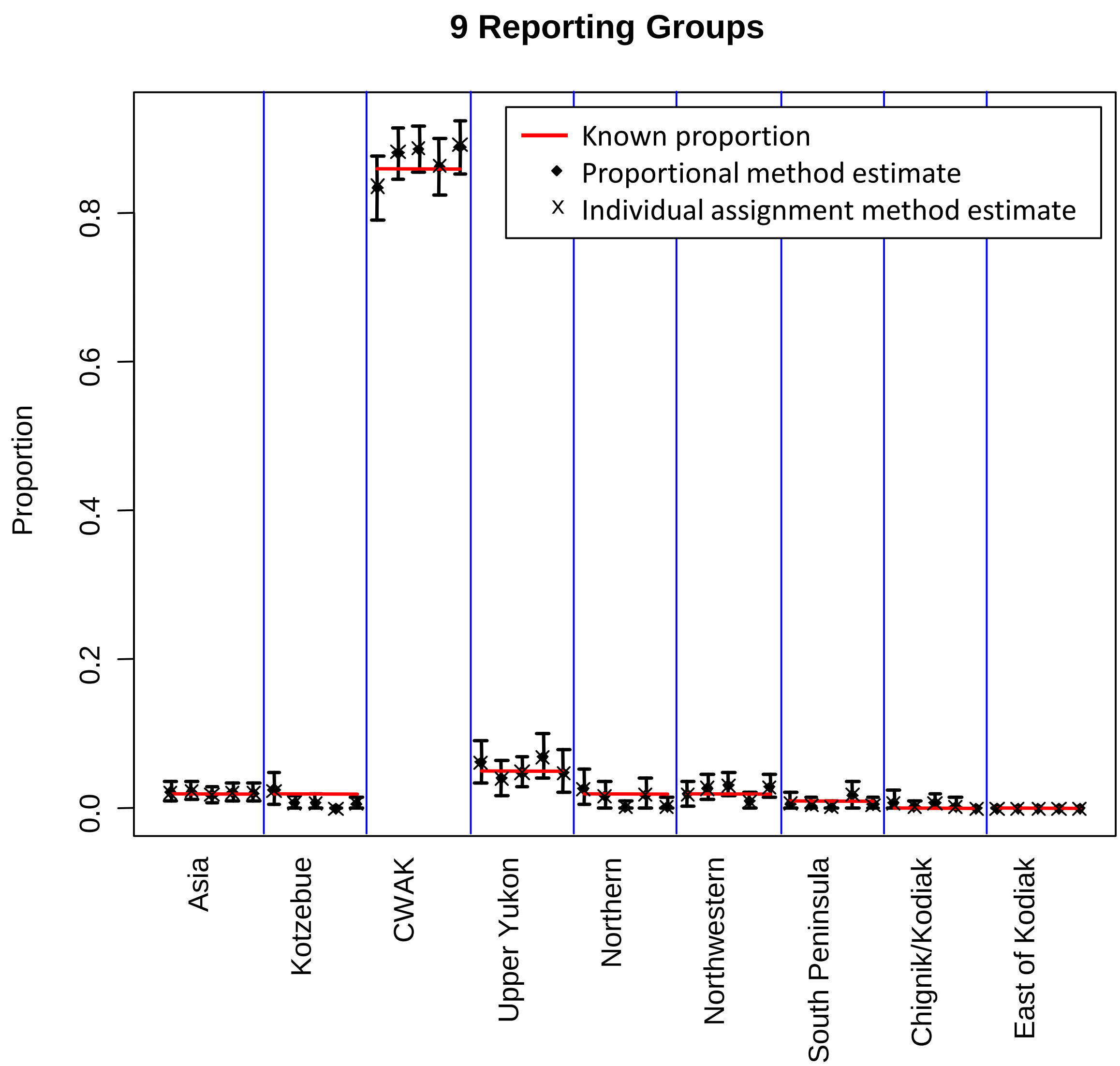

Figure 7.–BAYES estimates for 5 replicate samples for the fishery-based proof test *Kusko Bay* (Habicht et al. 2012, Figure 7) for 9 reporting groups where Coastal Western Alaska (CWAK) is a single reporting group..

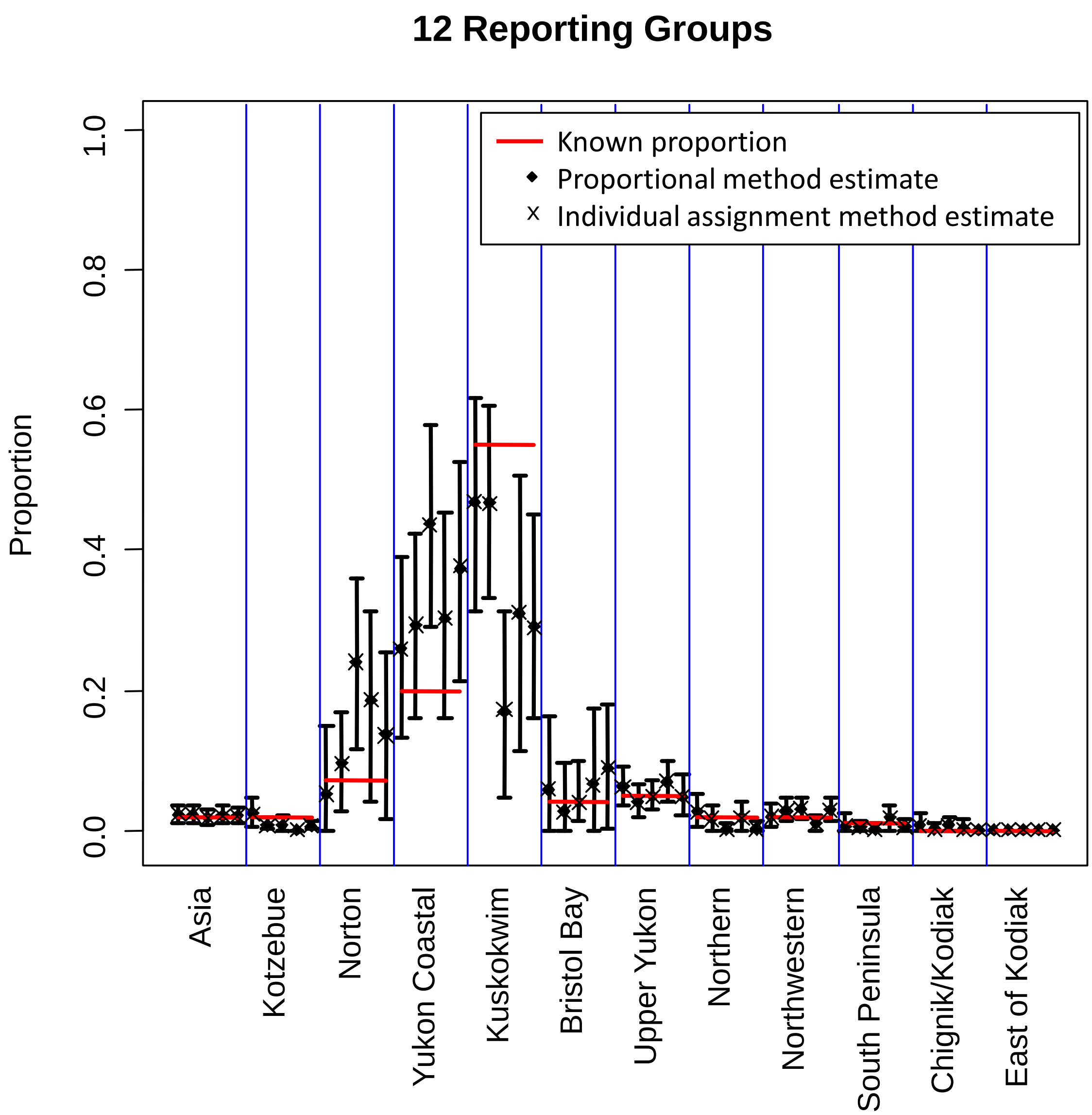

Figure 8.–BAYES estimates for 5 replicate samples for the fishery-based proof test *Kusko Bay* (Habicht et al. 2012, Figure 8) for 12 reporting groups where Coastal Western Alaska (CWAK) is divided into 4 reporting groups.