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# The Commercial Size Limit for the Pacific Halibut Fishery off Alaska and its Relationship to Observer-Derived Estimates of At-sea Discard

J. Cahalan and J. Gasper

**February 2022**

U.S. DEPARTMENT OF COMMERCE  
National Oceanic and Atmospheric  
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# **The Commercial Size Limit for the Pacific Halibut Fishery off Alaska and its Relationship to Observer-Derived Estimates of At-sea Discard**

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## **U.S. DEPARTMENT OF COMMERCE**

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## Abstract

January 2013 marked the beginning of a new method of deploying at-sea observers into the Federal groundfish and Pacific halibut (*Hippoglossus stenolepis*) fisheries off Alaska. The new program provided for at-sea data collection on longline vessels participating in the Pacific halibut fishery. Previously data collections on these vessels were not authorized and had severely limited the National Marine Fisheries Service's ability to estimate incidental catch and at-sea discard of halibut and groundfish species. Vessels fishing for Pacific halibut have unique catch characteristics with fishing trips that contain both retained and discarded halibut. Halibut fisheries off Alaska operate under federal regulations requiring halibut intended for commercial sale be at least 32 inches (~ 81 cm) in total length. The minimum size limit complicates estimation of halibut discard due to the limited amount of disposition-specific data collected by observers available to calculate mean weights. Observers collect fish weights that are used to estimate the mean weight per fish from the unsorted (retained and discarded) catch. They also collect counts of retained fish to estimate the percent of the catch retained. The calculation of the mean weight per fish using observer data may overestimate the mean weight of discarded fish and underestimate the weight of retained fish. While estimates of retained catch are based on landings data and thus are not biased, the haul-specific estimates of at-sea discards of halibut in the halibut fishery are biased. This analysis assessed the impact of bias on the total discard estimates and proposes an adjustment to mitigate the bias.



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## Introduction

The North Pacific Observer Program (Observer Program) provides the regulatory framework for National Marine Fisheries Service (NMFS) to collect fishery-dependent data and monitor commercial groundfish and Pacific halibut fishing activity in the North Pacific. The Observer Program has a long history of successful data collection and has continually adjusted observer sampling methods to best integrate with the changing fisheries and evolving management needs. In 2013, NMFS restructured the Observer Program and changed how observers were deployed onto fishing vessels. Prior to 2013, sampling strata were defined by vessel length and whether fishing trips occurred in a catch share fishery (see NPFMC et al. 2010 for additional details about the restructuring of the Observer Program). With the restructuring of Observer Program deployment procedures, sample strata were redefined and a mechanism for randomization of observer deployments was implemented. In addition, the previously unobserved Pacific halibut (*Hippoglossus stenolepis*) commercial fishery became subject to observer coverage. This is the only federally managed non-recreational fishery in Alaska with a minimum retention size required by regulation.

Expansion of the Observer Program to cover the Pacific halibut fishery brought with it a suite of sampling challenges. Observer-sampling methods on longline vessels were well established and observers were experienced in the longline fisheries; however, several aspects of the Pacific halibut fishery differed substantially from the fisheries that were historically subject to observer coverage. Vessels participating in this fishery tend to be smaller than longline vessels participating in other monitored fisheries and, as such, have smaller living areas, smaller set sizes, and less space available to the observer to collect and process samples. As the Observer Program gained experience in this fishery, the limitations to observer sampling methods were recognized by NMFS and, in response, the Observer Program updated sampling methods to accommodate smaller vessels and unique fishing operations.

Although most sampling challenges were surmountable, the regulatory requirement for small halibut to be discarded at sea remains incompatible with established bycatch data collection and estimation processes. Regulations require halibut < 32 inches (~ 81.3 cm) to be discarded and larger fish to be retained if the fishing operation has individual fishing quota (IFQ)

available. In other fisheries, discards consist of quota and bycatch cap overages, damaged catch, and catch that drops off the gear ('drop-offs'); hence, the size distribution of discarded catch can be assumed to be the same as the size distribution of the total catch. However, in the directed fishery, halibut are not only discarded for all of the previously identified reasons, they are also discarded if they are under the minimum size limit. The size-specific discard requirement creates a unique data collection issue because observers collect data from the unsorted (retained and discarded) catch without inferring which fish would be discarded by the vessel. Hence, the mean weight per fish that is calculated from a sample of combined discarded and retained fish overestimates the mean weight of discarded fish and underestimates the weight of retained fish. While estimates of retained catch are based on landings data and thus are not biased, the haul-specific estimates of at-sea discards of halibut in the halibut fishery are biased under these estimation methods.

Unfortunately, changing sampling methods so that observers could obtain disposition-specific data in the directed halibut fishery is problematic on such space-limited vessels and would require changes to sampling protocols and vessel sorting procedures. In addition, current database and data transmission software does not support adding these additional data elements. Other methods such as using Electronic Monitoring (EM) for length measurement or binning halibut by size class prior to being discarded before the fish are brought onboard the vessel are not yet viable alternatives.

Given the constraints on changing observer sampling protocols, this paper used data collected under current sampling methods to evaluate analytical approaches that account for bias in haul-specific estimates of halibut discard. Our focus was to evaluate conversion methods that can be universally applied to observer data from the directed halibut fishery.

## **Methods**

### Observer Data Collection and Halibut Discard Estimation Methods

Observer sampling methods on longline vessels are built around random sampling, the observer's ability to access to the catch, and the logistics of working safely on a commercial fishing vessel. For any sampled set, there are two broad types of samples collected: the first type

is a larger sample used to collect species composition and fish disposition data, and the second type is for the collection of biological specimens and other data (e.g., individual fish lengths, weights, otoliths).

To collect the species composition sample, the observer first divides the longline into equal-sized sample units, often delineated by gear segments or a pre-specified number of hooks. Fish counts and disposition data are collected from a random selection of these sample units, generally equivalent to approximately a third of the set. These selected sample units are collectively referred to as the 'species composition sample' or 'tally period'. The observer counts (tallies) all catch in the species composition sample (selected sample units) as the longline gear is being retrieved, noting how many of a species or species grouping are retained (brought onboard) and the number of fish that are discarded (generally not brought onboard). There are two methods used by observers to determine the weight of halibut in these samples. In the first method (preferred), halibut lengths are estimated visually to the nearest 10 cm for *all halibut in the sample*. These estimated lengths are converted to weights using a length-to-weight table and summed to estimate the total weight of halibut in the sample. In the second, less-preferred method, the observer collects 10 to 20 randomly selected halibut to be brought on board and weighed during a separate, non-tally time period. The mean weight per fish is computed from this secondary sample and used to estimate the total weight of fish tallied in the species composition sample (number tallied multiplied by the mean weight per fish<sup>1</sup>). This method is used on hauls where the observer may not have time to estimate and record lengths of all halibut caught during the tally period. Under either method only the total number and weight of halibut in the species composition sample are captured in the database; individual length measurements and weights are not available from the species composition samples. We can compute the mean weight per halibut from the species composition sample because it contains the total number and total weight of sampled halibut, and the proportion of halibut retained. These data are used to estimate the weight of each species caught for the haul (both retained and discarded) by the expanding the species' sample weight to the entire set based on the fraction of the gear sampled; the sample weight for those samples where weights are not available for all halibut is the product of the number in the sample (the tally) and the species-specific mean weight per fish

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<sup>1</sup> This method is used to estimate the weight of fish in the sample for non-halibut species: the number of fish in the sample is converted to weight using the mean weight per fish computed from a sample of fish.

(approximately 2% of hauls). The percentage retained for each species is estimated as the proportion of a species (or grouping) that is retained, based on the observer count and converted to a percentage.

The second type of samples collected by observers is used to obtain biological specimen samples of non-target species (biological specimen sample). For these samples, the observer requests the crew set aside, for sampling, all non-target species encountered during the tally period (species composition sample). The observer determines the length and weight for all non-target species fish brought onboard and collects biological specimens such as otoliths (see AFSC 2021, p. 13-23 to 13-26 for specimen collection priority lists). In addition, a pre-determined number of the target species are also brought on board during a different sampling period and are used for the collection of biological data from the target species. The collection of biological specimens includes an assessment of the condition of halibut in the sample. Using a dichotomous key developed by the International Pacific Halibut Commission (IPHC), halibut are classified into four condition categories based on their hooking injuries: dead, minor injuries, moderate injuries, excellent condition. These condition categories are associated with the estimated post-capture survival of discarded halibut and are used to estimate the discard mortality rate (DMR) for halibut discarded outside of the halibut IFQ fisheries. Halibut that the crew determines will be retained by the vessel are not assessed, however their length is measured. Starting in 2016, observer sampling of halibut for collection of length and condition data was changed to be consistent with non-halibut species encountered in longline fisheries. This change results in an observer randomly selecting 10 halibut per sampled haul for the purposes of collecting biological data; length measurements are collected from each halibut, and if the crew indicates the halibut will be discarded, a condition assessment is conducted. This data collection is feasible because only a small number of fish (10 per haul) are selected, unlike during the tally periods where many halibut are landed and discarded. Additional details of observer sampling methods can be found in the Observer Sampling Manual (AFSC 2021).

Since condition assessments are only conducted on discarded halibut, we can infer which individual halibut in the biological specimen sample are retained (length measurement but no condition assessment) or discarded (both length measurement and condition assessment) in the directed fishery. Hence, the 2016 change in sampling not only increased the reliability of the

length and condition data collected, it also allowed for haul-specific estimation of mean weight per fish based on the disposition of a sampled halibut (i.e., retained or discarded).

### Discard Estimation Methods and Bias of the Estimator

The estimated weight of each species caught is the product of the number of each species in the observer's sample and the mean weight of each species (see Cahalan et al. 2014 for addition catch estimation details). The sample weight is then expanded to the total haul by dividing by the sample fraction ( $n/N$ , Eq. 1). This estimate of total weight of catch is unbiased with variance that depends on the variability between sample units (i.e., variance on the estimated total number of halibut) and the variability in mean weight per fish from the sample data. The estimate of catch weight for a species ( $\widehat{W}$ ) is given below where  $\widehat{N}$  is the estimated number of halibut caught,  $h$  is the number of halibut in the species composition sample,  $N$  is the number of gear segments fished,  $n$  is the number of gear segments in the observer sample,  $\widehat{w}$  is the weight of a sampled species, and  $\bar{w}$  is the mean weight per fish from either the composition sample or a separate sample of catch (not based on the assessed fish):

$$\widehat{W} = \frac{N}{n} h \bar{w} = \frac{N}{n} \widehat{w} = \widehat{N} \bar{w}. \quad (\text{Eq. 1})$$

The estimated at-sea discard of a species ( $\widehat{D}$ ) is the estimated catch weight multiplied by the proportion of the catch that is discarded ( $=1$ -proportion retained), where  $h$  is the number of halibut in the sample,  $h_r$  is the number of halibut in the sample that are retained, and  $h_d$  is the number of halibut in the sample discarded, and the other terms are as defined above:

$$\widehat{D} = \widehat{W} \left( 1 - \frac{h_r}{h} \right) = \widehat{N} \bar{w} \left( \frac{h_d}{h} \right). \quad (\text{Eq. 2})$$

These methods provide unbiased estimates of total catch. However, because there is a minimum size limit for halibut, the estimate of at-sea discards of halibut are biased. This estimator will be unbiased when the mean weight per discarded halibut equals the mean weight of all halibut, implying that the percent of halibut discarded, based on numbers, equals the percent of halibut discarded based on weight. While this is reasonable for non-halibut species since discarding behaviors are not driven by fish size, this assumption is not valid during directed halibut fishing because only halibut  $\geq 32$  inches are being retained by the vessel operator. To

correct this bias, we either need to convert the weight per fish caught to weight per fish discarded or we need to convert the percent number retained to percent weight retained. In addition, the correction procedure will need to be incorporated into the Observer Program and NMFS estimation processes (Cahalan et al. 2014) with minimal disruption to existing routines. For these analyses, we restricted the set of covariates to those currently collected or easily integrated into observer data collections and those with biological relevance.

### Overview of Data

Data from 2017 and 2018 were used to train models and data from 2019 were used to test model predictions. We chose this separation of training and testing data to be representative of how the model would likely be operationalized: a model developed and periodically updated based on recent-past data and then applied to current year collections. Although data are available in real time, the stability of estimates throughout a fishing year and transparency of estimation methods were prioritized over in-season estimation. Limited sample size and fishery representation early in the year would result in generation of models that would not be relevant to later fishing activities. These models would also need to be re-estimated on a continual basis throughout the year which would be computationally demanding and would create unstable numerical outcomes. The 2016 data, collected during the first year under the new methods, were not included because of the small sample size and large variability. Additionally, data were filtered to only include those hauls fished with longline gear where IFQ halibut were retained. The model was fit using the following data elements from both species composition sampling and biological specimen sampling.

From the observer's species composition sample:

- For each species composition sample (tally period), the mean weight of halibut calculated as the sum of the weight of halibut in all selected sample units divided by the sum of the number of halibut in the sample units (ratio estimator).<sup>2</sup>
- For each haul, the percent of the number of halibut retained: the count of retained halibut divided by the count of all halibut caught based on the observer's tallies as the longline is

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<sup>2</sup> Note that the weight of halibut is based on converting the halibut length to weight using the IPHC length weight conversion table included in the observer sampling manual (AFSC 2021). Halibut lengths from this sample are not retained in the database. In addition, the length-to-weight tables are not area- or year-specific.



retrieved. The disposition is tallied as catch is either brought on board or discarded at the rail during the collection of the species composition sample (the ‘tally’ phase).

From the observer’s biological specimen sample:

- For each assessed halibut, the length, weight, and presence of a condition assessment for a random selection of up to 10 halibut per sampled haul.
- The presence of a condition assessment was used to indicate that halibut were discarded since condition assessments are only conducted on discarded halibut. The absence of an assessment generally indicates the halibut was retained; however, other factors may result in halibut without condition assessment data including limited access to discarded halibut, data loss, and observer error. This would result in some discarded halibut being assigned to the retained category. These types of data loss are relatively rare and are assumed to be random with regard to size.

From landings data:

- Weight of total retained halibut for a trip was obtained from industry reports (e.g., fish tickets). These data are used in the latter part of the analysis to evaluate the magnitude of bias associated with the current methodology.

Only those hauls where some halibut were retained were included in the analysis regardless of the amount of IFQ that may be remaining. In addition, data were further filtered to only include hauls with data from both sample types, three or more assessed halibut, and where the proportion of halibut retained was greater than zero and less than one based on data from both sample types (tally of retained halibut and halibut in the biological specimen samples).

### Model Development and Selection

The bias in the estimates of discarded halibut weight arises from inconsistencies in how terms are defined. Specifically, Eq. 2 contains the product of three key terms: 1) the proportion of halibut discarded, 2) the estimated total number of halibut, and 3) the mean weight of halibut. Taking the first two of these, we have an unbiased estimate of the number of halibut discarded,  $\hat{N} \left(1 - \frac{h_r}{h}\right)$ , which is then multiplied by the mean weight of all fish regardless of disposition. The estimated discard weight will only be unbiased if the mean weight per fish equals the mean weight of discarded fish, which will only be unbiased for species with no size-selective

discarding. Concordantly, grouping the second two terms results in an unbiased estimate of total weight ( $N\bar{w}$ ) that, when multiplied by the percent number halibut discarded, will generate an unbiased estimate of weight discarded if the percent number discarded equals the percent weight discarded, which is not valid for species with size-selective discarding. Hence, there are two general approaches that could be used to adjust estimates of halibut discard weight using observer data: 1) convert the estimate of mean weight per fish to mean weight per discarded fish or 2) convert the percent number retained to percent weight retained.

1. *Conversion of mean weight per fish to mean weight per discarded fish*

A conversion of the mean weight per fish to the mean weight per discarded fish with an interaction term, is given by Eq. 3 where  $P_n$  is the proportion of the number of halibut discarded,  $\bar{w}$  is the mean weight per halibut, and  $\hat{w}_d$  is the predicted mean weight per discarded halibut,

$$\ln(\hat{w}_d) = \alpha + \beta_1 \ln(\bar{w}) + \beta_2 P_n + \beta_3 \ln(\bar{w})(P_n). \quad (\text{Eq. 3})$$

Because the relationship between weight and number was not linear, both the mean weight per halibut and mean weight per discarded halibut were natural log transformed. This model was fit using ordinary least squares linear regression, both with and without the interaction term, using the R programming language (R Core Team, 2020). Other covariates, such as geographic area and time were not evaluated since the conversion models (e.g., coefficients, fit) were not expected to vary spatially nor temporally.

2. *Conversion of Percent Numbers Retained to Percent Weight Retained*

Noting that the halibut discard weight is a function of both the percent number retained ( $P_n$ ) and the mean weight per fish ( $\bar{w}$ , Eq. 4), and noting that the mean weight per retained fish is a function of the percent retained (the larger the proportion of fish retained, the more large fish, and the greater the mean weight per fish  $\bar{w}_R = f_x(P_n)$ ), conversion of the percent number retained to the weight retained was evaluated using both the overall mean weight per fish and the percent number retained as covariates:

$$P_w = \frac{h_R \bar{w}_R}{h \bar{w}} = P_n \frac{\bar{w}_R}{\bar{w}}. \quad (\text{Eq. 4})$$

Using ordinary least squared regression (OLS), the model is given by Eq. 5 where  $P_w^2$  is the squared percent weight retained and other terms are as defined previously. The response variable ( $P_w$ ) was transformed (squared) so that the relationship between the  $P_w$  and the covariates was approximately linear:

$$P_w^2 = \alpha + \beta_1 P_n + \beta_2 \bar{w} + \beta_3 P_n \bar{w}. \quad (\text{Eq. 5})$$

Since the response variable ( $P_w$ ) is a proportion and in order to constrain predicted values on the same scale as the percent weight retained (i.e., bounded by 0% and 100%), we fit two generalized linear logistic regression models with a quasi-binomial link, each with and without the interaction term (Eq. 6).

$$\ln\left(\frac{P_w}{1-P_w}\right) = \alpha + \beta_1 P_n + \beta_2 \bar{w} + \beta_3 P_n \bar{w}. \quad (\text{Eq. 6})$$

Four candidate models were evaluated for the conversion of  $P_n$  to  $P_w$ : two OLS linear models (Eq. 5) and two GLMs (Eq. 6), each with and without the interaction term. Model selection was focused on predictive ability over interpretation of parameters. Covariates tested always included percent number retained and mean weight per fish since these are currently collected by observers. Sampling year was considered as a covariate; however, since only two years of data are available for the analysis and initial analyses did not show an effect, year was not included in model fitting. Model selection and covariate evaluation was evaluated using F-tests, analysis of deviance, residual analysis, and ex-sample predicative ability. As with the development of models converting mean weight per halibut to mean weight per discarded halibut, geographic area and time were not evaluated since the conversion models (e.g., coefficients, fit) were not expected to vary spatially nor temporally.

The root mean squared error (RMSE) was computed as the square root of the mean squared differences between the predicted values derived from the test data (converted percent weight retained) and the actual percent weight retained based on assessed halibut (Eq. 7). These were computed from the percent number retained and mean weight of assessed halibut for each individual haul ( $i = 1, \dots, n$  hauls with assessed halibut in 2019) where  $\hat{P}_{wi}$  is the converted percent weight retained for haul  $i$  and  $P_{wi}$  is the actual value based on assessed fish in that haul.

$$RMSE = \sqrt{\frac{\sum_{i=1}^n (\hat{P}_{wi} - P_{wi})^2}{n}}. \quad (\text{Eq. 7})$$

A linear regression of the predicted  $\hat{P}_{wi}$  and actual  $P_{wi}$  was used to assess the degree of variance and potential bias over the range of  $P_{wi}$  values.

### Evaluation of Bias

To assess the magnitude of bias in estimates of at-sea discard of halibut in the directed fishery, percent number retained based on data from the composition samples was converted to percent weight retained. The percent number retained and mean weight per halibut from the composition samples are available for every haul sampled by observers and are part of the standard data collections conducted by observers. The converted percent weight retained was applied to the estimated total halibut catch to generate estimates of halibut discard and compared to estimates of discard weight using current methods.

To assess the bias associated with fishery-level discard estimates used in management, the adjusted haul-specific estimates of halibut discard were used to estimate fishery-specific discards using the same methods as the NMFS Catch Accounting System (CAS; Cahalan et al. 2014). Bycatch rates generated using the adjusted haul-specific discard estimates were applied to landing data to estimate adjusted total discards for vessels keeping legal-sized halibut.

## Results

### Data Exploration

There were 2,918 hauls for which both species composition and biological specimen sample data are available; that is, individual halibut lengths and inferred dispositions were available from halibut condition assessments and for which species composition data were available (773 in 2017, 1,148 in 2018, and 997 in 2019). For these hauls, an average of 7.13 halibut per haul were assessed (measured) and disposition inferred (Fig. 1). For each of these hauls, two estimates of the proportion of halibut retained are available, one based on data from the observer's composition samples and the other based on halibut in the biological specimen samples.

Hauls where assessed halibut were not selected randomly (selected opportunistically), hauls with two or fewer halibut in the biological specimen sample, and hauls where all halibut in the biological specimen sample were either retained or discarded (proportion discarded is either

zero or one based on the presence of a halibut assessment) were not included in the analysis. First, on some hauls the observer is unable to randomize the collection of halibut for collection of biological data (i.e., condition assessments); these hauls are not included in the analysis because of the lack of randomization. Second, hauls were excluded from the data when the biological specimen sample contained two or fewer halibut because the proportion of halibut discarded for the haul would be either zero or one based on the single halibut and with two halibut there are only three possible outcomes. Last, because the proportion of the number of halibut discarded, based on the presence of an assessment for halibut in the biological specimen samples, encompassed a wide range of values relative to the proportion of the number discarded determined during the observer's tally sample (Fig. 2), additional hauls were removed when the inferred disposition based on the presence of a halibut assessments indicated full retention or complete discard (proportion of halibut with an assessment was zero or one). After removing these hauls, there were 2,144 hauls (627 in 2017; 751 in 2018; 766 in 2019) remaining in the analysis dataset. Additionally, hauls where the observer tally showed either all or no halibut were discarded (based on species composition sample not by presence of condition assessment) were also removed from the analysis. The final dataset included hauls with data from both sample types, the biological specimen sample contained three or more halibut, and where the proportion of halibut retained was greater than zero and less than one based on both the presence of halibut assessments in the biological specimen sample and based on the number of retained halibut tallied by the observer during the species composition sample (tally period). This results in 1,579 hauls (475 in 2017; 560 in 2018; and 544 in 2019) being included in the analysis, which was split into training (2017-2018, 1,035 hauls) and testing data (2019, 544 hauls).

The proportion of numbers of halibut retained on a haul varied considerably between estimates based on the species composition sample data and the presence of assessments for halibut in the biological specimen samples (Fig. 2). This was not unexpected because different sampling methods are associated with the estimates. The number of halibut in the biological specimen samples was generally much smaller than the number encountered during species composition sampling. In addition, the disposition of halibut being inferred from the presence of a condition assessment (i.e., not directly measured by an observer) contributes to the differences in the estimates of proportion retained, which contributed to variability in the estimates of percent retained. The difference between these estimates, relative to proportion of the number

retained, decreased as the ratio of the number of halibut in the biological specimen sample to the number of halibut encountered in the composition samples increased, although we note there was a high degree of variability in the relationship (Fig. 2).

The conversion of the mean-weight-per-fish to the mean weight of discarded fish and the conversion of the proportion of the number retained to the proportion of the weight retained were both contingent on our ability to determine catch disposition (retained or discarded). For this reason, we pursued model development using data from halibut in the biological specimen sample where catch disposition could be inferred (i.e., based on the presence of a condition assessment). We assumed that for the species composition sample versus the biological specimen sample, the relationships between weight per fish discarded and total weight, and between proportion of the number and proportion of the weight retained were the same.

### Model Fitting and Selection

Two separate sets of models were developed to convert 1) the mean weight of fish to mean weight of discarded fish (Models W1 – W4) and 2) to convert the percent number retained to percent weight retained (Models PR1 – PR4). Both sets of conversion models used percent number retained and mean weight per fish as covariates.

#### *1. Conversion of mean weight per fish to mean weight per discarded fish*

The observed composition data showed that the mean weight per discarded halibut was stable over the range of percent numbers discarded; however, the mean weight of halibut increased with the percent number of halibut retained (Fig. 3). This result was not unexpected because as the proportion of the catch that is above the minimum size limit (i.e., retained halibut) decreases, the overall mean weight of halibut also decreased.

Looking only at data from assessed halibut, there was a high amount of variability in haul-specific mean halibut weights across the range of both mean weight per fish (Fig. 4; right panel) and percent retained values (Fig. 4; left panel). As evidenced by small  $R^2$  values, the mean weight per discarded halibut had a very weak positive relationship with the mean weight per halibut ( $R^2 = 0.023$ ,  $F = 24.66$  on 1 and 1,033 df, res. std. err. 0.26; Appendix A Model W1).

Similarly, the mean weight per discarded halibut had a very weak positive relationship with percent retained ( $R^2 = 0.023$ ,  $F = 24.65$  on 1 and 1,033 df, res. std. err. 0.26; Appendix A Model W2). In both cases, the covariate and intercept were statistically significantly different from zero based on a t-statistic with P-values  $< 0.001$  (Appendix A).

Although larger mean weights were associated with higher percent number retained, the mean weight per discarded fish did not vary greatly with either percent number retained or mean weight. The inclusion of both covariates did not improve the model fit ( $R^2 = 0.029$ ,  $F = 15.21$  on 2 and 1,032 df, res. std. err. 0.26; Appendix A Model W3), nor did inclusion of the interaction term ( $R^2 = 0.04$ ,  $F = 14.51$  on 2 and 1,032 df, res. std. err. 0.26; Appendix A Model W4). Model summaries and residual plots are presented in Appendix A.

Because there was little variation in mean weight per discarded fish with the mean weight per fish or with the mean weight per fish in combination with percent number retained, the ability to predict the mean weight of discarded halibut from these two variables was limited. The conversion of mean weight per fish (from total catch to discarded catch) was not pursued further; however, the conversion of percent number retained to percent weight retained was developed.

## *2. Conversion of Percent Numbers Retained to Percent Weight Retained*

There was a non-linear relationship between percent retained by weight and percent retained by number, with a larger mean weight per fish at higher retention levels (Fig. 5). This stronger relationship was used to develop a conversion between percent number and percent weight retained. The model fitting objectives were to 1) evaluate and model assumptions about distribution and variance structure of the data and 2) determine whether interaction terms substantially improved model fit.

In all four models, the models explained a substantial amount of the variance in the data: for both linear models, the  $R^2$  values were over 90% and there was a large reduction in deviance with the inclusion of covariates in the two GLM models. Individual terms were significant based on F-test (OLS models) and likelihood ratio tests (analysis of deviance, GLMs). For both main effects models, sampling year was included as a covariate; however, in both cases this term was insignificant (p-value = 0.3 in both the linear model and GLM). Sampling year was not

considered further during modeling. Inspection of residual patterns and examination of test-data predictions did not indicate poor model fit for any of the four models. The inclusion of an interaction term in the linear model increased the  $R^2$  value from 0.90 to 0.92. Addition of the interaction term to the GLM did not significantly increase the model fit (likelihood ratio test  $P$ -value = 0.5). Residual patterns for all models were found to be satisfactory and are presented along with model summaries in Appendix B.

To test the ex-sample predicative ability, the final conversion equation based on the 2017 and 2018 training data was applied to the test data collected in 2019 from assessed halibut and compared to actual percent weight retained estimated from the same assessed halibut (Table 1; Fig. 6, Appendix B). Linear regressions of the predicted percent weight retained against the actual values had  $R^2$  values of 0.83 for OLS models and 0.85 for GLMs. The root mean square error (RMSE) was computed as square root of the mean squared differences between the predicted values on their original scale (i.e., back-transformed) and the actual percent weight retained values (Table 1). The majority of predictions for the preferred model, Model PR3, were within 10 percentage points of the observed value (Fig. 6). For other models tested, the distribution of differences between predicted and observed values (5% and 95% percentiles) was larger and there was greater variability in the comparison of predicted and observed values (Table 1, Fig. 6, Appendix B).

Model PR3 was our preferred model because it had the best overall goodness of fit, better ex-sample (testing data) prediction than the linear model and, following principles of parsimony, the interaction term in Model PR4 did not improve fit enough to justify the added complexity. Further, an analysis of deviance (likelihood ratio test) revealed Models PR3 and PR4 to be statistically similar ( $P$ -value = 0.38).

### Evaluation of Bias

In order to assess the magnitude of the bias in estimated discard weight, we made predictions with Model PR3, the preferred model. The adjusted weight of discarded halibut was generated by multiplying the modeled predicted percent weight retained and the estimated catch of halibut for each haul (Fig. 7, left panel). A linear regression of the haul-specific adjusted estimated percent weight retained on the original estimate, through the origin, has a slope of 0.65



indicating that the original haul-specific estimates overestimated halibut discard by approximately 35%<sup>3</sup> (Fig. 7).

Additionally, adjusted discard estimates were compared to original estimates generated by CAS for each landing, indicating that a bias persists in the final estimates of discards (Fig. 7, right panel). Current methods overestimate discards of halibut in the directed fisheries by approximately 40%<sup>4</sup>.

## Discussion

The estimation of at-sea discards of halibut in the directed halibut fishery is constrained by a lack of data specific to the disposition of the catch. While implementing sampling methods that support the collection fish size independently for each catch disposition category would be the best solution to address this data collection gap, the space available for sampling activities and the development new fishery-specific sampling methods present significant challenges. The types of changes that would be needed are not trivial and would affect the ability for observers to meet other sampling goals and programing priorities. The analytical solution that we have proposed would correct for bias and would not require the logistical issues in the field.

Since observer workload leaves little time for other sampling activities, any changes to the sampling methods that would allow collection of fish size by disposition would result in decreasing other data collections such as collections of biological specimens (otoliths) from non-target species. Another consideration is the inability of the current database to house disposition-specific data without significant changes to the database structure. Observer data are transmitted while observers are deployed and automatically imported into the Observer Program database multiple times per day. The data entry software, database structure, and automated error checking systems would require changes in order to accommodate the new data.

Model PR3 was the preferred model because it had good predictive capability and relied solely on standard observer data collections conducted on sampled hauls. Moreover, the model

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<sup>3</sup> The bias is calculated as follows:  $[1 \text{ (perfect linear slope)} - 0.65 \text{ (regression slope)}] * 100 = 35\%$ .

<sup>4</sup> Calculated as  $[1 \text{ (perfectly linear slope)} - 0.60 \text{ (fitted slope)}] * 100 = 40\%$ .

and model formulation could easily be incorporated into the current estimation processes to correct for biases, and be periodically evaluated with new data to determine if the model needs updating. Under this model, the previous estimates of at-sea discard of halibut in the directed fisheries are overestimated by approximately 40%. Although the estimates of directed fishery discard is not currently used for quota management nor stock assessment; application of this conversion model will reduce the amount of bias in the directed halibut fishery discard estimates and thus increase their utility to stock assessors and other researchers.

Results from this study also suggest that the conversion of mean weight to mean retained weight per halibut would result in an estimate of the total weight of retained halibut for the haul and allow estimation of discarded halibut weight as the difference between estimated total halibut catch and estimated retained catch. However, because direct conversions of mean weight or percent retained are simpler to estimate and rely on a single conversion, the conversion of mean weight per halibut to mean weight per retained halibut was not pursued. Similarly, models to convert the mean weight of halibut to mean weight of discarded halibut did not have strong predictive ability and hence, models to predict mean weight per discarded halibut were not selected for further evaluation or testing.

### Changes to Estimation Protocol

Use of the proposed conversion would only require small changes to the at-sea discard estimation protocols, and no changes to data infrastructure or current observer sampling methods. For future implementation, we recommend the following changes be made:

- Use the observer's estimate of percent number retained for any hauls where either all halibut are retained or all halibut are discarded. In these cases, the percent weight retained and the percent number retained will be equal (i.e.,  $\%R_n = \%R_w = 0$  or  $100\%$ ).
- Use the GLM regression developed to convert the percent number retained recorded by observers to percent weight retained for each sampled haul where some, but not all, halibut are discarded using the following methodology:

- Estimate log-odds ratio of percent retained (P) using the preferred Model PR3:

$$P = \logOdds(\%R_w) = 3.620\%R_n + 0.108\bar{w} - 1.801$$

- Transform the log-odds ratio to estimate the percent weight retained:
 
$$\%R_w = \frac{\exp(P)}{\exp(1-P)}$$
- Convert %R only for hauls where  $\%R_n > 0$  and  $< 100$ .
- Incorporate adjusted percent retained values into the observer tables that are used to present haul-specific catch and bycatch estimate to data users. These are the tables accessed by the Catch Accounting System in the bycatch estimation processes.
- Although, there did not appear to be a year effect, we also recommend that the regression be evaluated with new data on a regular basis to ensure accurate predictability over time.

The IPHC is in the process of evaluating the minimum size limit for halibut (Stewart and Hicks 2018, Stewart et al. 2021). Implementing costly changes to observer sampling methods and data infrastructure now may be premature if the IPHC removes the minimum size limit in the near future. The analytic solution would be applicable before and unnecessary after a decision on size limit removal and hence be robust to future management changes.

Pacific halibut is the only groundfish species in Alaska with a regulatory minimum size limit. Because this directed fishery had not been monitored prior to 2013, data collection methods and database infrastructure were not developed for this situation and estimates of halibut discard computed using methods suitable for other species. Computation of estimates of halibut discard within the directed fishery were overestimated by approximately 40% (this study). The analytic method proposed under our preferred model is unbiased, simple to implement, and does not require changes to established protocols.



## **Acknowledgments**

We extend our gratitude to the many professional fisheries observers who collect these data to support sustainable fisheries in Alaska. This manuscript benefitted from comments provided by Dr. Ian Stewart, Dr. Kari Fenske, and Ms. Jennifer Mondragon.



Table 1 -- Model results for the four conversions of  $P_n$  to  $P_w$  that we tested. Note that  $P_n$  = proportion retained by number,  $P_w$  = proportion retained by weight, and  $\bar{w}$  = mean weight per halibut. Training dataset included trimmed data from 2017 and 2018, and the testing data was trimmed data from 2019. Residual standard errors and degrees of freedom (df) are provided for OLS models fit to training data while residual deviance is presented for GLMs. Deviance for both GLM null models ( $y = 1$ ) was 224.38 on 1034 df. Regressions of predicted values on actual values for the 2019 testing data were all significant (P-value < 0.001) with  $R^2$  values for both OLS models = 0.83 and for both GLMs = 0.85. Intercept and slope values are presented along with RMSE.

Model	Model Number	Fitted Coefficients	Training Res Std. Error (lm) or Res Deviance (glm)	Testing RMSE, (lm intercept, slope)
Linear Model $P_w = \sqrt{y}$	PR1	$y = P_w^2 = 0.895P_n + 0.016\bar{w} - 0.078$	0.084 on 1,032 df	0.0749 (0.11, 0.85)
	PR2	$y = P_w^2 = 1.261P_n + 0.048\bar{w} - 0.046(P_n\bar{w}) - 0.318$	0.075 on 1,031 df	0.0753 (0.08, 0.89)
GLM $P_w = \frac{y}{1-y}$	PR3 (preferred)	$y = \logOdds(P_w)$ $= 3.620P_n$ $+ 0.108\bar{w} - 1.801$	20.67 on 1,032 df	0.0725 (0.06, 0.92)
	PR4	$y = \logOdds(P_w)$ $= 4.200P_n$ $+ 0.150\bar{w}$ $- 0.072(P_n\bar{w})$ $- 2.104$	20.31 on 1,031 df	0.0727 (0.05, 0.92)

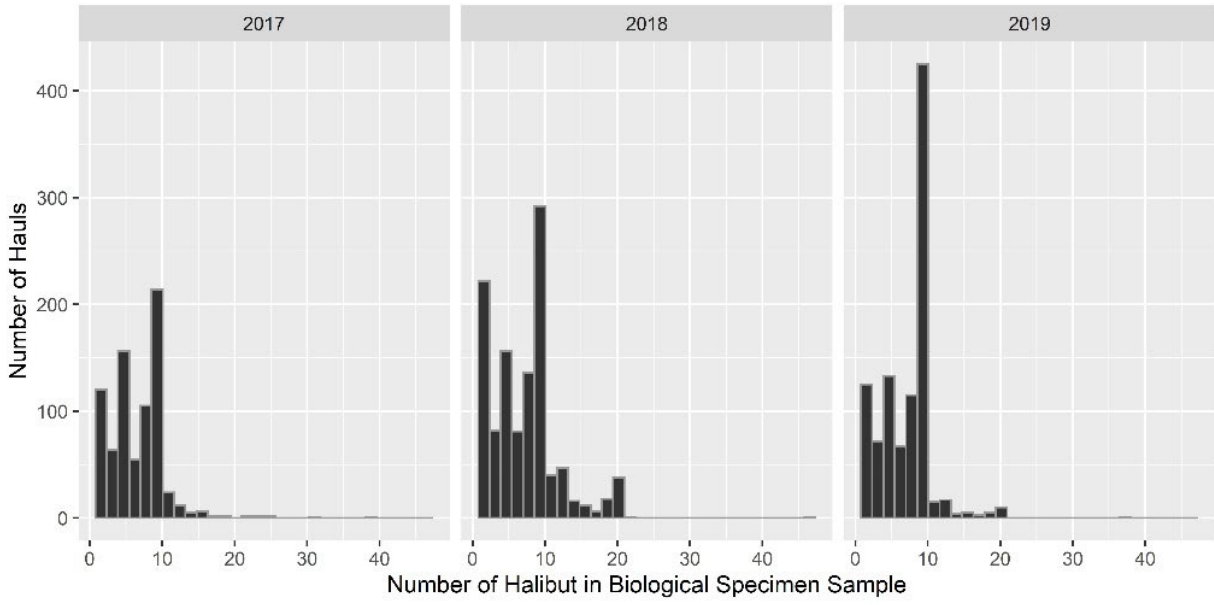


Figure 1 -- Distribution of number of assessed halibut per haul for 2017, 2018, and 2019.



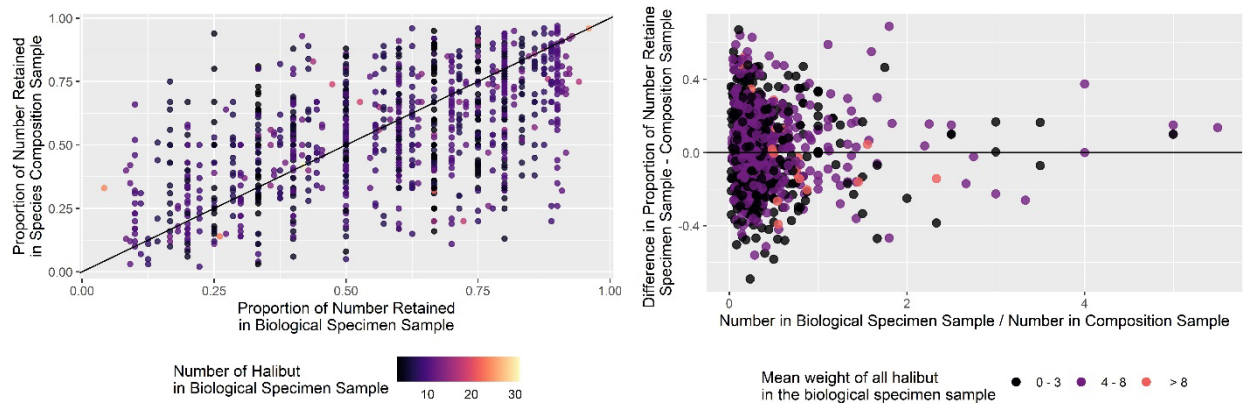


Figure 2 -- Comparison of proportion of halibut assessed and proportion of halibut in species composition samples. Left panel: Comparison of estimated proportion of the number of halibut retained based on composition sample (y-axis) and biological specimen sample data (x-axis). Right panel: Difference between the estimated proportion of the number of halibut retained as a function of the ratio of the number of halibut in the biological specimen sample to the number encountered in the composition sample. Since these samples are independent, the ratio of assessed halibut to halibut encountered in the species composition sample may exceed one.

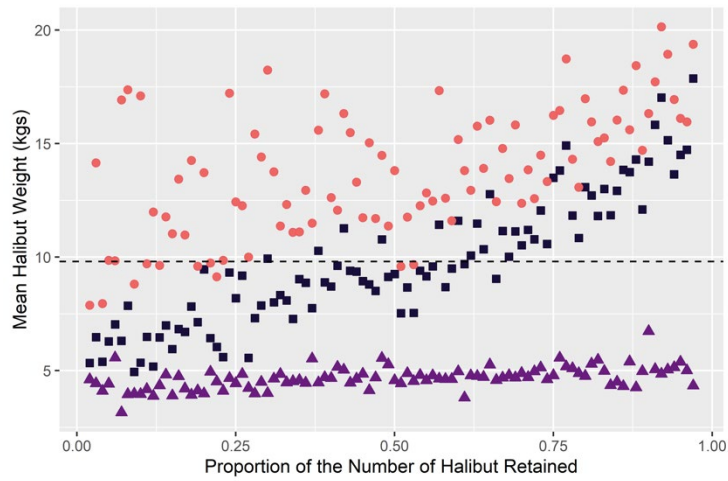


Figure 3 -- Mean weight of halibut based on assessed fish as a function of the percent of halibut retained (by number) based on species composition sample data. Mean weight is estimated across all hauls within a percentage retained (i.e., one mean weight for each percent retained value). Mean halibut weight for all size classes is indicated by the black squares, red circles indicate the mean weight per retained halibut, and purple triangles indicate mean weight per discarded halibut. The dotted line references the overall average combined mean halibut across all percent retained values.

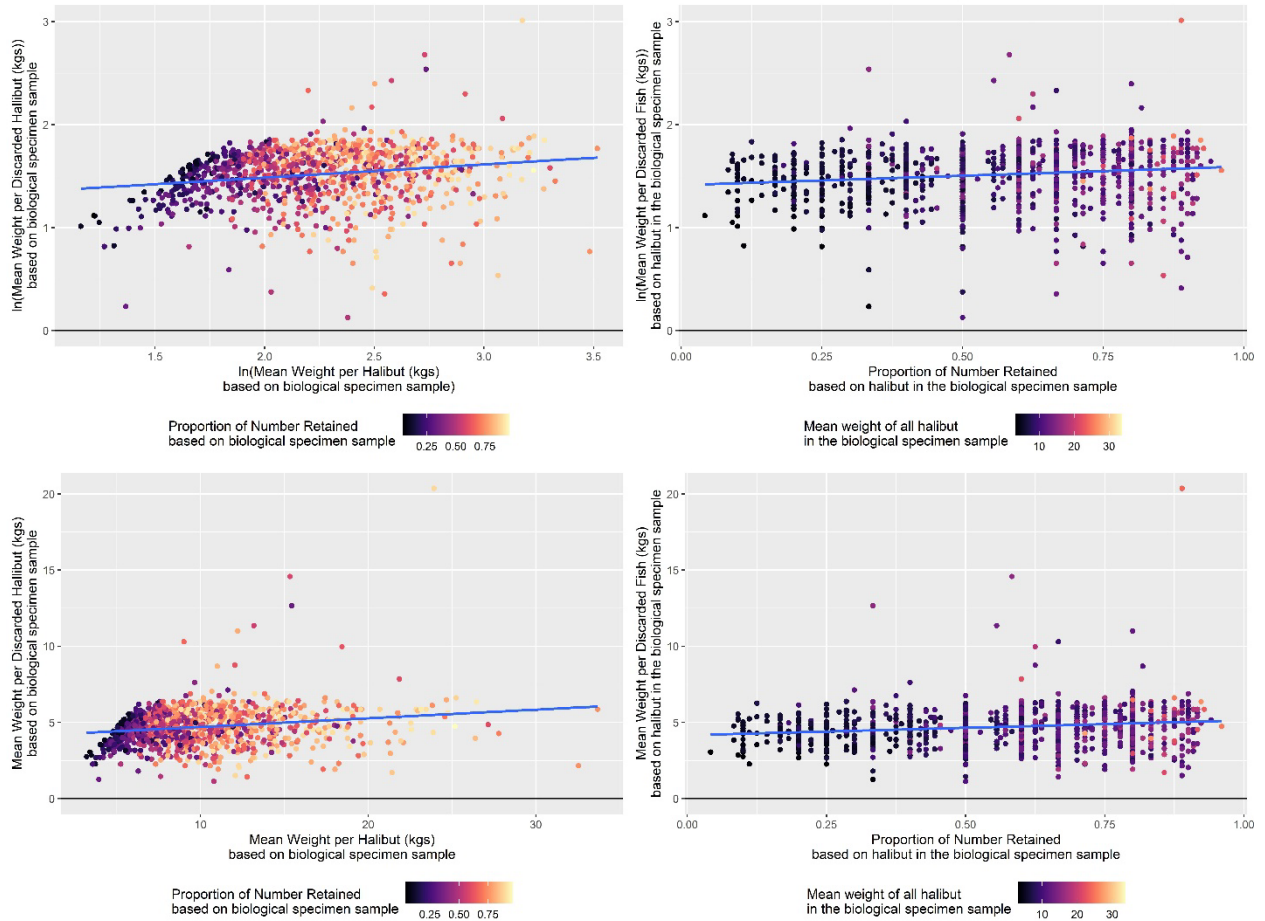


Figure 4 -- Natural log of mean weight per discarded halibut as a function of the natural log of overall mean weight per halibut and colored by the percent number retained (left panels) and as a function of proportion retained by number colored by natural log of the overall mean weight per halibut (right panels). Upper panels depict the transformed data while the lower panels show results on the original scale of the data. Each data point represents haul-specific values based on assessed halibut. Blue lines on the upper panels are the linear fit of the natural log of mean weight of discarded halibut on the mean weight per halibut (upper left) and proportion retained by number (upper right), Blue lines on the lower panels (untransformed data) are the linear fit of the mean weight of discarded halibut to the mean weight per halibut (lower left) and proportion retained by number (lower right).

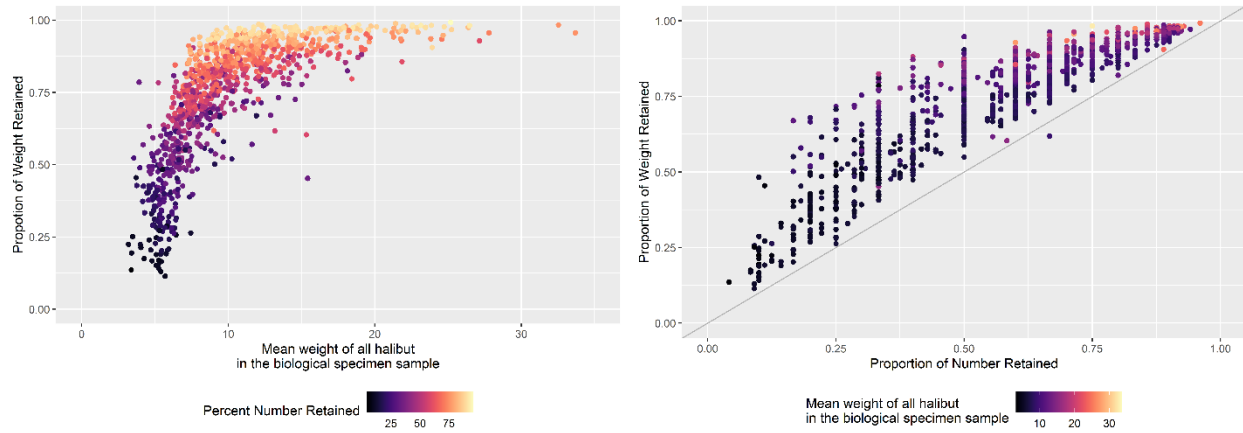


Figure 5 -- Percent weight retained as function of mean weight per fish (left) and percent number retained (right). Each data point represents a haul. The color of the data points reflects the percent number retained in the left panel and the mean weight per fish in the right panel for the haul. The reference line in the right panel is where the percent weight retained equals the percent number retained (i.e., slope = 1 and intercept = 0).

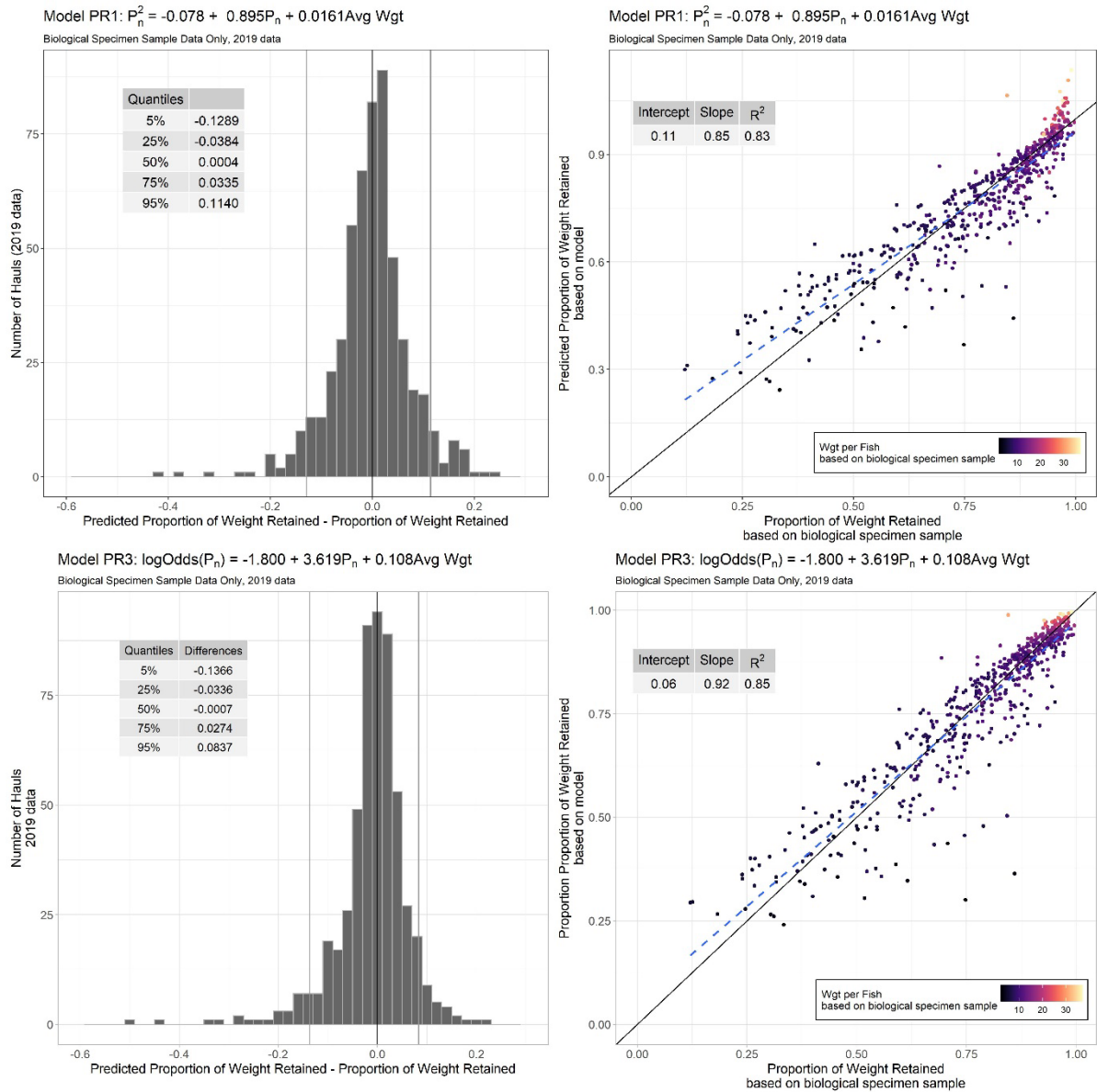


Figure 6 -- Distribution of differences between predicted and actual percent weight retained (left) and comparison of predicted and observed values (right) for Model PR1 (top) and Model PR3 (lower). Grey reference line on histogram (left panels) indicate the 5<sup>th</sup> and 95<sup>th</sup> quantiles. One-to-one (solid grey) and least squares regression fit (blue dashed) lines are included on scatter plots (right panels). Model testing results for Models PR2, and PR4 are included in Appendix A.

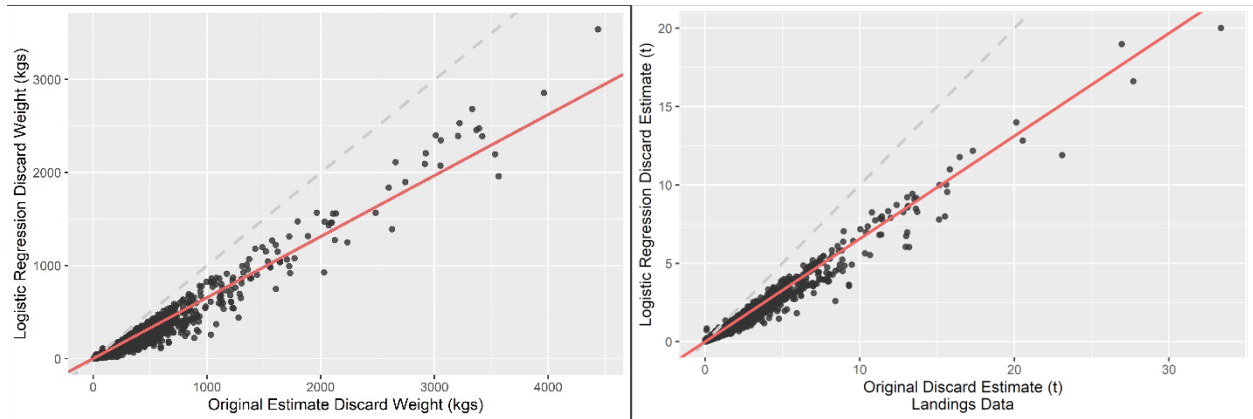


Figure 7 -- Comparison of adjusted and original estimates of halibut discard weight. Each data point represents the estimates for kilograms of discard for individual hauls (left panel) and tons of discards for individual fishing trips (deliveries, right panel). The dashed grey line is a 1:1 line through the origin, and the solid red line is the linear model fit the prediction.

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## Appendix A: Output Model Summaries for Conversion of Mean Weight per Halibut

*Model W1*:  $\ln(\text{mean weight per discarded halibut}) = a + b_1 \%R_n$

This model is fit using ordinary least squared (OLS) regression without inclusion of an interaction term. The response variable (mean weight per discarded halibut) is log transformed (using the natural log) so that the regression is linear. The model is fit using the `lm` function in R (R Core Team 2020).

### Summary of Model Results

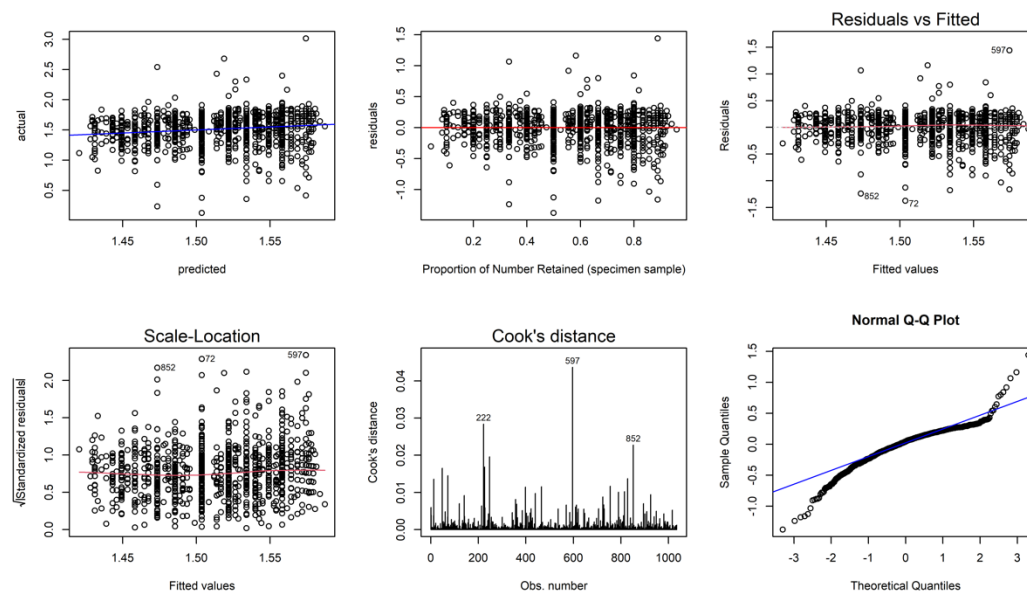
Distribution of Residuals:

Min	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Max
-1.37706	-0.12608	0.04265	0.17398	1.43981

Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	1.41296	0.02244	62.974	< 2e-16
$\%R_n$ ( $b_1$ )	0.18162	0.03658	4.964	8.06e-07

Residual standard error: 0.2637 on 1033 degrees of freedom  
 Multiple R-squared: 0.0233, Adjusted R-squared: 0.02236  
 F-statistic: 24.65 on 1 and 1033 DF, p-value: 8.056e-07



*Residual plots for Model W1:  $\ln(\text{mean weight/halibut}) = \text{percent number retained}$ .*

Model W2:  $\ln(\text{mean weight per discarded halibut}) = a + b_1(\text{mean weight per fish})$

This model is fit using ordinary least squared (OLS) regression without inclusion of an interaction term. The response variable (mean weight per discarded halibut) is log transformed (using the natural log) so that the regression is linear. The covariate is  $\%R_n$ . The covariate is the mean weight per fish. The model is fit using the lm function in R (R Core Team 2020).

**Summary of Model Results**

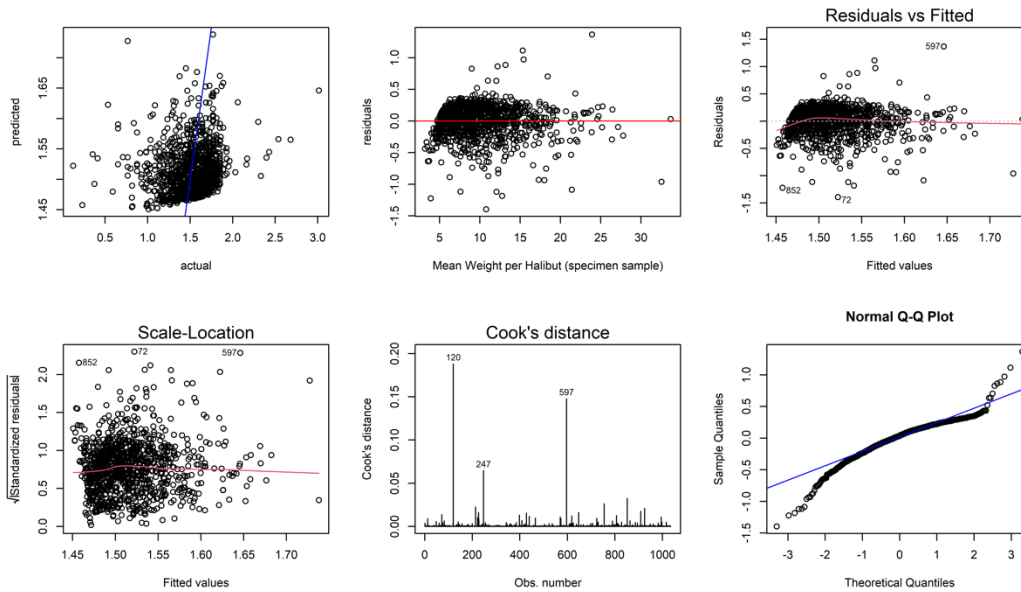
Distribution of Residuals:

Min	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Max
-1.39565	-0.13296	0.03475	0.17380	1.36809

Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	1.420631	0.021001	67.645	<2e-16
Mean Weight / assessed halibut (b <sub>1</sub> )	0.009427	0.001898	4.966	8e-07

Residual standard error: 0.2637 on 1033 degrees of freedom  
 Multiple R-squared: 0.02331, Adjusted R-squared: 0.02237  
 F-statistic: 24.66 on 1 and 1033 DF, p-value: 8.003e-07



Residual plots for Model W2:  $\ln(\text{mean weight/halibut}) = \text{mean weight} / \text{halibut}$ .

*Model W3*:  $\ln(\text{mean weight per discarded halibut}) = a + b_1(\%R_n) + b_2(\text{mean weight per fish})$

This model is fit using ordinary least squared (OLS) regression without inclusion of an interaction term. The response variable (mean weight per discarded halibut) is log transformed (using the natural log) so that the regression is linear. The covariates are both  $\%R_n$  and the mean weight per fish. The model is fit using the `lm` function in R (R Core Team 2020).

### Summary of Model Results

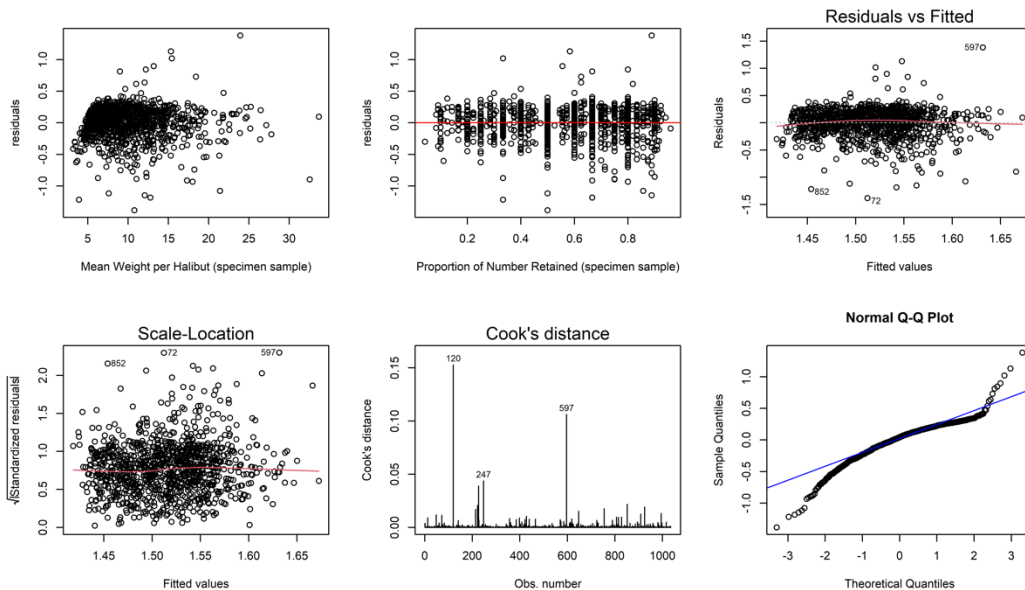
Distribution of Residuals:

Min	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Max
-1.38554	-0.12486	0.04079	0.17231	1.38255

Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	1.393990	0.023764	58.661	<2e-16
$\%R_n$ ( $b_1$ )	0.111503	0.046911	2.377	0.0176
Mean Weight / assessed halibut ( $b_2$ )	0.005793	0.002434	2.380	0.0175

Residual standard error: 0.2631 on 1032 degrees of freedom  
 Multiple R-squared: 0.02863, Adjusted R-squared: 0.02675  
 F-statistic: 15.21 on 2 and 1032 DF, p-value: 3.091e-07



*Residual plots for Model W3:  $\ln(\text{mean weight/halibut}) = \text{percent number retained} + \text{mean weight/halibut}$ .*

*Model W4*:  $\ln(\text{mean weight per discarded halibut}) = a + b_1(\%R_n) + b_2(\text{mean weight per fish}) + b_3(\%R_n) (\text{mean weight per fish})$

This model is fit using ordinary least squared (OLS) regression with inclusion of an interaction term. The response variable (mean weight per discarded halibut) is log transformed (using the natural log) so that the regression is linear. The covariates are  $\%R_n$ , the mean weight per fish, and the interaction between  $\%R_n$  and the mean weight per fish. The model is fit using the `lm` function in R (R Core Team 2020).

### Summary of Model Results

Distribution of Residuals:

Min	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Max
-1.41640	-0.12493	0.03996	0.17814	1.47849

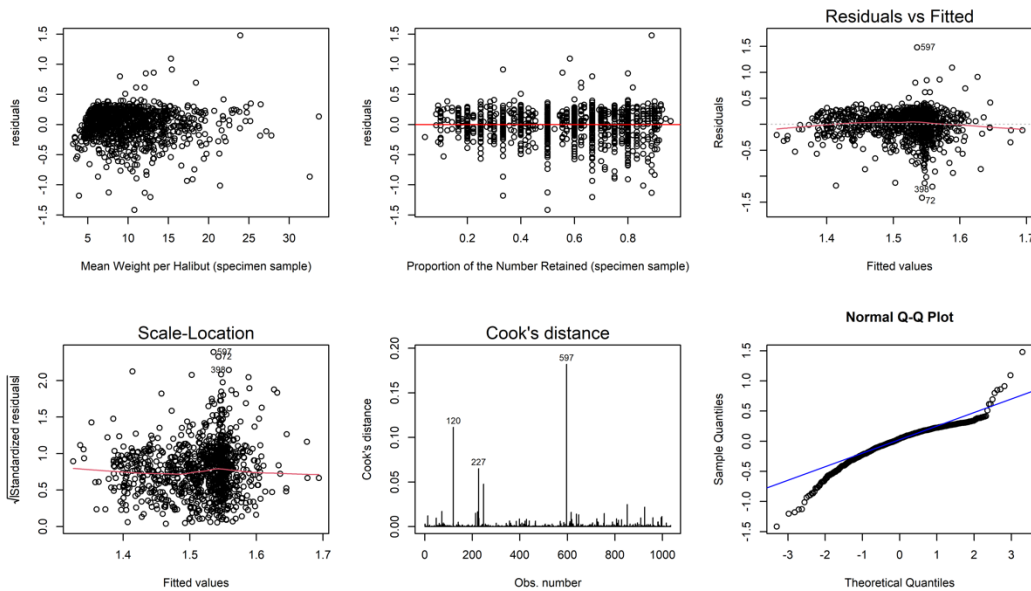
Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	1.211471	0.056286	21.523	< 2e-16
$\%R_n$ ( $b_1$ )	0.390443	0.090947	4.293	1.93e-05
Mean Weight / assessed halibut ( $b_2$ )	0.030121	0.007227	4.168	3.33e-05
$\%R_n * \text{Mean Weight / assessed halibut}$ ( $b_1 * b_2$ )	-0.034959	0.009785	-3.573	0.00037

Residual standard error: 0.2616 on 1031 degrees of freedom

Multiple R-squared: 0.04051, Adjusted R-squared: 0.03772

F-statistic: 14.51 on 3 and 1031 DF, p-value: 2.91e-09



*Residual plots for Model W4*:  $\ln(\text{mean weight/halibut}) = \text{percent number retained} + \text{mean weight/halibut} + \text{interaction}$ .

## Appendix B: Output Model Summaries for Conversion of Percent Number Retained

*Model PR1* is fit using ordinary least squared (OLS) without inclusion of an interaction term. The response variable (percent weight retained,  $\%R_w$ ) is squared (transformed) so that the regression is linear. The model is fit using the `lm` function in R (R Core Team 2020).

Model PR1:  $(\%R_w)^2 = a + b_1 \%R_n + b_2$  (mean weight per halibut)

### Summary of Model Results

Distribution of Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.327	-0.055	-0.004	0.047	0.354

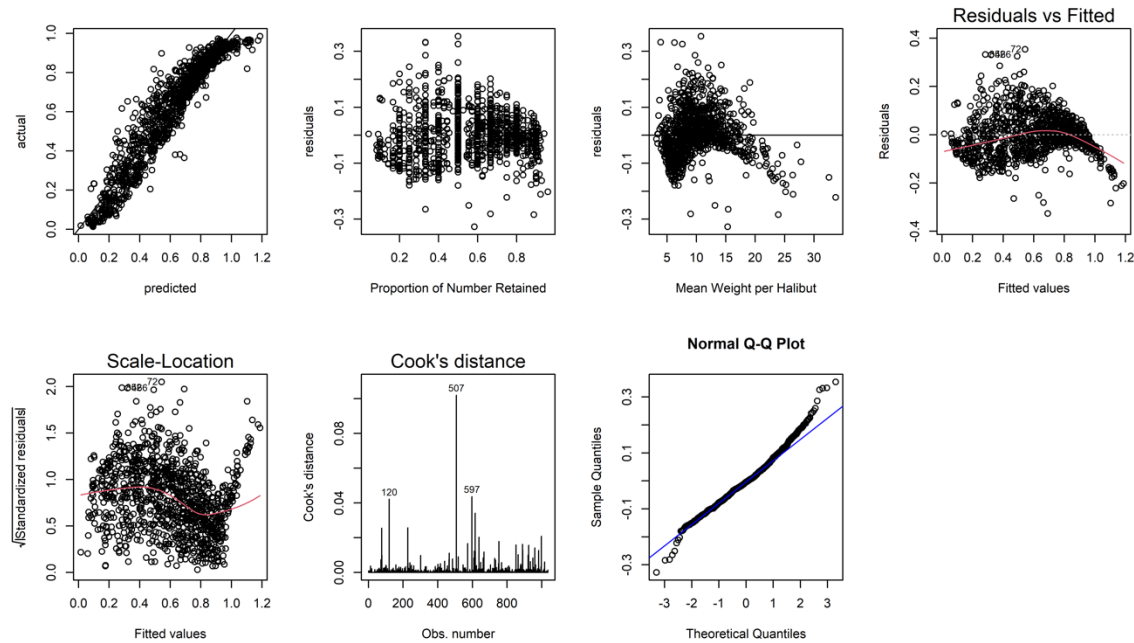
Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	-0.078	0.0076	-10.19	<2e-16
$\%R_n$ ( $b_1$ )	0.895	0.0150	59.58	<2e-16
Mean Weight / halibut ( $b_2$ )	0.016	0.0008	20.70	<2e-16

Residual standard error: 0.08419 on 1032 degrees of freedom

Multiple R-squared: 0.8985, Adjusted R-squared: 0.8983

F-statistic: 4566 on 2 and 1032 DF, p-value: < 2.2e-16



Residual plots for percent retained Model PR1:  $(\%R_w)^2 = a + b_1 \%R_n + b_2$  (mean weight per halibut)

Model PR1: Regression of predicted values on actual 2019 training data

Model PR1 predicted percent weight retained based on 2019 training data (assessed halibut) regressed against actual percent weight retained using ordinary least squared (OLS) methods.

**Summary of Regression Results**

Distribution of Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.402	-0.031	0.013	0.041	0.233

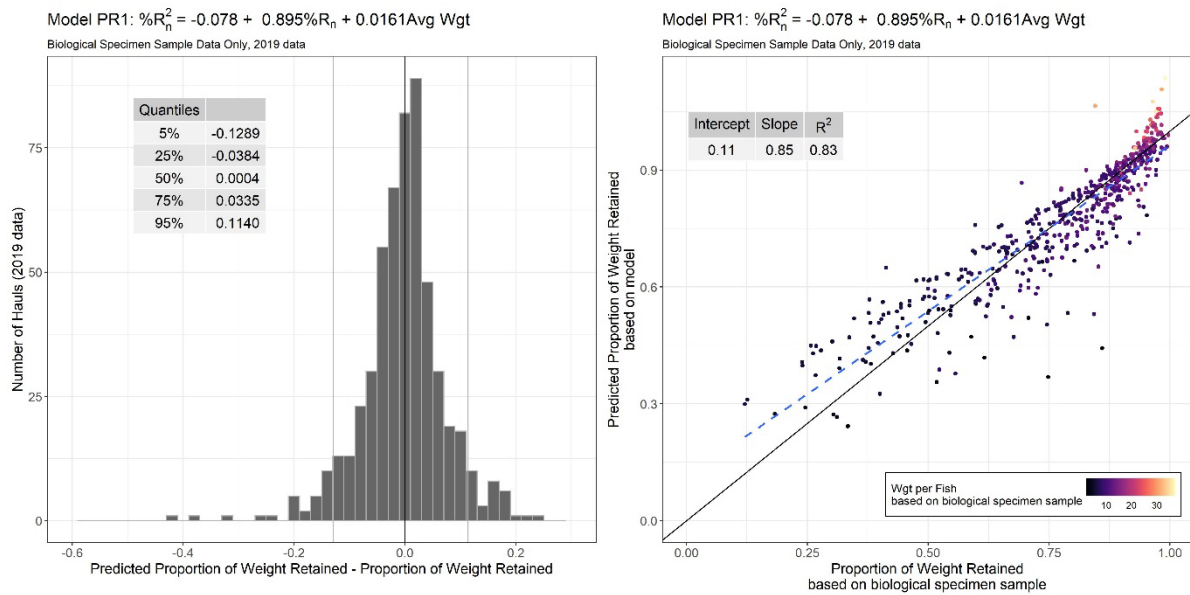
Estimated Coefficients, standard error of estimates, and significance test for intercept = 0 and slope =1:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	0.112	0.0132	8.55	<2e-16
%R <sub>w</sub> (b <sub>1</sub> )	0.851	0.0164	6.07	2.37e-09

Residual standard error: 0.06986 on 542 degrees of freedom

Multiple R-squared: 0.832, Adjusted R-squared: 0.8317

F-statistic: 2684 on 1 and 542 DF, p-value: < 2.2e-16



*Distribution of differences between predicted and actual percent weight retained (left) and comparison of predicted and observed values (right) for Model PR1. Grey reference line on histogram (left panels) indicate the 5<sup>th</sup> and 95<sup>th</sup> quantiles. One-to-one (solid grey) and least squares regression fit (blue dashed) lines are included on scatter plots (right panels).*

Model PR2 is fit using ordinary least squared (OLS) with inclusion of an interaction term. The response variable (percent weight retained,  $\%R_w$ ) is squared (transformed) so that the regression is linear. The model is fit using the lm function in R (R Core Team 2020).

Model PR2:  $(\%R_w)^2 = a + b_1 \%R_n + b_2$  (mean weight per halibut) +  $b_3 (\%R_n)$  (mean weight per halibut)

**Summary of Model Results**

Distribution of Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.404	-0.042	-0.0008	0.040	0.385

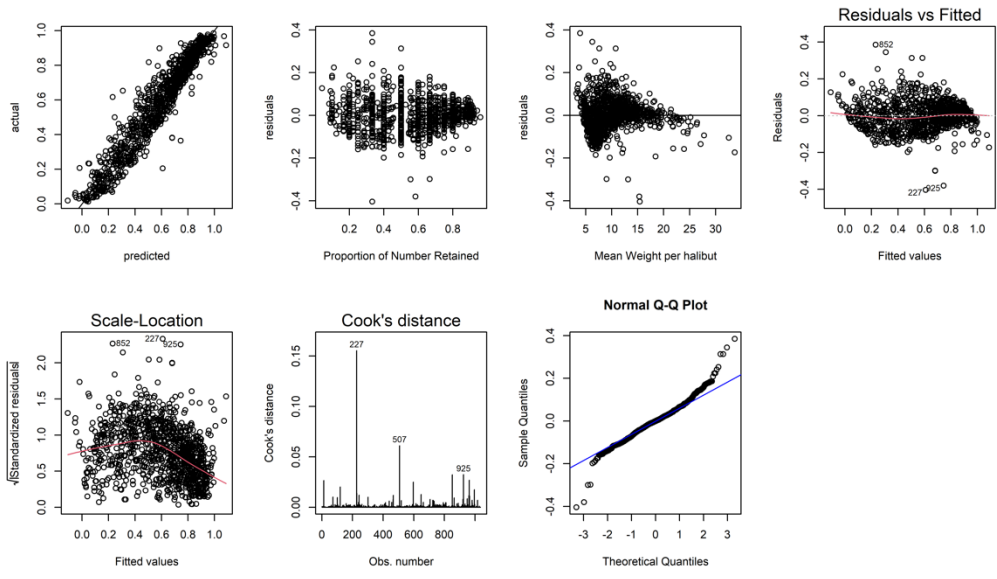
Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	-0.318	0.0161	-19.67	<2e-16
$\%R_n$ ( $b_1$ )	1.261	0.0261	48.36	<2e-16
Mean Weight / halibut ( $b_2$ )	0.048	0.0021	23.22	<2e-16
$\%R_n$ * Mean Weight / halibut ( $b_1 * b_2$ )	-0.046	0.0028	-16.38	<2e-16

Residual standard error: 0.07503 on 1031 degrees of freedom

Multiple R-squared: 0.9194, Adjusted R-squared: 0.9192

F-statistic: 3922 on 3 and 1031 DF, p-value: < 2.2e-16



Residual plots for percent retained Model PR2



Model PR2: Regression of predicted values on actual 2019 training data

Model PR2 predicted percent weight retained based on 2019 training data (assessed halibut) regressed against actual percent weight retained using ordinary least squared (OLS) methods.

**Summary of Regression Results**

Distribution of Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.613	-0.021	0.012	0.035	0.206

Estimated Coefficients, standard error of estimates, and significance test for intercept = 0 and slope =1:

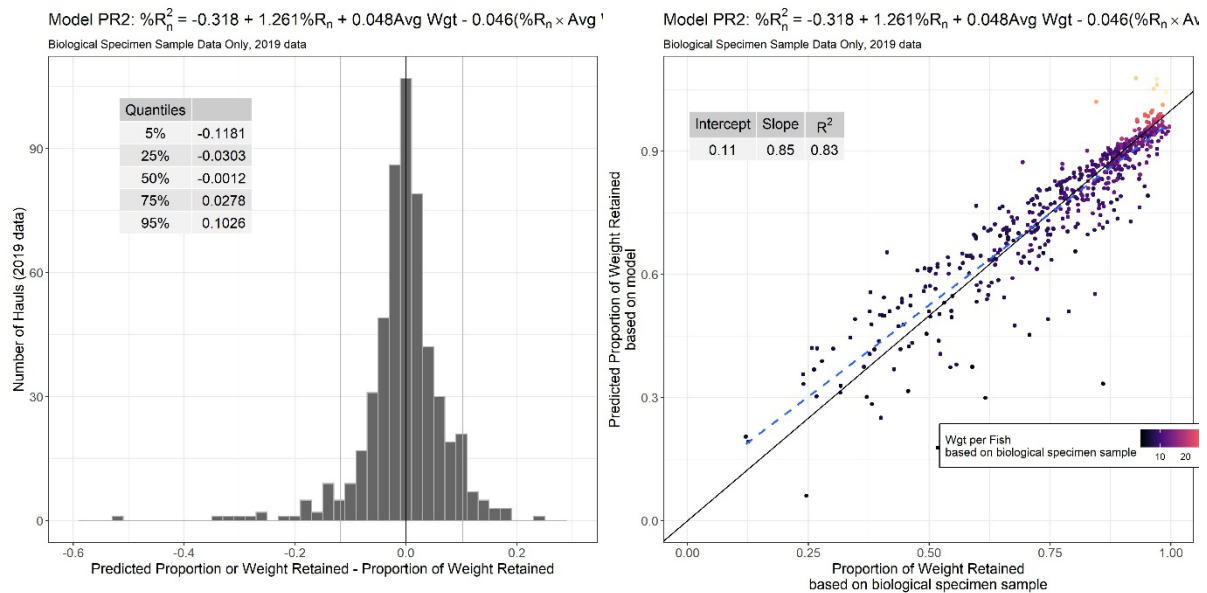
	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	0.079	0.0142	5.576	3.89e-08
%R <sub>w</sub> (b <sub>1</sub> )	0.893	0.0177	9.052	<2e-16

Residual standard error: 0.07311 on 538 degrees of freedom

(4 observations deleted due to missingness)

Multiple R-squared: 0.8254, Adjusted R-squared: 0.8251

F-statistic: 2543 on 1 and 538 DF, p-value: < 2.2e-16



*Distribution of differences between predicted and actual percent weight retained (left) and comparison of predicted and observed values (right) for Model PR2. Grey reference line on histogram (left panels) indicate the 5<sup>th</sup> and 95<sup>th</sup> quantiles. One-to-one (solid grey) and least squares regression fit (blue dashed) lines are included on scatter plots (right panels).*



*Model PR3* is fit using generalized linear models (GLM) with a logit link (family – quasi-binomial). The response variable is the log-odds of percent weight retained,  $\text{LogOdds}(\%R_w)$ . The covariates are the  $\%R_n$ , the mean weight per fish. The model is fit using the `glm` function in R (R Core Team 2020).

Model PR3:  $\text{LogOdds}(\%R_w) = P = a + b_1 \%R_n + b_2$  (mean weight per halibut)

$$\%R_w = \exp(P)/\exp(1-P)$$

### Summary of Model Results

Distribution of Deviance Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.69385	-0.08397	-0.00381	0.08302	0.67014

Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	-1.800631	0.033651	-53.51	<2e-16
$\%R_n$ ( $b_1$ )	3.619399	0.069967	51.73	<2e-16
Mean Weight / halibut ( $b_2$ )	0.108431	0.004548	23.84	<2e-16

(Dispersion parameter for quasi-binomial family taken to be 0.02013808)

Null deviance: 224.380 on 1034 degrees of freedom

Residual deviance: 20.671 on 1032 degrees of freedom

Number of Fisher Scoring iterations: 5

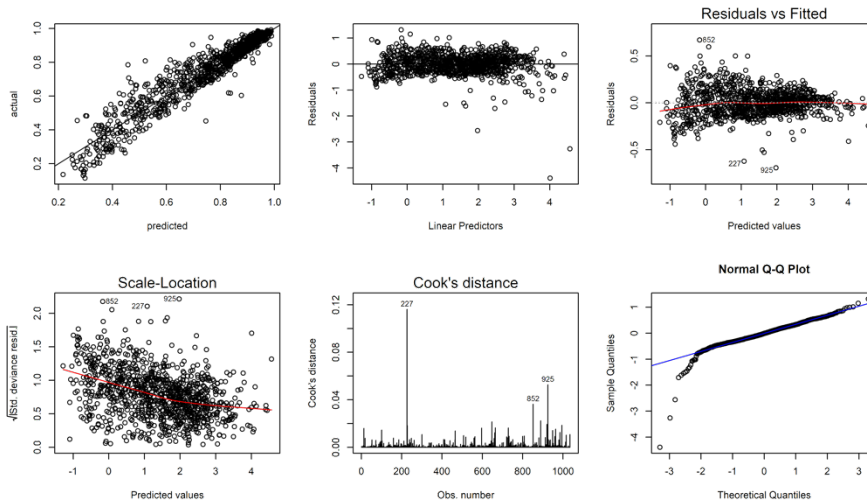
*P-value for Model 3 fit (small p-value (5.8e-45) favors full model over null model):*

for  $X \sim \chi^2_{(1034 - 1032)}$ ,  $P(X > 20.671) = 5.8e-45$

### Summary of Overall Model Fit

Analysis of Deviance Table (terms added sequentially, first to last):

	df	Deviance	Residual Df	Residual Deviance	P(>Chi)
Intercept (a)			1034	224.380	
$\%R_n$ ( $b_1$ )	1	190.756	1033	33.624	<2e-16
Mean Weight / halibut ( $b_2$ )	1	12.953	1032	20.671	<2e-16



*Residual plots for percent retained Model PR3*

Model PR3: Regression of predicted values on actual 2019 training data

Model PR3 predicted percent weight retained based on 2019 training data (assessed halibut) regressed against actual percent weight retained using ordinary least squared (OLS) methods.

**Summary of Regression Results**

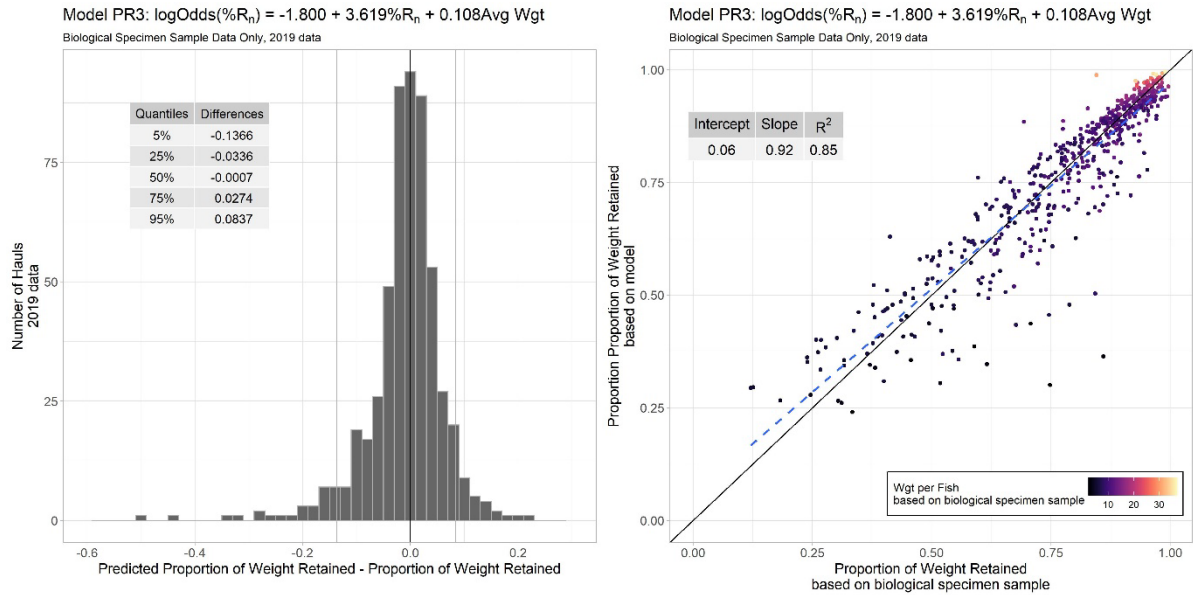
Distribution of Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.480	-0.020	0.014	0.040	0.195

Estimated Coefficients, standard error of estimates, and significance test for intercept = 0 and slope =1:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	0.056	0.0132	4.233	2.71e-05
%R <sub>w</sub> (b <sub>1</sub> )	0.916	0.0165	5.093	4.87e-07

Residual standard error: 0.07033 on 542 degrees of freedom  
 Multiple R-squared: 0.8497, Adjusted R-squared: 0.8494  
 F-statistic: 3064 on 1 and 542 DF, p-value: < 2.2e-16



*Distribution of differences between predicted and actual percent weight retained (left) and comparison of predicted and observed values (right) for Model PR3. Grey reference line on histogram (left panels) indicate the 5<sup>th</sup> and 95<sup>th</sup> quantiles. One-to-one (solid grey) and least squares regression fit (blue dashed) lines are included on scatter plots (right panels).*

*Model PR4* is fit using generalized linear models (GLM) with a logit link (family: quasi-binomial). The response variable is the log-odds of percent weight retained,  $\text{LogOdds}(\%R_w)$ . The covariates are the  $\%R_n$ , the mean weight per fish, and the interaction term. The model is fit using the `glm` function in R (R Core Team 2020).

Model PR4:  $\text{LogOdds}(\%R_w) = P = a + b_1 \%R_n + b_2 (\text{mean weight/halibut}) + b_3 \%R_n (\text{mean weight/halibut})$   
 $\%R_w = \exp(P)/\exp(1-P)$

**Summary of Model Results**

Distribution of Deviance Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.702	-0.084	0.0004	0.084	0.692

Estimated Coefficients, standard error of estimates, and significance test for individual coefficients = 0:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	-2.104	0.0784	-26.835	< 2e-16
$\%R_n$ ( $b_1$ )	4.196	0.1502	27.945	< 2e-16
Mean Weight / halibut ( $b_2$ )	0.150	0.0107	14.055	< 2e-16
$\%R_n * \text{Mean Weight / halibut}$ ( $b_1 * b_2$ )	-0.072	0.0167	-4.327	1.66e-05

(Dispersion parameter for quasi-binomial family taken to be 0.01980871)

Null deviance: 224.380 on 1034 degrees of freedom

Residual deviance: 20.306 on 1031 degrees of freedom

Number of Fisher Scoring iterations: 6

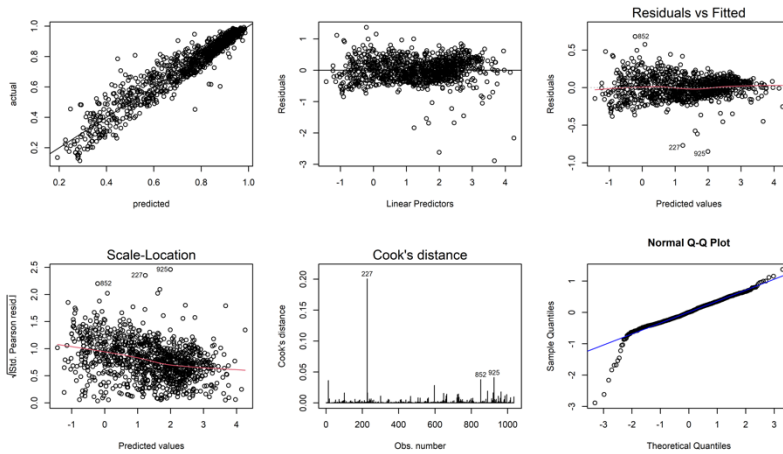
*P-value for Model 4 fit (small p-value (5.5e-44) favors full model over null model):*

for  $X \sim \chi^2_{(1034 - 1031)}$ ,  $P(X > 20.306) = 5.5e-44$

**Summary of Overall Model Fit**

Analysis of Deviance Table (terms added sequentially, first to last):

	df	Deviance	Residual Df	Residual Deviance	P(>Chi)
Intercept (a)			1034	224.380	
$\%R_n$ ( $b_1$ )	1	190.756	1033	33.624	< 2.2e-16
Mean Weight / halibut ( $b_2$ )	1	12.953	1032	20.671	< 2.2e-16
$\%R_n * \text{Mean Weight / halibut}$ ( $b_1*b_2$ )	1	0.364	1031	20.306	1.79e-05



*Residual plots for percent retained Model PR4*

Analysis of deviance did not support inclusion of an interaction term (i.e. did not support Model PR4 over Model PR3). Small change in deviance with the addition of the interaction term yielded large P-value (0.55) which favors the reduced model over the model with the interaction.

Analysis of Deviance Table: Model 3, Model 4

	Residual Df	Residual Deviance	df	Deviance	P(>Chi)
Model 3	1032	20.671	1		
Model 4	1031	20.306	1	0.365	0.55

Model PR4: Regression of predicted values on actual 2019 training data

Model PR4 predicted percent weight retained based on 2019 training data (assessed halibut) were regressed against actual percent weight retained using ordinary least squared (OLS) methods.

Summary of Regression Results

Distribution of Residuals:

Minimum	1 <sup>st</sup> Quartile	Median	3 <sup>rd</sup> Quartile	Maximum
-0.500	-0.017	0.014	0.038	0.201

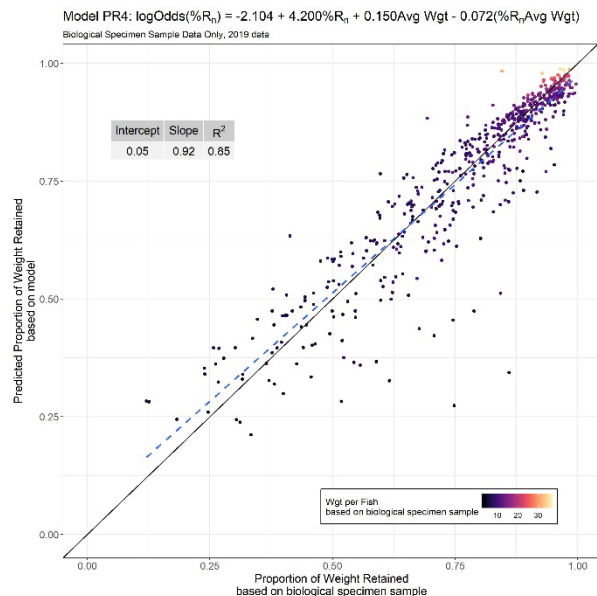
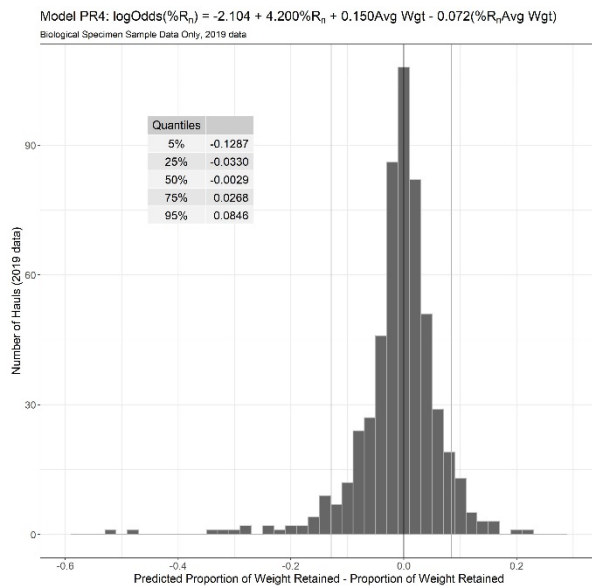
Estimated Coefficients, standard error of estimates, and significance test for intercept = 0 and slope =1:

	Estimate	Std. Error	t value	Pr(> t )
Intercept (a)	0.053	0.0133	3.996	7.32e-05
%R <sub>w</sub> (b <sub>1</sub> )	0.920	0.0166	4.841	1.69e-06

Residual standard error: 0.07067 on 542 degrees of freedom

Multiple R-squared: 0.8495, Adjusted R-squared: 0.8493

F-statistic: 3060 on 1 and 542 DF, p-value: < 2.2e-16



Distribution of differences between predicted and actual percent weight retained (left) and comparison of predicted and observed values (right) for Model PR4. Grey reference line on histogram (left panels) indicate the 5<sup>th</sup> and 95<sup>th</sup> quantiles. One-to-one (solid grey) and least squares regression fit (blue dashed) lines are included on scatter plots (right panels).



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