



**Abstract**—Collecting age-composition data is a critical aspect of stock assessment; however, there are no biological or statistical investigations that support optimization of the distribution of sample size across species. Sample sizes for both collection and age-reading are often set by using ad hoc or historical values. Investigations into quantifying the trade-offs when allocating sample sizes across species are needed because resources for age determination are always limited. In this study we performed analyses to investigate the distribution of sample sizes to determine ages across multiple species by using methods derived from sampling theory and simulation testing of stock assessment models. We found that, in terms of methods based on sampling theory, distribution of sample size under 2-stage sampling could be significantly related to the life-history characteristics of the species. Results from simulation analysis illustrated that the influence of sample sizes required to determine age composition of fish on uncertainty in stock assessment models was related to uncertainty in a survey index and recruitment variability of the species being assessed. The simulation analysis highlighted cases in which larger age-composition sample size did not appreciably decrease uncertainty in the stock assessment model, in particular, for species with lower recruitment variability and larger survey index uncertainty.

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## Investigations into the distribution of sample sizes for determining age composition of multiple species

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Age-composition data sets provide the fundamental information necessary for application of statistical catch-at-age assessment (SCAA) models used to estimate population dynamics and to manage commercial fisheries (Quinn and Deriso, 1999; Maunder and Punt, 2013). Age composition data allow the tracking of year classes through time, providing an improved understanding of population dynamics compared with that gained from analyzing fishery catch per unit of effort or survey biomass indices alone. Although theoretically the uncertainty in age composition can be reduced by increasing sample size, agencies have limited age-reading capacity (because of budgetary constraints on the number of hours age-reading scientists can spend reading ages from otoliths, as well as the number of age-reading scientists that a science center can employ.

A formal method for determining the most efficient distribution of sample size across species would be useful for the allotment of limited time, personnel, and funding; however, there is little to no existing guidance in the literature. The lack of scientific rigor used in choosing sample sizes for determining age composition at the NOAA Alaska Fisheries Science Center (AFSC) was noted in

the 2013 NOAA Office of Science and Technology program review (AFSC<sup>1</sup>) of data collection and management. The reviewers noted that in light of potentially shrinking budgets, the current level of age-reading capabilities at AFSC may not be sustainable. Even though this conclusion was specific to the AFSC review, this topic is applicable globally, whenever agencies are balancing age-reading priorities with other data collection or assessment priorities in their stock assessment programs.

If a method were to be adopted that based age-composition sampling across species on a statistical or biological basis, the distribution of sample size would be different from that of the current method, and some species would experience an increase in the samples sizes used to determine age composition of fish [hereafter “the age-composition sample size”], while others would result in a decrease. A resulting important issue when discussing these changes in sample sizes for determining age composition is the subsequent influence of increasing or decreasing sample size

<sup>1</sup> AFSC (Alaska Fisheries Science Center). 2013. Summary report: Alaska Fisheries Science Center science data collection review, 40 p. [Available from [website](#).]

on the uncertainty of estimates determined from SCAA models. This is, however, a different investigation than the application of sample size within an SCAA model, or, the idea of effective sample size. The topic of effective sample size and the use of age or length composition data within stock assessments has received extensive attention in recent years (Francis, 2011; Maunder, 2011). This study is also a different investigation from that of optimizing the number of hauls from which age-composition samples are obtained (Pennington et al., 2002; Hulson et al., 2011). While effective sample size is certainly related to the precision and accuracy that results from an SCAA model (Hulson et al., 2012) and determining the number of tows to sample is an important practical consideration (Pennington and Vølstad, 1994), here we are interested in *how* to distribute age-composition sample sizes across species before the data are input in a stock assessment model and after decisions have been made on the number of samples within a tow.

We followed a 2-step procedure to address the 2 topics presented in the preceding paragraphs: 1) how to distribute age-composition sample sizes across species on a statistical or biological basis, and 2) what is the effect on SCAA model uncertainty for species with different life histories by increasing or decreasing age-composition sample size. In the first step we used methods derived from sampling theory to determine the minimum sample sizes necessary to achieve certain sampling goals for multiple species (Quinn and Deriso, 1999). Using this statistical procedure, we then attempted to relate these sample sizes to life-history characteristics of the species investigated to explore whether there exists a biological basis for distribution of sample size across multiple species. In the second step we used simulation to isolate and evaluate the influence of sample sizes that determine age composition from fishery-independent sources on resulting uncertainty in estimates from SCAA models. The simulation analysis was applied to 3 species types with different life-history and survey characteristics to evaluate how age-composition sample size, in combination with survey index uncertainty, influenced SCAA model results and if this influence is disproportionate among different species type life histories. In addition to exploring these 2 topics the underlying goal of the research of this study is to provide preliminary guidance for prioritizing the distribution of sample size for age composition across multiple species, which has not been previously attempted or provided in fisheries research.

## Materials and method

### Step 1: distribution of sample sizes to determine age composition across multiple species

Age and length observations from fishery-independent bottom trawl surveys conducted by the AFSC in the

Gulf of Alaska (GOA), Aleutian Islands (AI), and Bering Sea (BS) were used to evaluate the distribution of sample sizes needed to determine age composition (henceforth, the term “age sample sizes”). These surveys provided an excellent opportunity to evaluate sample sizes for age composition because of the longevity of the surveys and the number of different species sampled for ages. Data (AFSC bottom trawl surveys, [website](#)) were used from trawl surveys conducted in the GOA from 1984 to 2011 (triennially from 1984 to 1999 then biennially from 2001 to 2011, e.g., Raring et al., 2011), in the AI from 1980 to 2010 (triennially from 1980 to 1986 and from 1991 to 1997, then biennially from 2000 to 2006 and 2010 on, e.g., von Szalay et al., 2011), and in the BS from 1982 to 2011 (annually; e.g., Lauth and Conner, 2014). In the interest of brevity we refer to von Szalay et al. (2011) for a detailed description of how the survey index and age-length compositions are estimated from the surveys. Our interest was the distribution of age-composition sample sizes across species before indices are estimated; therefore the details concerning the indices are not provided here.

Species included were those for which the number of aged otoliths were greater than 3000 across the time series of the trawl surveys. Within a given haul, the majority of species are sampled for ages with 2-stage sampling: 1) with a fixed allocation method, and 2) the remainder of species sampled with simple random sampling (SRS). Species were categorized into 3 types that included ‘flatfish,’ ‘rockfish,’ and ‘roundfish’ (Table 1). Including rougheye (*Sebastes aleutianus*) and blackspotted (*Sebastes melanostictus*) rockfish, which are assessed as a complex and considered a ‘single species’ in the context of this study (Spencer and Rooper<sup>2</sup>; Shotwell et al.<sup>3</sup>), there were 15 species and 23 stocks investigated across all areas, including 10 flatfish, 7 rockfish, and 6 roundfish stocks. Otoliths that were read by both a ‘reader’ and a ‘tester’ were also collected for each of these species to evaluate the influence of aging error on estimates of age-composition sample size.

We estimated sample sizes for age composition following the method for 2-stage sampling outlined in Quinn and Deriso (1999, chapter 8). In the first stage of sampling a subsample of fish from the total catch is taken to obtain lengths (either total or fork length depending on the species) and in the second stage of sampling a subset of these fish are then sampled for age determination within each predetermined length bin. There are several methods proposed to obtain the

<sup>2</sup> Spencer, P. D., and C. N. Rooper. 2014. Assessment of the blackspotted and rougheye rockfish stock complex in the Bering Sea/Aleutian Islands. *In* Stock assessment and fishery evaluation report for the groundfish resources of the Bering Sea/Aleutian Islands regions. North Pacific Management Council, Anchorage, AK. [Available from [website](#).]

<sup>3</sup> Shotwell, S. K., D. H. Hanselman, J. Heifetz, and P.-J. F. Hulson. 2015. Assessment of the rougheye and blackspotted rockfish stock complex in the Gulf of Alaska. *In* Stock Assessment and fishery evaluation report for the groundfish resources of the Gulf of Alaska. North Pacific Management Council, Anchorage, AK. [Available from [website](#).]

Table 1

Total mean length and age-composition sample sizes per survey and total number of ages sampled combined across years from the NOAA Alaska Fisheries Science Center bottom trawl surveys for the Gulf of Alaska (GOA, 1984–2011), Aleutian Islands (AI, 1980–2010), and Bering Sea (BS, 1982–2011) for the species investigated for this study. The “/” used between Rougheye and blackspotted rockfish denotes that these species are assessed as a complex rather than individual species.

Species: common name (scientific name, acronym)	Region	Mean sample size for length	Mean sample size M for ages	Total sample size for ages
<b>Flatfish</b>				
Alaska plaice ( <i>Pleuronectes quadrituberculatus</i> , AP)	BS	11,934	347	5800
Flathead sole ( <i>Hippoglossoides elassodon</i> , FS)	BS	17,354	458	7997
Northern rock sole ( <i>Lepidopsetta polyxystra</i> , NRS)	BS	34,045	441	6751
Yellowfin sole ( <i>Limanda aspera</i> , YS)	BS	32,025	707	20,539
Arrowtooth flounder ( <i>Atheresthes stomias</i> , AF)	GOA	61,142	924	9244
Dover sole ( <i>Microstomus pacificus</i> , DS)	GOA	7064	404	4642
Flathead sole ( <i>H. elassodon</i> , FS)	GOA	21,364	572	5723
Northern rock sole ( <i>Lepidopsetta polyxystra</i> , NRS)	GOA	8337	434	3474
Rex sole ( <i>Glyptocephalus zachirus</i> , RS)	GOA	15,687	423	4563
Rock sole ( <i>L. bilineata</i> , SRS)	GOA	10,136	455	3638
<b>Rockfish</b>				
Northern rockfish ( <i>Sebastes polyspinis</i> , NR)	AI	7405	483	4990
Pacific ocean perch ( <i>S. alutus</i> , POP)	AI	19,878	1068	10,876
Rougheye/blackspotted rockfish ( <i>S. aleutianus/melanostictus</i> , RB)	AI	1701	428	3611
Light dusky rockfish ( <i>S. variabilis</i> , LDR)	GOA	1883	385	4191
Northern rockfish ( <i>S. polyspinis</i> , NR)	GOA	4195	413	4521
Pacific ocean perch ( <i>S. alutus</i> , POP)	GOA	19,658	1119	11,511
Rougheye/blackspotted rockfish ( <i>S. aleutianus/melanostictus</i> , RB)	GOA	3950	516	5279
<b>Roundfish</b>				
Atka mackerel ( <i>Pleurogrammus monopterygius</i> , AM)	AI	9187	598	6068
Walleye pollock ( <i>Gadus chalcogrammus</i> , WP)	AI	16,087	1280	12,498
Pacific cod ( <i>Gadus macrocephalus</i> , PC)	BS	12,241	883	21,731
Walleye pollock ( <i>G. chalcogrammus</i> , WP)	BS	106,317	1455	42,078
Pacific cod ( <i>G. macrocephalus</i> , PC)	GOA	12,138	607	6676
Walleye pollock ( <i>G.s chalcogrammus</i> , WP)	GOA	31,387	1428	17,139

second stage sample and 2 are investigated here: proportional allocation (selecting samples proportional to the length distribution) and fixed allocation (a fixed number of samples from each length class). The method outlined in Quinn and Deriso (1999) allows estimation of minimum sample sizes necessary to achieve a target level of precision (on the basis of a specified coefficient of variation [CV] for all ages in the age composition data. The primary components used to estimate sample size is the estimated proportion-at-age ( $\hat{\theta}_a$ ), the within-length interval variance component of the estimated proportion-at-age ( $F_a$  for fixed allocation,  $V_a$  for proportional allocation) and the between-length interval variance component of the estimated proportion-at-age ( $B_a$ ). In simple terms, one can think of within-length interval variance as the variability of ages within a given length bin (or, the number of ages represented for a given length) and between-length interval variance as the variability in length bins within a given age (or, the number of lengths represented for a given age). From Quinn and Deriso (1999) an unbiased estimator under 2-stage random sampling is represented by the following equation:

$$\hat{\theta}_{a,y} = \sum_{l=1,\dots,J} \hat{\alpha}_{1,y} \hat{\theta}_{1,a,y}, \quad (1)$$

where  $\hat{\alpha}_{1,y}$  = the observed proportion of fish at length  $l$  in year  $y$  (the number of observations at length  $l$  divided by the total number of length observations); and

$\hat{\theta}_{1,a,y}$  = the observed proportion of fish of length  $l$  and age  $a$  in year  $y$  (the number of age observations at length  $l$  and age  $a$  divided by the number of age observations at length  $l$ ).

The within-length interval variance for fixed allocation sampling ( $F_{a,y}$ ) is defined as

$$F_{a,y} = J \sum_{l=1,\dots,J} \hat{\alpha}_{1,y}^2 \hat{\theta}_{1,a,y} (1 - \hat{\theta}_{1,a,y}), \quad (2)$$

where  $J$  = the total number of length intervals; and  $\hat{\alpha}_{1,y}$  and  $\hat{\theta}_{1,a,y}$  are as defined above.

For proportional allocation, the within-length interval variance ( $V_{a,y}$ ) is defined by Quinn and Deriso (1999) as:

$$V_{a,y} = \sum_{l=1,\dots,J} \hat{\alpha}_{1,y} \hat{\theta}_{1,a,y} (1 - \hat{\theta}_{1,a,y}). \quad (3)$$

Finally, the between-length interval variance ( $B_{a,y}$ ) is given as

$$B_{a,y} = \sum_{l=1,\dots,J} \hat{\alpha}_{l,y} (\hat{\theta}_{l,a,y} - \hat{\theta}_{a,y})^2. \quad (4)$$

For fixed allocation, the formula to estimate the age-composition sample size in year  $y$  ( $A_y$ ) is given by

$$A_y = \frac{F_{a,y}}{\hat{\theta}_{a,y}^2 CV^2 - B_{a,y} / L_y} + J, \quad (5)$$

where  $F_{a,y}$  = the within-length interval variance (Eq. 2);

$\hat{\theta}_{a,y}$  = the proportion of fish at age  $a$  (Eq. 1);

$CV$  refers to the target CV in the age composition;

$B_{a,y}$  = the between-length interval variance (Eq. 4);

$L_y$  = the number of length observations in year  $y$ ;  
and

$J$  = the number of length intervals.

Age-composition sample size at some level of precision given proportional allocation was estimated with

$$A_y = \frac{V_{a,y}}{\hat{\theta}_{a,y}^2 CV^2 - B_{a,y} / L_y}, \quad (6)$$

where  $V_{a,y}$  = the within-length interval variance (Eq. 3) and the other terms are the same as in Equation 5.

For consistency across species, the length classes were set at 1-cm bins and were not grouped.

We also estimated the sample size necessary to obtain some target CV under SRS. Under SRS, the age-composition sample size at some level of precision was estimated with

$$A_y = \frac{(1 - \hat{\theta}_{a,y})}{\hat{\theta}_{a,y} CV^2}, \quad (7)$$

which is derived from the variance of a multinomial distribution.

Four sampling goals to achieve some target level of precision in age composition were investigated that represented 2 general categories based on 1) a single age class, or 2) a group of age classes that were related to the total number of ages in the population. The overall point of each of these sampling goals was to investigate standardized sampling goals across species that achieved the same level of uncertainty in the age-composition data. The first sampling goal was to achieve the target CV for the most frequently caught age (i.e., the age class with the largest annual proportion-at-age). The second sampling goal was to achieve the target CV for the age class with the maximum within-length interval variance (i.e., the age class with the least information on age from the length data). The third sampling goal was to achieve the target CV for the top 25% of age classes caught (i.e., proportionally the same number of age classes across species). Finally, the fourth sampling goal was to achieve the target CV for age classes with proportions-at-age that were on average (across time) greater than the inverse of half of the maximum age (i.e., greater than some proportion that is related to the longevity of the species in-

vestigated). As an example of this final sampling goal, for a maximum age of 84 years for Pacific ocean perch (*Sebastes alutus*), we would try to achieve a CV for all ages with proportions that were on average greater than 1/42 or 2.4%. It should be noted that it is often difficult to set a sampling goal without prior sampling having been completed.

The CVs ranging from 10 to 25% were initially evaluated (by 5% intervals) to estimate age-composition sample sizes under fixed and proportional allocation across the species investigated. We investigated estimated sample sizes with the same age-composition CV across species to form a basis for comparison. The trends and patterns in distribution of sample size across species, which was our focus, were extremely similar across the different CVs and we present only the results of a target CV of 15%. The overall estimated sample sizes and proportions of the total sample size presented for each species were the median across the years of the bottom trawl surveys needed to obtain the target CV in the age composition. To show the distribution of sample size across species we calculated the species-specific proportion of the total sample size within each sampling goal (dividing the species-specific estimated sample size for some sampling goal by the sum of the estimated sample sizes across species for that sampling goal).

We also investigated the use of species-specific aging error in the estimation of sample sizes. Reader-tester agreement data was compiled for all the species and stocks investigated from the AFSC Age and Growth Laboratory. Two aging error cases were investigated: the first was when aging error was not incorporated, the second was when aging error was incorporated. The amount of aging error (i.e., the age-reading error standard deviation [SD] by age) was investigated for each species and stock according to the methods of Richards et al. (1992) and Hiefert et al. (1998). In order to construct and implement a generalized aging error method for all species and stocks, a constant CV was used across ages for each species and stock. Aging error was implemented into the estimates of sample size by multiplying the species-specific aging error matrix by the observed proportion of fish of length  $l$  and age  $a$  in year  $y$  ( $\hat{\theta}_{l,a,y}$ ).

We evaluated the relationships between the distribution of age-composition sample size across species and life-history characteristics of species by comparing the proportion of total sample size estimates with 4 statistics. The 4 statistics were focused on instantaneous growth rates (i.e., the slope of the tangent of the growth curve at some age), calculated as the derivative of the von Bertalanffy growth curve (von Bertalanffy, 1938). The life-history statistics investigated included the natural log of 1) the instantaneous growth rate at 20% of the maximum age observed; 2) the instantaneous growth rate of the age at 50% of the asymptotic length ( $L_\infty$ ); 3) the mean population instantaneous growth rate (the instantaneous growth rate at age weighted by the observed proportions at age); and 4)

the minimum lifetime growth rate (simply calculated as  $L_\infty$  divided by the maximum age observed). Growth for each species was estimated by using the von Bertalanffy growth curve fitted to the mean age and length observations by using AD Model Builder (Fournier et al., 2012). Estimates of the von Bertalanffy growth curve parameters for each of the species investigated when aging error is not included and when it is included (along with the maximum age observed in the bottom trawl surveys) are provided in [Supplementary Table 1](#). Relationships between the distribution of age sample size and other life-history characteristics were also investigated (including the von Bertalanffy estimated growth coefficient,  $\kappa$ ), but for brevity we show these 4 statistics because they resulted in the strongest relationship with the distribution of age-composition sample sizes.

## Step 2: sample size for determining age composition and SCAA model uncertainty

A simulation approach was used to evaluate the influence of the magnitude of fishery-independent survey uncertainty (including both age composition and biomass) on resulting SCAA model uncertainty across species types. Operating models for the species types were constructed with simplified versions of the stock assessments for 3 species: GOA arrowtooth flounder (*Atheresthes stomias* [Turnock and Wilderbuer<sup>4</sup>]) as an example for the flatfish species type, Pacific ocean perch ([Hanselman et al.<sup>5</sup>]) as an example for the rockfish species type, and walleye pollock (*Gadus chalcogrammus* [Dorn et al.<sup>6</sup>]) as an example for the roundfish species type.

The operating models for the 3 species types were constructed by fitting standard SCAA models to similar data sources for each example species. Catch-at-age in year  $y$  ( $C_{a,y}$ ) was modeled with the Baranov (1918) catch equation and numbers-at-age in year  $y$  ( $N_{a,y}$ ) were estimated by following the theory of survival presented by Ricker (1975), which are given by

$$C_{a,y} = N_{a,y} \frac{F_{a,y}}{Z_{a,y}} (1 - e^{-Z_{a,y}}) \text{ and} \quad (8)$$

$$N_{a+1,y+1} = N_{a,y} e^{-Z_{a,y}}, \quad (9)$$

where  $Z_{a,y}$  = the instantaneous total mortality, composed of natural mortality,  $M_{a,y}$ , and fishing mortality,  $F_{a,y}$ .

Fishing mortality was modeled as year-specific and age-specific factors (Doubleday, 1976),

$$F_{a,y} = s_a f_y, \quad (10)$$

where  $s_a$  = age-specific selectivity (asymptotic); and  $f_y$  = the annual fishing mortality rate for fully selected fish.

Data that were fitted in the objective function to construct the operating models included total catch biomass (lognormal), commercial fishery age and length compositions (multinomial, effective sample size set at the square root of sample size), bottom trawl survey biomass (lognormal), and bottom trawl survey age composition (multinomial, effective sample size set at square root of sample sizes). The primary differences between the actual stock assessment models and the simplified SCAA models used here included combined-sex rather than sex-specific models, time-invariant survey catchability and selectivity, time-invariant fishing selectivity, and effective sample sizes used. The point of constructing the operating models was not to replicate the exact results of each assessment but to obtain reasonable parameter estimates indicative of the 3 species type life histories. Parameter estimates from the final 30 years of the time series of the operating models for each species type were treated as ‘true’ values from which process error in recruitment and observation error in survey age compositions and biomass were generated. The parameter estimates used in the operating models for each of the 3 species types investigated are provided in [Supplementary Table 2](#). The same time scale and amount of data (annually) were used for each species type so that resulting uncertainty in the estimation models was not sensitive to the length or quantity of the data time series.

Process error in recruitment was generated from the operating models with the lognormal distribution. Recruitment deviation parameters were generated independently following the estimation method used in the stock assessment SCAA models (as opposed to using autocorrelation or a stock-recruitment model). The mean recruitment on the log-scale was 6.3 (SD 0.32) for arrowtooth flounder, which was comparable to the 2011 assessment values with a log-scale mean of 6.3 (SD 0.29) from 1980 to 2011 (Turnock and Wilderbuer<sup>4</sup>). For Pacific ocean perch the log-scale mean recruitment used was 3.9 (SD 0.45), which was similar to the 2011 assessment mean from 1980 to 2011 of 3.9 (SD 0.49) (Hanselman et al.<sup>5</sup>). The log-scale mean recruitment was 6.23 (SD 0.70) for walleye pollock, the mean was slightly larger than the assessment mean of 6.0, and the SD was smaller from the assessment value of 0.92 from 1980 to 2011 (Dorn et al.<sup>6</sup>).

For each process error replicate of recruitment, observation error was then generated in age composition

<sup>4</sup> Turnock, B. J., and T. K. Wilderbuer. 2011. Assessment of the arrowtooth flounder stock in the Gulf of Alaska. In Stock assessment and fishery evaluation report for the groundfish resources of the Gulf of Alaska. North Pacific Management Council, Anchorage, AK. [Available from [website](#).]

<sup>5</sup> Hanselman, D., S. K. Shotwell, P. J. F. Hulson, J. Heifetz, and J. N. Ianelli. 2011. Assessment of the Pacific ocean perch stock in the Gulf of Alaska. In Stock assessment and fishery evaluation report for the groundfish resources of the Gulf of Alaska. North Pacific Management Council, Anchorage, AK. [Available from [website](#).]

<sup>6</sup> Dorn, M., K. Aydin, S. Barbeaux, M. Guttormsen, K. Spalinger, and W. Palsson. 2011. Assessment of the walleye pollock stock in the Gulf of Alaska. In Stock assessment and fishery evaluation report for the groundfish resources of the Gulf of Alaska, p. 51–146. North Pacific Management Council, Anchorage, AK. [Available from [website](#).]

**Table 2**

Minimum and maximum estimated age sample sizes across sampling goals under simple random sampling (SRS), proportional allocation (PA), and fixed allocation (FA) from the NOAA Alaska Fisheries Science Center bottom trawl surveys for the Gulf of Alaska (GOA, 1984–2011), Aleutian Islands (AI, 1980–2010), and Bering Sea (BS, 1982–2011). Estimated sample sizes without aging error are shown on the left of the “|” symbol and sample sizes including aging error are shown on the right (species acronyms are provided in Table 1). The top row for each species type contains the average of the minimum and maximum. Species acronyms are explained in Table 1.

Species	Region	SRS	PA	FA
<b>Flatfish</b>				
Avg.	Min–Max	269–730   301–737	205–659   244–706	447–1354   523–1374
AP	BS	286–687   300–716	224–666   259–676	530–1330   616–1298
FS	BS	278–640   318–604	197–565   236–574	356–1079   389–1066
NRS	BS	192–570   208–727	136–380   152–406	370–882   446–890
YS	BS	232–662   249–676	150–614   178–630	314–1358   338–1365
AF	GOA	240–458   254–615	151–410   190–548	369–836   445–941
DS	GOA	460–1686   560–1515	377–1614   492–1785	646–3058   820–3124
FS	GOA	268–616   297–594	222–556   258–570	600–1416   718–1432
NRS	GOA	210–579   226–564	174–526   188–530	400–1028   430–1025
RS	GOA	217–888   257–852	187–801   224–843	478–1699   576–1700
SRS	GOA	310–516   342–504	236–462   265–498	410–853   447–898
<b>Rockfish</b>				
Avg.	Min–Max	406–1823   516–2967	348–1977   467–3002	805–4805   1072–6494
NR	AI	360–1433   427–1533	335–1400   402–1516	566–3082   1024–3386
POP	AI	319–2000   416–6319	261–2702   366–6218	650–4882   782–12224
RB	AI	678–2522   989–2523	661–2822   980–2662	1928–8584   2871–7710
LDR	GOA	258–1030   290–1172	210–1044   206–1146	524–2726   516–3040
NR	GOA	406–1423   464–1456	342–1371   421–1433	660–4139   860–3918
POP	GOA	346–1670   370–5015	231–1718   249–5300	473–3886   338–9380
RB	GOA	477–2684   655–2751	396–2781   642–2740	837–6333   1116–5801
<b>Roundfish</b>				
Avg.	Min–Max	126–350   133–329	55–255   62–256	147–509   200–576
AM	AI	110–174   112–180	72–150   75–155	155–342   178–379
WP	AI	170–499   191–427	110–446   135–374	238–849   334–876
PC	BS	109–262   117–254	20–137   40–188	134–299   187–389
WP	BS	108–490   109–510	50–404   8–412	92–827   105–942
PC	GOA	138–294   143–242	69–133   105–157	191–323   318–427
WP	GOA	118–383   125–359	6–260   8–250	70–413   75–440

and biomass from survey data. Observation error in survey age-composition data from the operating model was generated with the multinomial distribution. To evaluate the influence of age-composition sample size in a fishery-independent survey on SCAA model results, 13 sample sizes were used to generate trawl survey age composition data that ranged from 10 to 100,000 (by multiples of 2.5 and 2, e.g., 10, 25, 50, 100, 250, 500...).

The influence of survey biomass uncertainty was evaluated concurrent with age composition uncertainty with 4 index uncertainty cases. These cases focused on the CV used to generate observation error in the log-normal survey biomass time series. Index case E0 generated log-normal survey biomass data with a CV set at the average obtained by the AFSC bottom trawl survey in the GOA (CV≈9% for arrowtooth flounder, 25% for Pacific ocean perch, and 18% for walleye pollock). Index case E1 multiplied the CV in case E0 by 2. Index

case E2 set the CV at 10% for all species types, and E3 set the CV at 25% for all species types. Although some of the index cases may not occur in reality (for example, setting the CVs equal across species), our goal was to investigate the relationship with survey index CV as well as age composition based on survey data and a range of values is needed. Unlike the actual AFSC bottom trawl survey time series in the GOA (which is triennial from 1984 to 1999 and biannual from 1999 to 2011) this simulation analysis generated annual trawl survey biomass and age-composition data, so that variability in model estimation results was not sensitive to gaps in the time series based on data from the trawl surveys.

In the estimation models, the same number of parameters was estimated for each species type so that resulting uncertainty was more directly comparable and was not sensitive to parameter differences. Estima-

tion models had 35 parameters that included log-scale mean recruitment (1), recruitment deviations (30), natural mortality (1), survey catchability (1), and logistic parameters for survey selectivity (2). The models fitted age-composition data from the trawl survey with the multinomial distribution and biomass data from the trawl survey with the log-normal distribution. The sample sizes and CVs used to generate the age composition and biomass data, respectively, from the trawl data were treated as known and used in the estimation models so that uncertainty was not misspecified.

For each of the 100 replicates of recruitment that were generated, 100 replicates of survey age composition and index were generated and fitted by the estimation models. For presentation we focus on the CV of the total biomass of the final year estimated by the SCAA model because this particular quantity allows consideration of the uncertainty in potential quantities of interest to management.

## Results

### Step 1: distribution of sample sizes to determine age composition across multiple species

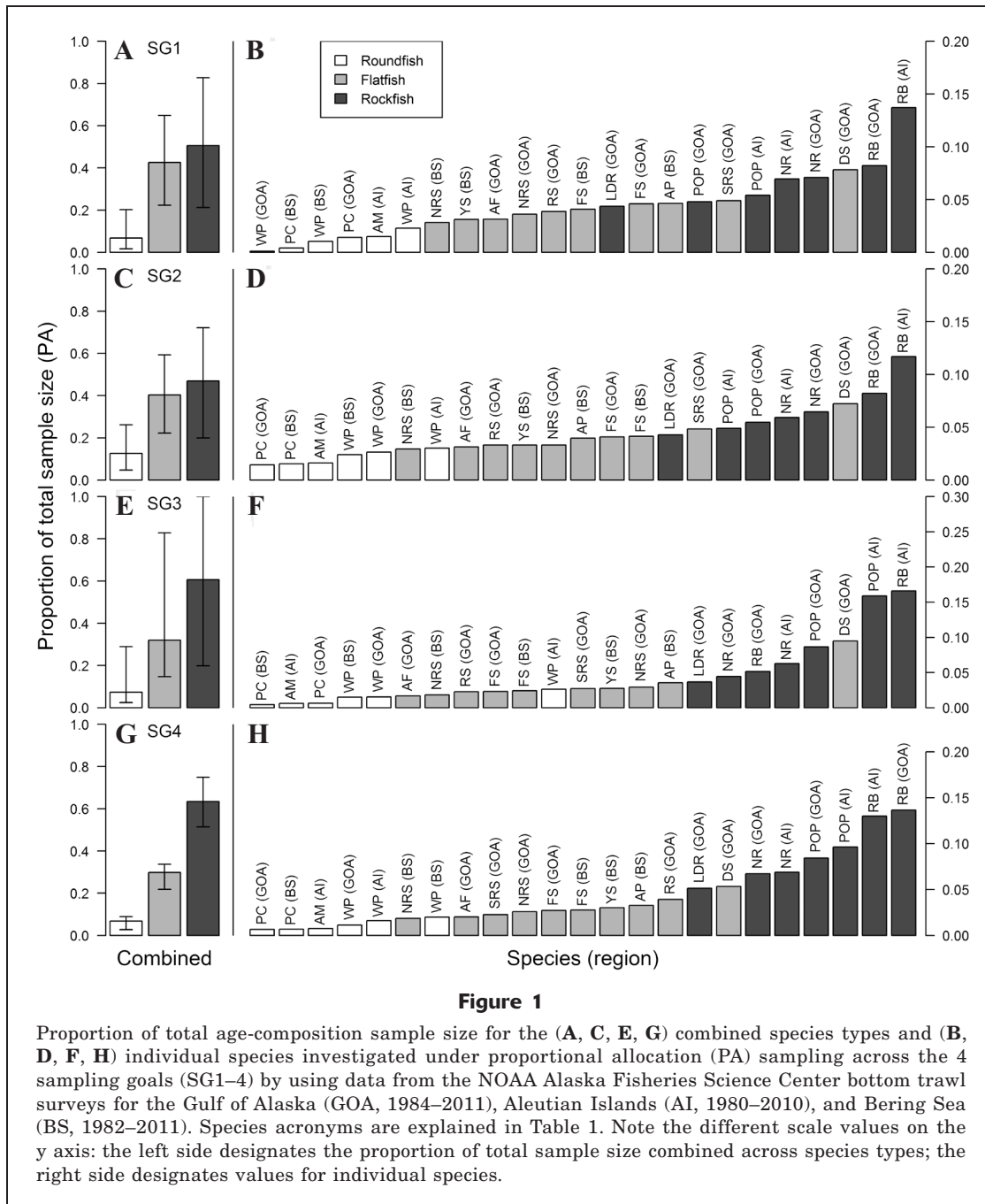
Overall, the results of the distribution of sample size for age-composition among the species types investigated with the AFSC bottom trawl survey data were consistently similar across sampling goals (Fig. 1), sampling methods (Fig. 2), and whether or not aging error was included (Fig. 3, A–D). Proportionally speaking, the distribution of age samples was in general the smallest for roundfish, intermediate for flatfish, and largest for rockfish (Figs. 1–3). Upon combining sample sizes across species types, we found that the distribution of sample size for the collection of otoliths for age reading was around 10% for roundfish, 30–40% for flatfish, and 50–60% for rockfish (left panels, Figs. 1–3). An interesting species that was a counter-example to the general results was Dover sole (*Microstomus pacificus*) in the GOA, which is the longest lived flatfish species investigated. In some sampling goals Dover sole resulted in a larger proportion of the total sample size than some rockfish species. Consistent patterns or large differences in the distribution of sample sizes in relation to location (e.g., among the GOA, AI, or BS) were not apparent across sampling goals, sampling methods, or cases of aging error for species that resided in more than one region investigated.

A few minor differences resulted in the distributions of sample size for individual species across sampling goals (Fig. 1) and sampling methods (Fig. 2); however, the overall pattern of distribution by species type dominated the results of the distribution of sample size for collecting age samples. When aging error was included in the distribution of sample size, there were some differences in total sample size proportions among some of the roundfish and flatfish species but there were no differences when aging error was not included (for ex-

ample, AI Atka mackerel (*Pleurogrammus monopterygius*) or GOA Arrowtooth flounder), although, the overall distribution by species type was again consistent (Fig. 3, A and C). When directly comparing across species, sampling goals, and sampling methods, we found that the sample sizes required when aging error was included were predominantly larger than when aging error was not included (Table 2). The slope parameter from a linear regression between estimated sample sizes that did and did not include aging error was significantly greater than 1 and the intercept parameter was significantly greater than 0, indicating that estimated sample sizes when aging error was included are larger than when aging error was not included (Fig. 3E). On average, when aging error was included, the sample size needed to increase by around 10% for flatfish and roundfish, and over 40% for rockfish to achieve the same level of uncertainty as when aging error was not included.

Upon investigating the within- and between-length interval variance components across species there were patterns that emerged that could explain the resulting distribution of sample size across species (Fig. 4). In general, the between-length interval variance was smallest for rockfish, intermediate for flatfish, and largest for roundfish. Alternatively, the within-length interval variance (under both proportional and fixed allocation) was, in general, smallest for roundfish, intermediate for flatfish, and largest for rockfish. Significant relationships resulted among all 4 life-history statistics investigated and the proportion of total sample size across sampling goals (Fig. 5, including aging error, shown as an example). The weakest relationship was between the log of estimated sample size and the log of the growth rate at 50% of  $L_{\infty}$  with coefficient of multiple determination ( $R^2$ ) values of 0.61 (Fig. 5B). The strongest relationship was found between the log of median sample size and the log of the minimum lifetime growth rate with  $R^2$  values of 0.88 (Fig. 5D).

Estimated sample sizes were comparable to AFSC bottom trawl survey sample sizes. Across the flatfish species investigated, the range between the average minimum and maximum sample sizes to achieve the sampling goals investigated was between 205 and 1374 samples (Table 2), which contains the actual average sample size taken by the AFSC bottom trawl surveys and is approximately 500 samples per year (Table 1). For the rockfish species investigated, the range of average minimum and maximum sample sizes to achieve our sampling goals was from 348 to 6494 samples (Table 2), which also contains the actual average yearly sample size of 630 samples taken by the AFSC bottom trawl surveys (Table 1). The range of the average minimum and maximum sample sizes to achieve the sampling goals for the roundfish investigated was between 55 and 576 samples (Table 2), the average annual sample size taken by the AFSC bottom trawl surveys of around 1040 samples (Table 1) was larger than this range. The estimated sample sizes were, in general,



**Figure 1**

Proportion of total age-composition sample size for the (A, C, E, G) combined species types and (B, D, F, H) individual species investigated under proportional allocation (PA) sampling across the 4 sampling goals (SG1–4) by using data from the NOAA Alaska Fisheries Science Center bottom trawl surveys for the Gulf of Alaska (GOA, 1984–2011), Aleutian Islands (AI, 1980–2010), and Bering Sea (BS, 1982–2011). Species acronyms are explained in Table 1. Note the different scale values on the y axis: the left side designates the proportion of total sample size combined across species types; the right side designates values for individual species.

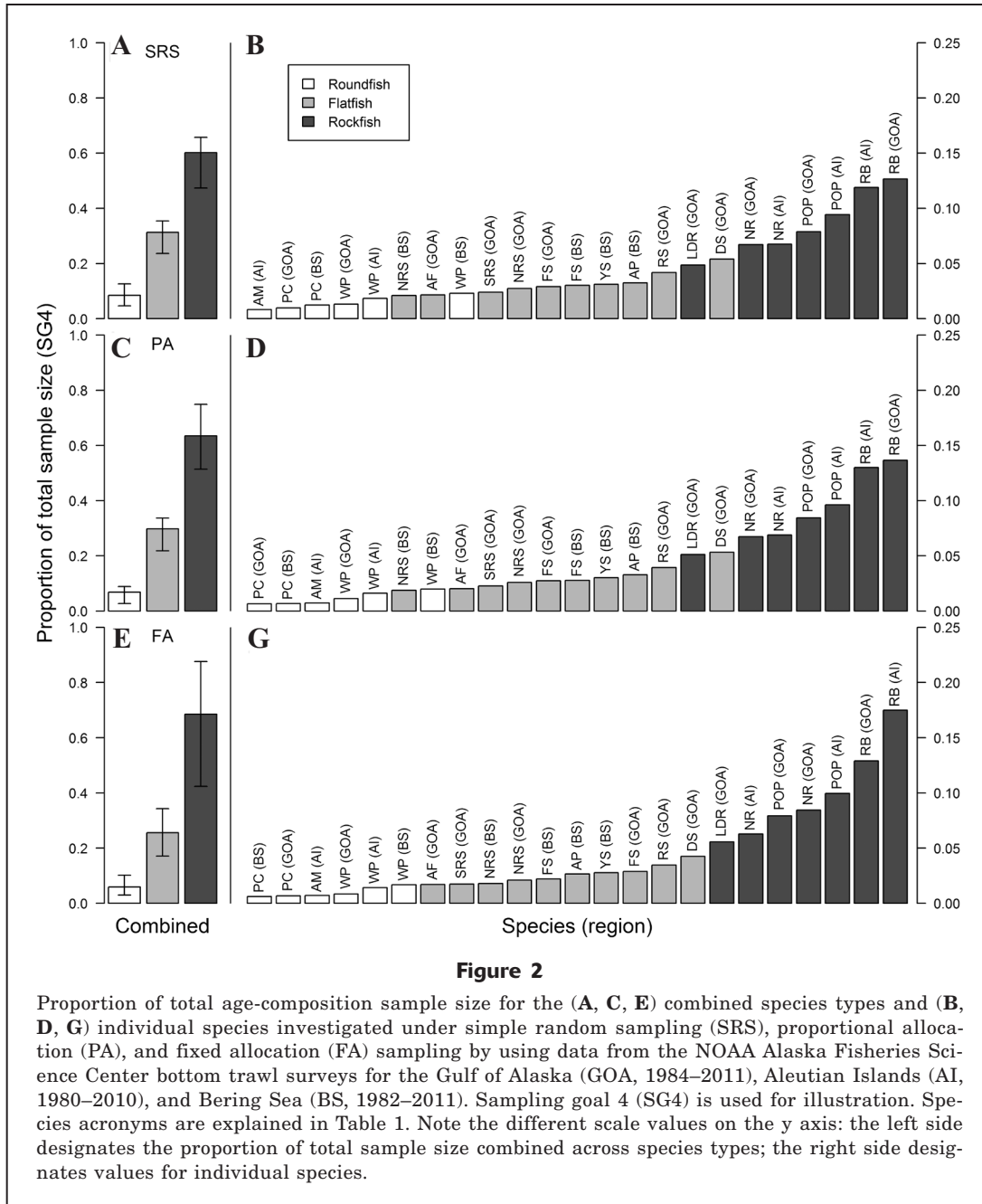
of similar magnitude between SRS and proportional allocation sampling across the sampling goals. Both SRS and proportion sampling required almost half the number of age samples to achieve the same amount of uncertainty as that obtained with fixed allocation, which is the current method for the majority of species sampled by the AFSC bottom trawl survey. Compiled results of the estimated sample sizes sampling goals investigated are shown in Table 2 to reduce the number of results presented; the estimated sample sizes for each species investigated across the sampling goals,

sampling methods, and whether or not aging error was included are provided in [Supplementary Tables 3–5](#).

**Step 2: sample size for determining age composition and SCAA model uncertainty**

The CV of total biomass in the final year of the estimation models for flatfish, rockfish, and roundfish decreased at different rates with increasing age-composition sample size from survey data and eventually approached a minimum value for the index uncertainty

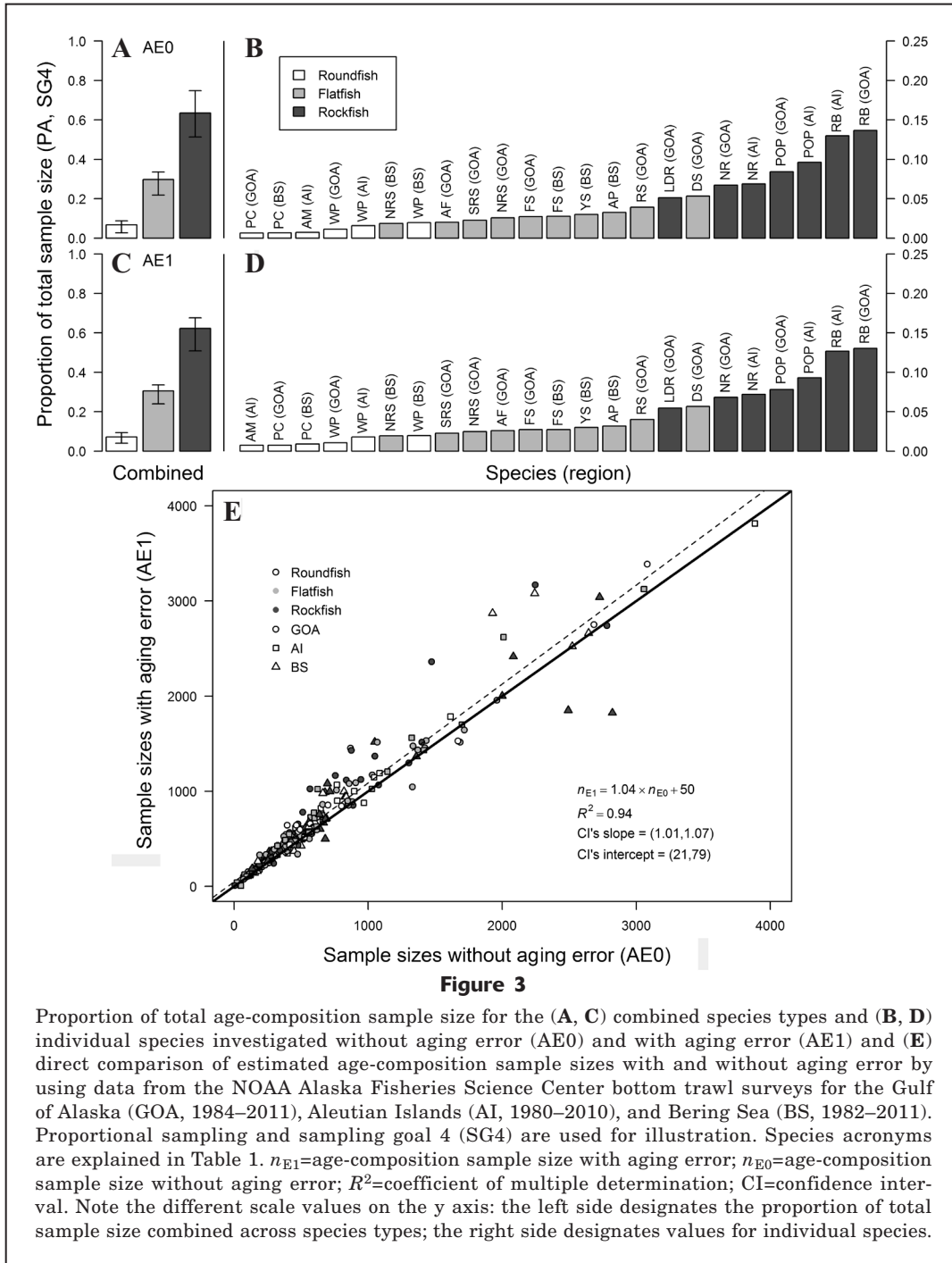




cases E0–E3 (Fig. 6). For each of the index uncertainty cases the minimum CV obtained, or baseline, was related to the underlying magnitude of the CV in survey biomass. In uncertainty cases E0 and E1 (Fig. 6, A and B), the baseline CV of the final year’s total biomass was smallest for flatfish, intermediate for roundfish, and largest for rockfish, which followed the relative magnitude of the underlying uncertainty in the survey index data for these 3 species types. In all index uncertainty cases, CV reduction resulting from increased age-composition sample size (the maximum CV obtained compared to the baseline) was greatest for the

roundfish group (text in top right corner of each plot in Fig. 6) and the smallest for the flatfish group, with rockfish intermediate.

The sample size for which the CV in the total biomass of final year changed by less than 2.5% for all species types, which we define as the point of diminishing returns, and was larger in cases with smaller survey index uncertainty than in cases with larger survey index uncertainty (vertical lines with arrows in Fig. 6). For example, the sample size at the point of diminishing returns for case E0 of 2500 samples was larger than the sample size of 500 samples for case E1 (verti-

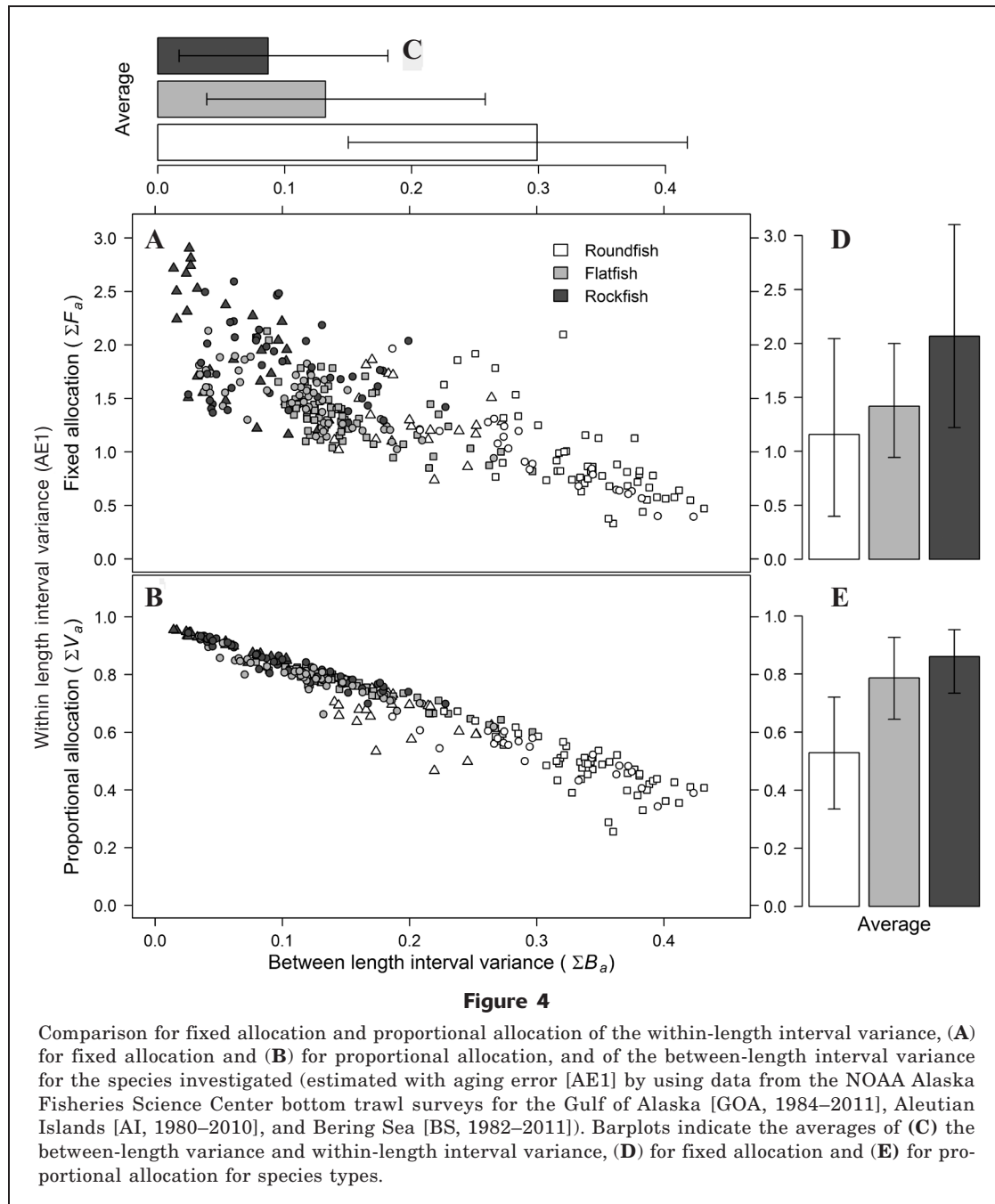


**Figure 3** Proportion of total age-composition sample size for the (A, C) combined species types and (B, D) individual species investigated without aging error (AE0) and with aging error (AE1) and (E) direct comparison of estimated age-composition sample sizes with and without aging error by using data from the NOAA Alaska Fisheries Science Center bottom trawl surveys for the Gulf of Alaska (GOA, 1984–2011), Aleutian Islands (AI, 1980–2010), and Bering Sea (BS, 1982–2011). Proportional sampling and sampling goal 4 (SG4) are used for illustration. Species acronyms are explained in Table 1.  $n_{E1}$ =age-composition sample size with aging error;  $n_{E0}$ =age-composition sample size without aging error;  $R^2$ =coefficient of multiple determination; CI=confidence interval. Note the different scale values on the y axis: the left side designates the proportion of total sample size combined across species types; the right side designates values for individual species.

cal lines with arrows in each plot in Fig. 6). Likewise, the sample sizes at the point of diminishing returns were greater for E2 (5000) compared with E3 (500).

Correlation analysis between changes in the estimates of the CV in the biomass of the final year, recruitment variability, and survey index uncertainty from the estimation model emphasized the relationship between these quantities and sample size. The percent change in the CV of the total biomass of the final year

(relative difference between largest CV compared with baseline CV, or, the minimum CV obtained) was positively correlated with recruitment variability (0.54; Fig. 7A). Conversely, the uncertainty in the survey index was negatively correlated with the percent change in the CV of biomass in the final year (-0.57; Fig. 7B). Taken alone, however, neither of these correlations was as strong as when the percent change in the CV of total biomass in the final year was correlated with the

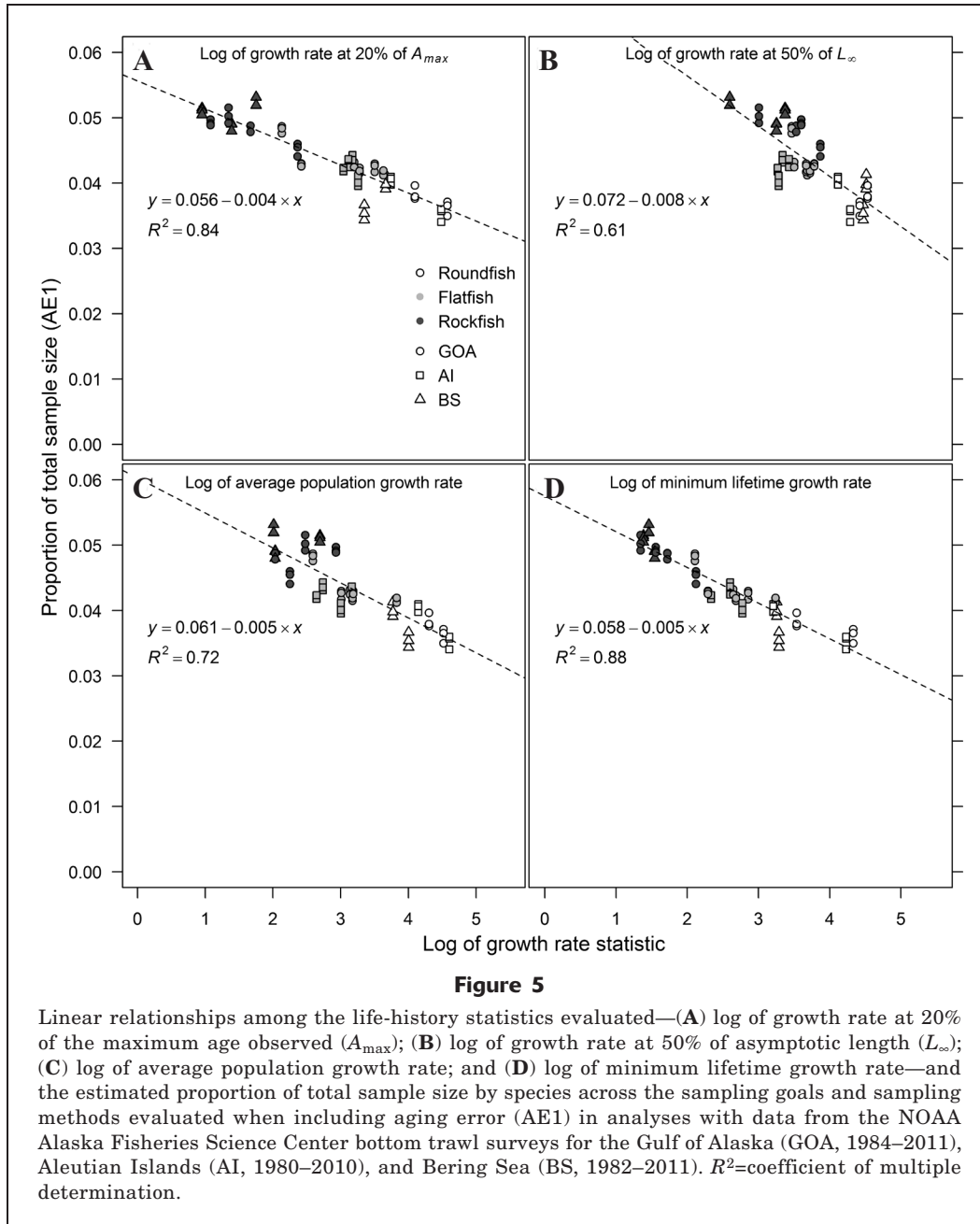


ratio of recruitment variability divided to the survey index uncertainty, which was 0.96 (Fig. 7C).

## Discussion

When thinking about the most efficient and appropriate manner to distribute sample sizes for age across multiple species, whether in a fishery-independent survey or from a commercial or recreational fishery, there are a number of factors to consider. All of these can be

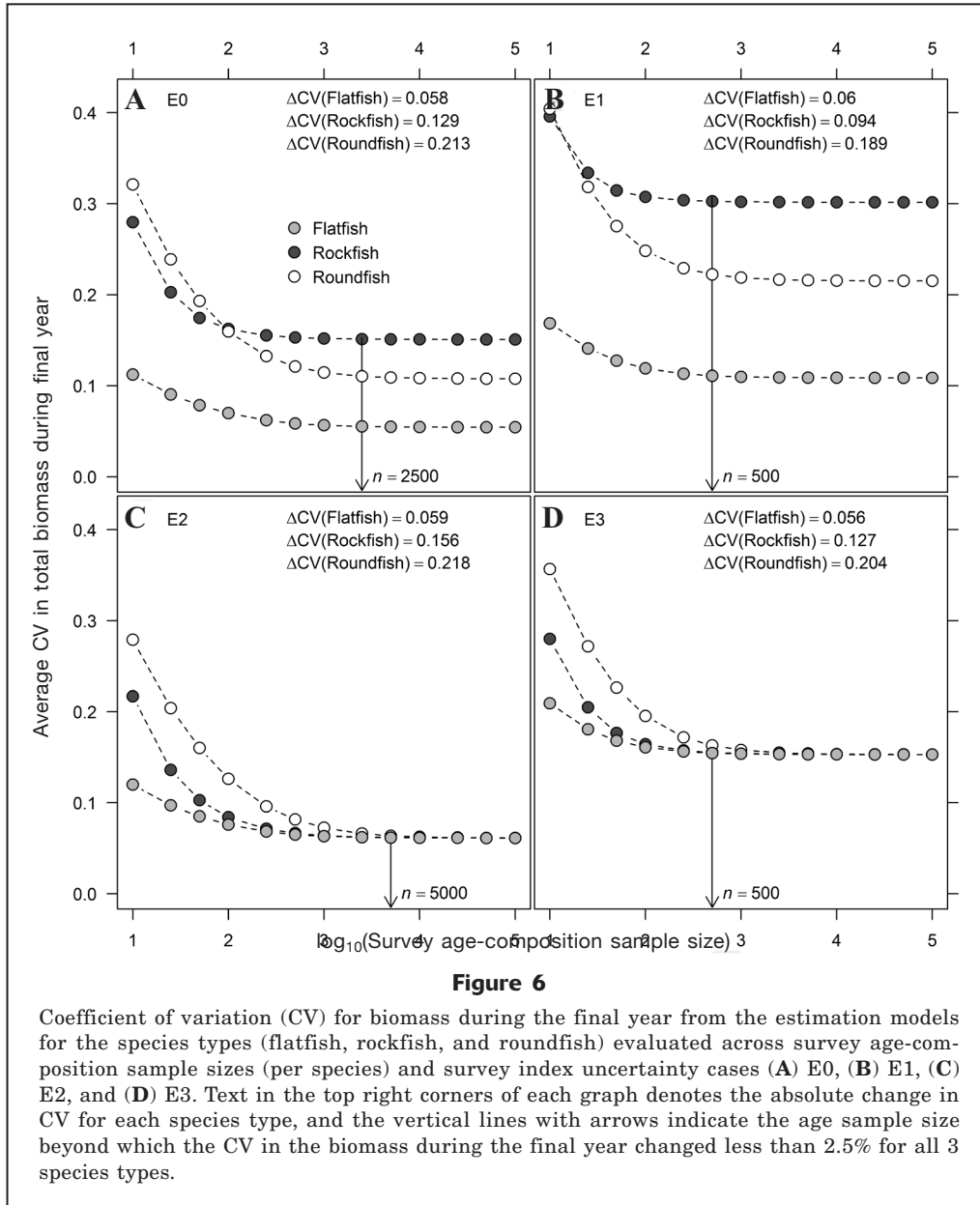
reduced to answering a single question: What is the relative value of each additional otolith to stock assessment? Although this can be posed as a simple question, it is not simple to answer. It is an optimization problem that requires balance among biology and life-history, statistics and stock assessment, and the commercial value and importance of the fisheries to user groups. Although this study is the first attempt in the fisheries literature to directly address this question, we recognize that many more factors than those considered here should be investigated to obtain a more



definitive answer to this question. Although, at some point it must be recognized that the uncertainty inherent in collecting and analyzing fisheries data, and the simplifications that are unavoidable in simulation analyses, make a comprehensive answer to this question unobtainable. In this study we have, however, provided several useful and interesting results that can be considered when approaching the issue of age sample size distribution and its subsequent influence on stock assessment.

The use of sampling theory, to estimate age sample sizes for each species, resulted in surprisingly consistent patterns in comparisons of the resulting sample

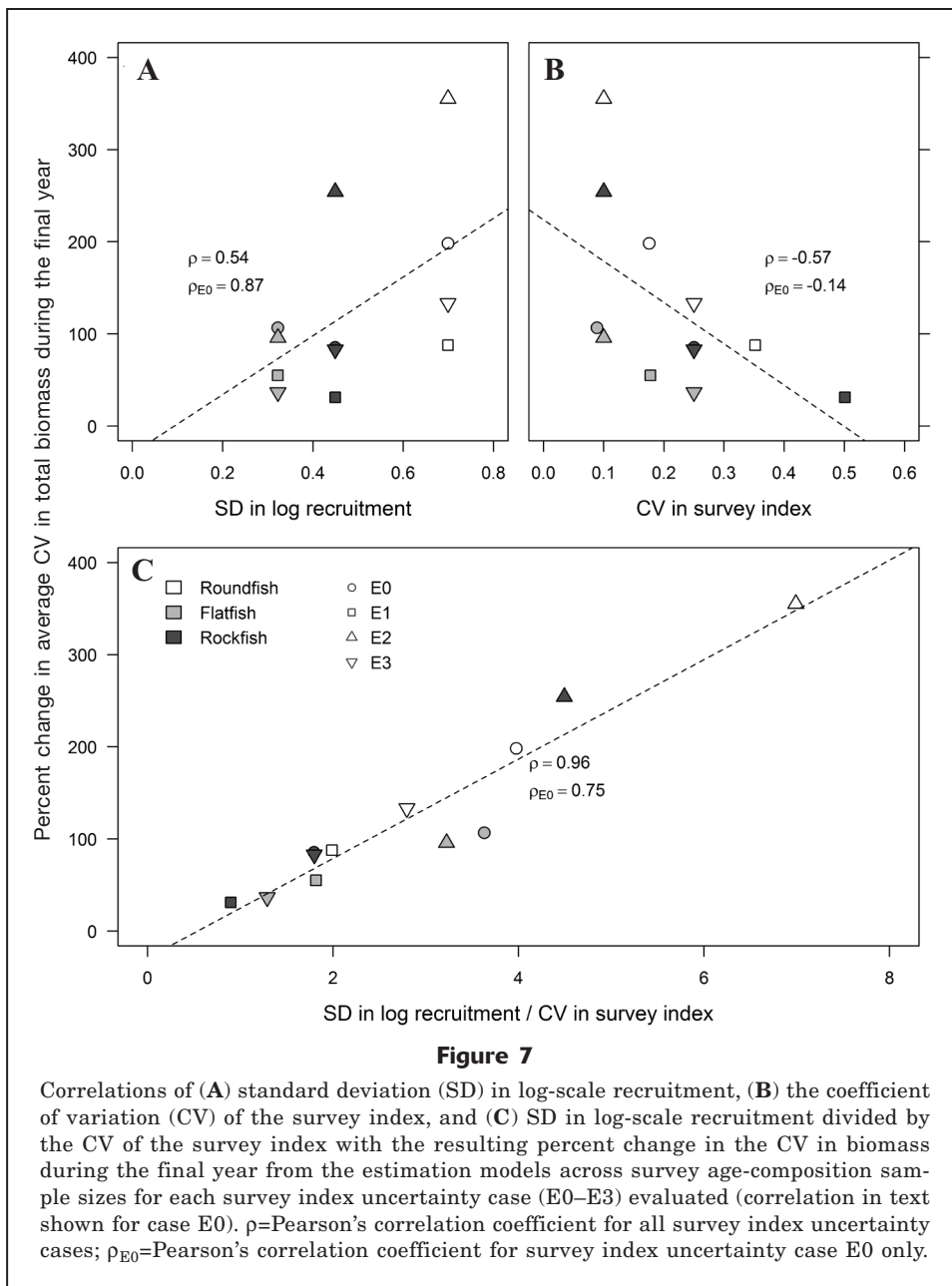
sizes across species in a distributional sense rather than by restricting the results to only species-specific evaluation. Upon viewing the species-specific sample sizes as a proportion of total sample size, regardless of the sampling goal, sampling method, or whether aging error was applied, the same pattern emerged. The rockfish species type required the largest proportion of total sample size, flatfish were intermediate, and roundfish required the lowest proportion of total sample size. Potentially the most interesting results of this study were the relationships between the distributions of sample size and life-history characteristics, in particular growth. It was shown that the rela-



tive proportion of sample size could be related to the growth rates of the species considered. The significant relationships between the proportion of age-composition sample sizes by species and life-history statistics could be due partially to the patterns in the variance between- and within-length intervals that resulted with species types.

On the basis of our results of this study, species that are relatively slower growing require more samples to determine age composition than those that are relatively faster growing. The overall idea being that for relatively faster growing species, there is more distinction between the lengths at a given age; thus, the length composition is relatively more informative regarding age than it is for slower growing species, and fewer

age samples are need to determine the age composition when performing 2-stage sampling. These results are also generalizable beyond just the species sampled by the AFSC bottom trawl surveys. Any fisheries science organization around the world will be constrained by the total number of otoliths it can process in a given year when considering how to distribute age sample size in a fishery-independent survey or fishery. The guidance that this study provides is that the growth characteristics of the species being sampled can help determine the relative magnitude of the sample size that should be used for each species. However, the results of this study should be taken in light of the caveats inherent to the method used to determine the distribution of sample size. We will discuss 3 of these: 1)



cost, 2) intrahaul correlation, and 3) commercial value of the species.

Cost, in terms of collecting age samples, would be defined as the cost in time (which is proportional to labor costs) required to both collect and read any given otolith. For example, when otoliths are collected, it is somewhat more difficult to obtain an otolith from a rockfish than from a roundfish or flatfish. There could also be differences in the amount of time it takes to obtain lengths of certain species. In terms of reading otoliths, more time is required to read a rockfish otolith than a flatfish or roundfish otolith, if for no other reason than that rockfish are longer-lived and have more

annuli to count than flatfish or roundfish. Additionally, we found that aging error had a relatively larger influence on rockfish species than on roundfish or flatfish. This finding would increase the cost in time because more otoliths would need to be read to obtain the same amount of information in the age-composition data. Cost could also be a function of sampling method, with the highest cost associated with fixed-allocation 2-stage sampling and lower costs associated with proportional allocation 2-stage sampling or SRS (in terms of the sample size necessary to achieve the same amount of uncertainty). Methods have been developed to include cost in estimating sample sizes required for age com-

position (Schweigert and Sibert, 1983; Lai, 1987), however, the data on cost for the species sampled by the AFSC was not available at the time of this study.

Intrahaul correlation arises owing to the similarity of fish ages within a given haul or the spatial distribution of these ages in comparison with the spatial distribution of sampling, which then leads to over-dispersion of uncertainty when compared with what would be determined from multinomial sampling (McAllister and Ianelli, 1997). Intrahaul correlation in sampling for ages has recently been the subject of several studies (Pennington et al., 2002; Hulson et al., 2011), as well as investigations of how to account for intrahaul correlations in SCAA models (Francis, 2011; Maunder, 2011; Hulson et al., 2012). Although intrahaul correlation has received attention in the literature in terms of integration into stock assessment models, it is not clear at this point in time how intrahaul correlation could be incorporated in estimating optimal distribution of age-composition sample sizes across species before a stock assessment. The magnitude of the difference between effective sample size and the actual sample size collected is influenced by the age aggregations within schools or the spatial distribution of the species sampled, which may not be consistent across species. This should be a topic for future consideration but is beyond the scope of the current study.

Value in this case would be defined as the value of the fishery, the sampling efforts of which are supporting stock assessment. Using fisheries assessed by the AFSC as an example, the walleye pollock fishery in the eastern BS supports one of the largest and most valuable groundfish fisheries in the world (Ianelli et al.<sup>7</sup>). The stock would require a decrease in age-composition sample size if the results of the current study were implemented in the AFSC bottom trawl age-sampling design. Including value into the sampling theory method has not been previously explored but, mathematically speaking, it could be implemented in a similar manner to that of cost. It is more challenging, however, to determine how age sample size affects the potential value of a fishery. The results of the simulation analysis show that changing sample size in age composition affects the resulting uncertainty in an SCAA model. Methods have been proposed that would take into account uncertainty when setting management quantities such that when uncertainty in SCAA model results increase, the harvest target rate decreases to account for this uncertainty (Prager and Shertzer, 2010). The eastern BS pollock assessment employs a buffer based on the uncertainty of the estimation of the harvest target. Therefore, if sample sizes were decreased and SCAA model uncertainty increased substantially, the potential value of the fishery could decrease. A more rigorous

analysis of value would have to include the numerous other factors that are a part of the overall value of a fishery (e.g., a decrease in quota could increase the price per kilogram or increase long-term value). Age-composition sample size may indeed be a very small factor in terms of value, but value is unquestionably one of the main factors influencing how age-composition sample sizes are currently allocated by the AFSC.

The simulation analyses with the SCAA model provide guidance on the factors to consider when adjusting age-composition sample sizes in a multispecies data collection program. The results suggest that life-history and survey index uncertainty play key roles in determining the magnitude of influence that changing age-composition sample size has on SCAA model uncertainty. The results of the simulation analysis indicated that age-composition sample size has a greater impact on the resulting uncertainty in SCAA models for species with high recruitment variability or low survey index uncertainty, or both. In contrast, for species with low recruitment variability or high survey index uncertainty, or both, changes in age-composition sample size have a smaller influence on the resulting uncertainty from a SCAA model. Returning to the eastern BS walleye pollock example, the recruitment variability of this stock is higher than that of most species, and it has intermediate survey index uncertainty (intermediate between rockfish and flatfish species); therefore, decreasing age-composition sample size would potentially have a larger impact than decreasing sample size for a flatfish species, for example, that has lower recruitment variability and low survey index uncertainty.

To isolate the effect of the fishery-independent survey data sources (index and age composition) we made several simplifying assumptions in our simulation. These involved including process and observation error in the fishery data sources (e.g., different catch histories and different levels of uncertainty in the catch data) which would also influence the uncertainty resulting from an SCAA model and could decrease the relative influence of the fishery-independent survey data sources. An additional consideration that was not made in our simulation is the potential for gaps in the fishery-independent survey data (which is the case for the AI and GOA bottom trawl survey data) and how that influences age-composition sample size in the resulting SCAA model uncertainty. The strength of the relationships between increasing or decreasing age-composition sample size and recruitment variability and survey index uncertainty is possibly due to the simplifying assumptions made in the simulation analysis. Although, magnitudes in changes to the SCAA model uncertainty could be different with the use of more sophisticated simulations, we hypothesize that these correlations may be qualitatively the same regardless of the complexity of the simulation analysis. We recommend that future research into investigating the influence of age-composition sample size on SCAA model results, and how that relates to optimal distribution of sample size across species, should be under-

<sup>7</sup> Ianelli, J. N., T. Honkalehto, S. Barbeaux, and S. Kotwicki. 2015. Assessment of the walleye pollock stock in the Eastern Bering Sea. *In* Stock assessment and fishery evaluation report for the groundfish resources of the Bering Sea/Aleutian Islands regions. North Pacific Management Council, Anchorage, AK. [Available from [website](#).]

taken with more complex simulation analyses than the scope of this article allows.

We have attempted to synthesize the use of sampling theory with SCAA model simulation analyses to address 2 primary questions: 1) how to distribute age-composition sample sizes across species, and 2) what is the effect on SCAA model uncertainty by increasing or decreasing age-composition sample size for species with different life histories. In addressing the first question, if a goal of sampling is to obtain age compositions with a similar degree of uncertainty across species, the sample sizes should be distributed on the basis of life-history characteristics, in particular growth rates. In addressing question 2, at the same time one should keep in mind that the relationship between age-composition sample size and resulting SCAA model uncertainty can be disproportionate because of species-specific characteristics, and is related to the recruitment variability and survey index uncertainty of the species modeled. We had to make several simplifying assumptions because of the breadth of the topic of optimal distribution of age-composition sample size across species. It is due to these simplifying assumptions that we are reluctant to suggest absolute ranges of age sample sizes for each species, but we do contend that there are life-history characteristics, in particular growth, that can be considered when discussing the distribution of sample size. Optimal allocation of sample size has historically been an extremely important topic, although not one that has received attention in the literature. As fisheries research resources appear to be shifting away from traditional survey and stock assessments toward process studies, government agencies will continue to seek guidance for current allocation strategies. We suggest that future developments be focused on developing both sampling theory to take into account various aspects of sampling that currently are not considered and more sophisticated simulation analyses with SCAA models to place the discussion of sample size distribution across species in terms of risk of overfishing, accuracy of results, and value to managers and stakeholders.

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