Procedures for calculating discard mortality rates for Pacific halibut

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Summary

Discard mortality rates (DMRs) for Pacific halibut are needed to estimate the fraction of the discarded halibut which die from the capture/handling/discard process. Fishery observers sample halibut immediately prior to discard, using a dichotomous key to identify injuries and body condition to determine viability. The resulting vessel sample data are extrapolated up to target fishery, which are then used to estimate fishery DMRs. Three data sets are obtained from the North Pacific Observer Program, which undergo some reformatting and merging to align the data into a layout from which DMRs are calculated.

Background

Discard mortality rates (DMRs) were first investigated by Hoag (1975), when he examined the survival of halibut released from trawl vessels. An approach was developed in which stress could be measured by the degree of physical activity at the time of release. Using body condition and opercular movement, the release viability of a halibut could be placed into one of five distinct condition categories. Survival of released fish was subsequently estimated by tagging the fish prior to release, and using the ratio of recovery rates of each condition category to the recovery rate of fish in the best condition. Based on data from halibut tagged on trawl vessels off British Columbia, Hoag concluded that survival "was probably close to 50%". Subsequent analyses by IPHC used an assumed DMR of 50%, or 0.50, for all trawl fisheries.

By 1990, all foreign and joint venture fishing for groundfish off Alaska had been mostly replaced by U.S. vessels. Fishery observers were tasked with sampling the discarded halibut for release viability. IPHC was interested in a more accurate estimate of mortality than what an assumed DMR would provide, so observer data were analyzed by Williams (1990) and Wilderbuer (1991) to calculate DMRs for those sampled fisheries, using approaches similar to Hoag's. As halibut bycatch management employed mortality limits, calculating trawl DMRs became an annual exercise by IPHC, to be used both internally by IPHC and by NMFS in monitoring inseason bycatch against the trawl bycatch mortality limits.

DMR estimation procedures were subsequently developed for longlines and groundfish pots. The procedures follow the same general approaches as used for trawl gear, i.e., mortality rates are applied to viability factors. The initial longline approach was based on body condition criteria, similar to trawl procedures. The approach was revised by Kaimmer and Trumble (1998) based on the results of a comprehensive tagging project which identified mortality rates for specific sets of hook release injuries. An approach for estimating mortality of halibut caught in groundfish pots is based on body condition and the presence of certain injuries. Halibut condition in pots is affected by the length of the soak and the presence of other animals in the pots, especially crabs, whose spiny carapaces have been observed to scratch and abrade the skin of the captive halibut. Mortality studies for pot caught halibut have not been conducted, so the approach which is used takes a conservative approach with assumptions of mortality assigned to each condition class. Williams (1997) describes the rationale.

The analyses have continued to this day, the most recent iteration being completed by Williams (2013). For the most part, the same approach has been followed, with few if any substantive changes. While the general approach is described as part of the annual reporting of results, a fuller, more comprehensive description has not been written. This report seeks to provide that documentation.

General approach

The mortality rate m varies among gear types and represents the aggregate effects of external and internal injuries to the fish and the presence of predation by amphipods or marine mammals. The mortality rates for various release conditions have been determined through long-term tagging studies conducted by IPHC. See Clark et al. (1992) for trawls, Williams (1997) for pots, and Kaimmer and Trumble (1998) for longlines. Estimated halibut mortality rates by gear and condition/injury were as follows:

Gear (g)	m_{exc}	m_{poor}	m_{dead}	
Trawl	0.20	0.55	0.90	
Pot	0.00	1.00	1.00	
	m_{minor}	$m_{moderate}$	m_{severe}	m_{dead}
Longline	0.035	0.363	0.662	1.00

DMRs are calculated to support the management needs of NMFS in managing halibut bycatch mortality within the PSC limit program. This requires determining DMRs by target fishery. Mean fishery DMRs and associated standard errors are estimated by assuming that each vessel acts as a separate sampling unit within a fishery. Thus, a DMR is calculated for each individual vessel in a target fishery. The DMR for a target fishery is then estimated as the mean of vessel DMRs, where each vessel's proportion of the total number of bycaught halibut is used as a weighting factor, as follows:

Let DMR_i = observed DMR on vessel i

p_i = proportion of total number of halibut caught on vessel i

Then $\overline{DMR}$ = $\sum_{i=1}^{n} p_i \times DMR_i$

Standard errors of the weighted mean DMR were estimated as:

$$V\left(\overline{DMR}\right) = \sum_{i=1}^{n} p_i^2 \times V\left(DMR_i\right)$$

and $SE\left(\overline{DMR}\right) = \sqrt{V\left(\overline{DMR}\right)}$

where $V\left(DMR_i\right)$ is the sample variance of all the DMR_i, and $V\left(\overline{DMR}\right)$ and $SE\left(\overline{DMR}\right)$ are the variance and standard error of $\overline{DMR}$, respectively.

Data Sources

The data necessary for the analysis are obtained from the North Pacific Observer Program (NPOP). Three data files are supplied:
1. Haul data – this file consists of data on individual hauls, i.e., vessel code, observer code, date, location, depth, gear type, vessel class, the Official Total Catch (OTC) in mt, etc. Each record in the file represents a distinct haul.
2. Species catch data – this file contains data on the catch (kg) of each species in a haul. This includes target as well as incidental and prohibited species. No information is supplied on whether anything is retained or discarded, i.e., the data represent only what came up. Each record in this file represents a species, identified by its NMFS species code, and the estimated catch in kg of that species in a specific haul.
3. Halibut length/viability data – this file contains information on the length (cm) and viability of sampled halibut. Each record represents a length/viability combination, with a frequency variable to denote the number of fish of that specific length/viability. The file also includes fish which were only measured for length without a viability taken. Thus, a haul is represented by a varying number of records, according to the number sampled.

The records within the files are linked via a key variable named haul_join, which is a number assigned internally by the NPOP, and is unique to a specific haul. A list of the variables in each file are provided in Table 1.

Description of specific steps

The data files are processed, merged, and DMRs calculated using the SPSS software application. Prior to MS Office 2010, Excel was unable to import the files due to their size, so I was dependent on SPSS to do the data manipulations. As I've become accustomed to SPSS, I've continued to use it, although for some steps I will export the data to Excel for a few calculations, then return them to SPSS.

What follows next is an outline of the specific steps undertaken to arrange the data, merge variables across files, and perform calculations. First, import the files into SPSS, creating native SPSS work files.

Step 1: the Haul file
1. Create new variables in the haul file:
    a. Region, where BSA = nmfs_area ≤599, GOA = nmfs_area 600-659, and WOC = nmfs_area ≥670
    b. Date, using the month, day, and year variables (SPSS has a specific date creation wizard). This step creates a single date variable.
    c. Gear2, where TWL = gear 1-4, POT = gear 6, and HAL = gear 8. Note that the two trawl codes (pelagic trawl and non-pelagic trawl) are combined into a single trawl code. No DMR analyses are done based on the specific trawl gear type, but on the target fishery only.
    d. Fishery, where 1 = open access, 2 = CDQ, 3 = IFQ. This step consolidates two separate variables and adds open access as an explicit variable value to simplify separating the file.

e. iphc_reg, which is an IPHC reg area variable. This is created based on the nmfs_area variable, using the following area conversion:

IPHC	nmfs_area
2A	≥ 670
2C	650-669
3A	630-649
3B	610-629
4A	516, 517, 518
4B	541, 542, 543
4CDE	506, 509, 512, 513, 514, 519, 521, 523, 524, 530 (i.e., everything but the above)

2. Create a Week # variable. This is necessary because the determination of target fishery is based on the species composition of a vessel's catch within a reporting week, i.e., Sunday through Saturday. So the weeks for each vessel/gear/region need to be kept separate and distinct. In a subsequent step, the catch by species on all hauls by a vessel/gear/region within a week will be rolled up and the catch totals run through a routine which assigns target.

Step 2: the species catch file
1. The goal with this step is to collapse the species file such that each record contains the catch by species (or species group) for each haul. The species and species groups have been unchanged since sometime in the mid-1990s, when the target fishery determination approach was adopted. Ultimately, the outcome of this step will be to use the haul_join variable to merge these catch data onto the haul file.
2. The data in this file are described by a species code, a catch weight (kg), and the number of animals. We'll only be using the weight variable for groundfish species, but also using the number variable for halibut.
3. Based on the species code, create new variables which represent the target species (or target groups) as shown in the following table:

Target species group	Variable name	NMFS Species Codes	Area(s)
Pollock	poll	201	BSA, GOA
Yellowfin sole	yfs	140	BSA
Pacific cod	pcod	202	BSA, GOA
Rock sole	rsol	104, 120, 121	BSA
Arrowtooth flounder	atf	141	BSA, GOA
Greenland turbot	turb	102	BSA
Flathead sole	flat	103	BSA
Rex sole	rex	105	GOA
Shallow water flatfish	swf	104,106,108,109,115,120,121,140,142,	GOA
Deep water flatfish	dwf	102, 107, 110	GOA
Other flatfish	ofla	105,107-112,114,115, 117, 137, 142, 144, 146, 148	BSA
Sablefish	sabl	203	BSA, GOA
Rockfish	rock	300-355	BSA, GOA
Atka mackerel	atka	204	BSA, GOA
Other species	ospe	50,51,60,61,63-69,78,90, 400,418,431,433,440, 601,602,604	BSA, GOA

Pacific halibut (numbers)	hal_num	101	BSA, GOA
Pacific halibut (weight)	hal_wgt	101	BSA, GOA

Step 3: merging the new species catch data to the haul file
1. Merge the catch data to the haul file, using the haul_join variable as the matching variable.
2. From this new haul file, split out the WOC hauls, the IFQ hauls, and the CDQ hauls records based on the fishery code. The CDQ hauls will be used later but the WOC and IFQ will not be used in this analysis.

Step 4: determine weekly species compositions
1. This step entails determining the weekly target based on the composition of the weekly catch.
2. Sum up a vessel's weekly catch using vcode/region/week/gear strata. Gear is included in this stratification because in the past we've found a few vessels which change gear types within a week.
3. Compute a new variable which represents the retained catch, which is used for the flatfish targets. When these analyses started, discard estimates were not available, so a default approach was employed which assumed all arrowtooth flounder caught in BSAI non-ATF flatfish fishing were discarded. So a variable is created named '*retained*', based on the following:
   a. Retained = OTC minus (atf/1000)
   b. The ATF divisor is needed because of the differing weight units of OTC and ATF.
4. Next, compute the species percentages. The target fishery assignment is based on the percentage represented by a species/species group in the week's catch by a vessel.

Step 5: Target fishery assignment
1. The weekly species catch percentages are compared to the specific criteria – see Table 2. The determination process is sequential, i.e., once a vessel/week has been assigned a target, it is removed from further consideration. The approach and the percentage criteria have remained unchanged since the mid-1990s.
2. Once the target is assigned to the vessel/week in the temporary working file, the target code is then assigned back to the primary haul file, to all of a vessel's hauls during each week of activity.

Step 6: Reformatting the length/viability file
1. Each record (or line) in the length/viability (L/V) file represents the sampled number of halibut at a given length and viability, at a specific length (cm), in an individual haul. So hauls will have varying number of records. The data need to be reformatted to enable the sample data to be appended to the records in the haul file. The downside of doing this is separating the length data from the viability data, however the paired length/viability data are not lost, and they're just not carried forward in this reformatting.
2. Once the above task is complete, append the viability sample data to the records in the haul file using haul_join to match the records.

Step 7: DMR and standard error calculation
1. Calculate the DMR for each sampled haul using the exc/poor/dead or minor/moderate/severe/dead distributions and the mortality rates in the table at the top of page 2.
2. Calculate the mean vessel DMRs for each vessel/fishery/gear/region stratum. This is a simple arithmetic mean. Do not include unsampled hauls.
3. Calculate a weighted mean fishery DMR, using the proportion of halibut caught by each vessel within a target fishery as the weighting.
4. Calculate the standard error – equation, page 2.

CDQ calculations
The same process is followed for CDQ data, with the exception that target assignment is done on the basis of the catch in the individual haul, and not on a weekly aggregation of a vessel's catch.

References

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Table 1. List of variables in each source file.

Haul file variables	Species file variables	Length/Viability file variables
CRUISE	CRUISE	T_TABLE
VESSEL	VESSEL	CRUISE
YEAR	YEAR	VESSEL
MONTH	MONTH	YEAR
DAY	DAY	MONTH
HAUL	HAUL	DAY
GEAR_TYPE	SPECIES	HAUL_OFFLOAD
PERFORMANCE	SEX	SPECIES
VESSEL_TYPE	EXTRAPOLATED_WEIGHT (kg)	VIABILITY
LATITUDE	EXTRAPOLATED_NUMBER	INJURY
LONGITUDE	HAUL_JOIN	LENGTH
NMFS_AREA		FREQUENCY
DURATION		HAUL_JOIN
FISHING_DEPTH_FATHOMS		
'F'		
OFFICIAL_TOTAL_CATCH (t)		
DEPLOYMENT_DATE		
DEPLOYMENT_TIME		
RETRIEVAL_DATE		
RETRIEVAL_TIME		
BOTTOM_DEPTH_FATHOMS		
'F'_1		
SKATES_IN_SET		
TOTAL_HOOKS_POTS		
HOOKS_PER_SKATE		
HAUL_JOIN		
CDQ_CODE		
IFQ		

Table 2. Groundfish target definitions and target determination criteria.

BSA		GOA	
Target	**Definition**	**Target**	**Definition**
A	Atka mackerel	A	Atka mackerel
B	Bottom pollock	B	Bottom pollock
C	Pacific cod	C	Pacific cod
F	Other flatfish	D	Deep water flatfish
K	Rockfish	H	Shallow water flatfish
L	Flathead sole	K	Rockfish
O	Other spp.	L	Flathead sole
P	Midwater pollock	O	Other spp.
R	Rock sole	P	Midwater pollock
S	Sablefish	S	Sablefish
T	Greenland turbot	W	Arrowtooth flounder
W	Arrowtooth flounder	X	Rex sole
Y	Yellowfin sole		

CDQ and Non-CDQ TARGET FISHERY DETERMINATION

Bering Sea/Aleutians

P	if pollock $\geq$ 95% of total catch, or
W	if arrowtooth flounder $\geq$ 65% of total catch.
Y/R/L/F	if (rock sole + other flatfish + yellowfin sole + flathead) is the largest component of the retained[1] catch using this rule:
Y	if yellowfin sole is $\geq$ 70% of (rock sole + other flatfish + yellowfin sole + flathead sole), or
R	if rock sole > other flatfish and rock sole > flathead sole, or
L	if flathead sole > other flatfish and flathead sole > rock sole, or
F	if none of the three conditions above are met.

If target is not P, W, Y, R, L or F, then target is whichever species or species group (A, B, C, K, O, S, or T) forms the largest part of the total catch.

[1] *Note: retained catch is defined as total catch minus all arrowtooth flounder catch.*

Gulf of Alaska

P	if pollock $\geq$ 95% of total catch, or
W	if arrowtooth flounder $\geq$ 65% of total catch.

If target is not P or W, then target is whichever species or species group (A, B, C, D, H, K, L, O, S, or X) forms the largest part of the total catch.