Unofficial NWFSC and SWFSC Groundfish Stock Assessment Handbook

Assessment teams at NWFSC and SWFSC

2024-10-15

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Preface

Note: this is a document for use by the NWFSC and SWFSC groundfish stock assessment groups. Nothing in this document is guaranteed to be accurate or up-to-date, to work for any particular species, to write your model for you, or to save you from getting grilled at a STAR panel.

Dear Reader,

This document is not intended to be followed blindly. Its purpose is to collect in an organized and accessible format some of the wisdom that has been accumulating in the heads of stock assessment authors (see list of past assessments). Where reasonable alternative approaches can be used, they should be listed here, with indications of the pros and cons of each approach. If you think something is missing, please add it–this is a work in progress. If you would prefer that assessment authors all make independent, arbitrary decisions, uninformed by what's been done in the past, and unaware of the issues associated with different approaches, feel free to stop reading this document at any time. Otherwise, please don't criticize these notes in public meetings.

Alternative sources for best practices

The SSC Groundfish Sub-committee has produced documents "ACCEPTED PRACTICES GUIDELINES FOR GROUNDFISH STOCK ASSESSMENTS". These documents, as well as the official groundfish stock assessment terms of reference, are both more up-to-date than this handbook and also carry more weight. However, they are also less comprehensive than this document. You should either follow their guidelines or be prepared to justify why you didn't. The accepted practices documents and the terms of reference are available at available at https://www.pcouncil.org/stock-assessments-star-reports-stat-reports-rebuilding-analyses-terms-of-reference/groundfish-stock-assessment-documents/ (search for "accepted" or "terms").

1 Data sources: notes, contact information, and links

1.1 Table of contacts

Contact info for various agencies (states, PacFIN, etc.) is listed in this Google Doc created by Jason Cope in 2009 (updated May 2021)

1.2 Requesting data from State partners

Starting with the 2023 cycle, there is a more formal process for making data requests to states for stock assessments. Details about the data requesting process, and steps for assessment leads to take, can be found in the document "Process for requesting data from states for 2023 cycle."

1.3 Regulations and catch limits

Jim Hastie has lived through many changes in regulations for west coast groundfish. Don Pearson has recently (Fall of 2014) created this online regulations database.

1.4 Catch data, lengths, ages, etc.

1.4.1 West Coast Groundfish Observer Program (WCGOP)

Jason Jannot says that it should be easier to request data this year, but we (or perhaps a few designated folks on the team) will get it in a more raw format that needs some processing. See section below on "Notes and best practices for observer data and discards" ADD LINK

1.4.2 At-Sea Hake Observer Program (ASHOP)

Vanessa Tuttle (Vanessa.Tuttle@noaa.gov) is the contact person for this. Unlike the shoreside subset of the hake fishery which has dockside sampling and bycatch reported in PacFIN, the observed bycatch in the at-sea sectors (motherships and catcher-processors) is reported to the NORPAC database housed at AFSC. A non-definitive list of "common" and "uncommon" species seen in the hake fishery (as of 2008, but Vanessa says it is still current as of 2022) is in Appendix A of this document.

1.4.3 PacFIN biological data (BDS)

Talk to John Wallace or Andi Stevens. To confirm sample sizes for BDS, go to this webpage which should give a recent tally of samples by state agency.

Generalized code to process the data are currently in {PacFIN.Utilities}.

You may see some discrepancies in CA data from 1985-1989 when compared to older extractions. Some samples were removed for some species. It is not clear why these samples were removed.

1.4.4 PacFIN landings

[**Add text here on how and where to get catch for ~~2019~~ 2023 assessments**]

Talk to John Wallace or Andi Stephens. Note that the PacFIN catch can be broken down by INPFC or month only for the trawl component, not the non-trawl gears. Also, beware double counting based on multiple levels of aggregation.

PSMFC areas do not contain all of the catch, thus it is best to use INPFC areas to aggregate catch.

Once you have catch values for all years, contact the state representative(s) for confirmation that the values are correct.

1.4.5 RecFIN

All states have in the past claimed that all rec. data is available on RecFIN. Users should check with state representatives for updated information on the recommended source for recreational data. One can pull historical catches here. Select the "Catch / Sample Data Reports" image which takes you to the reports dashboard. Alternatively, ODBC connections can be used to pull catch estimates directly from the Comprehensive Fish Ticket table. Some data sources (e.g. MRFSS, WA historic catch estimates) are not currently available via the public login, so you need to login with an account that has permission to view the tables. Additionally, once

you have catch values for all years, contact the state representative for confirmation that the values are correct.

Washington provides recreational catch in numbers. This leads to two decisions for putting catches into the model: keep catch in numbers, which stock synthesis converts to weights internally; or convert catch to weight using an external estimate. Both options have been done historically. The former causes challenges for projections, but if the former is chosen, it is useful to compare the model's calculated average weight of the catch to the value used to convert numbers to weight to see if there is large disagreement. For a partial history about this issue, and approaches for some past assessments see issue #52 from the canary rockfish git hub page.

To obtain length composition data,

1. Go to RecFIN
2. Select the "Catch / Sample Data Reports" image which takes you to the reports dashboard. There, select the "SD001 Biological Detail Report" option.
3. There is an automatic filtering applied, so to adjust select the 'filter' icon in the upper right (the upside down Erlenmeyer flask-like icon), and then download your data in either csv or excel format. Lengths come in imputed and measured, with T being total length and F being fork length. For questions on definitions of fields, the metadata is included as a selectable report in the reports dashboard.

E.J. Dick (SWFSC) and Jason Edwards (PSMFC) are developing tables with catch-weighted length compositions. Tables have been prepared for WA and OR, and CA is in prep. Contact E.J. (edward.dick@noaa.gov) if you have questions or would like to use the estimates.

1.4.6 Research catch

This is not automatically included in any of the other data sources. Gretchen Hanshew (Gretchen.Hanshew@noaa.gov) has been the source in the past. Talk to John Wallace and ~~Ian Taylor~~ about complexities regarding PacFIN records of landings from research catch.

1.5 Indices of abundance

At a team meeting on 13 March 2019, the team agreed on the following terminology for the surveys, where best practice would be to introduce the survey initially using the full name, with the short name in parentheses, and then use the short name after that. This will be the approach used in the write-up of the surveys as well.

- NWFSC West Coast Groundfish Bottom Trawl Survey (WCGBT Survey)

- AFSC/NWFSC West Coast Triennial Shelf Survey (Triennial Survey)

- AFSC West Coast Slope Survey (AFSC Slope Survey)

- NWFSC West Coast Slope Survey (NWFSC Slope Survey)

- NWFSC Southern California Shelf Rockfish Hook and Line Survey (H&L Survey)

- NWFSC Integrated Acoustic and Trawl Survey of Pacific Hake (Acoustic Survey)

Note: the names for the first 4 of these surveys in the {nwfscSurvey} package are "NWFSC.Combo", "Triennial", "AFSC.Slope", "NWFSC.Slope". The H&L and acoustic surveys are not currently available through that package.

1.6 Summary of NOAA fishery independent trawl surveys used for west coast assessments

1. Triennial Survey (1980–1992 & 1995–2004)

    a. early triennial (1980–1992, 55-366m, north of 36.8 (however the switch to north of 34.5 actually occurred in 1989))

    b. late triennial (1995–2004, 55-500m, north of 34.5)

    c. The 2007 Canary assessment (Stewart, 2007) seems to have been the first one to split the survey and includes info on justification (but there's an ongoing debate about the need to split).

    d. Must filter out water hauls and tows occurring outside the US EEZ (foreign tows)

    e. Note that 1977 is always tossed out.

    f. The 2005 and 2013 Shortspine Thornyhead assessments split the triennial into shallow vs. deep to create a single index from 1980-2004 for 55-366 m and a separate 366-500 m index for 1995-2004.

2. AKFSC Slope Survey (1997-2001, 183–1280m, north of 34.5)

    a. Years before 1997 surveyed small areas of the coast

    b. Must filter out tows occurring outside the US EEZ

3. NWFSC Slope Survey (1998-2002, 183-1280m, north of 34.5)

4. WCGBT Survey (2003-present, 55-1280m, entire US coast)

    a. Starting in 2004, there's a change in sampling intensity north and south of 34.5, so this strata boundary should be included (unless there's some specific reason not to)

    b. Note that there were changes in sampling intensity at 183 and 549 meters

c. This survey should be referenced as the "WCGBT Survey"

1.6.1 AFSC surveys

Data are now available through the NWFSC data warehouse which can be accessed by the functions in the {nwfscSurvey} package. Appendix B identifies which year the listed vessels participated in the Triennial and Slope Surveys. Each cruise is assigned a unique number which is contained within the 'CRUISEJOINS' column in the database. Checking that your data has all the cruises you expect for a given survey would be good practice. Although gear and personnel change over time, if a study looking at differences by vessel was undertaken, Appendix B shows which vessels participated in what year and survey.

1.6.1.1 More detail on these AFSC surveys

The the most recent RACE division species and data codes manuals are here.

The ADP Code Book has, for example, sex and performance code information. For convenience, here is the legacy coding for sex:

Sex

1 Male

2 Female

3 Undetermined

Note on design of the 2004 Triennial Survey

It is my (John Wallace) understanding that in the later years of Triennial survey (pre-2004), the survey became more of a fixed survey design as the skippers went back to the same locations as recorded on their vessel's instrumentation.

For the 2004 survey, I followed the design as put forth in:

2001 AFSC Triennial Survey Plan (converted from WordPerfect via Word)

without regard to any previously recorded tow locations.

For CRUISEJOIN info, see Appendix B.

1.6.2 NWFSC Survey Indices

Tech memo on "history, design, and description" of the survey is now available:

> https://www.nwfsc.noaa.gov/assets/25/8655_02272017_093722_TechMemo136.pdf
> Keller, A. A., J. R. Wallace, and R. D. Methot. 2017. The Northwest Fisheries
> Science Center's West Coast Groundfish Bottom Trawl Survey: History, Design,
> and Description. U.S. Department of Commerce, NOAA Technical Memorandum
> NMFS-NWFSC-136. DOI: 10.7289/V5/TM-NWFSC-136.

Additional information on the survey can be found in these documents from John Wallace:

> Strata Tow Percentages for NWFSC Bottom Trawl Survey for 2004-Current
>
> Calcs for Strata Tow Percentages and Station Selection for the NWFSC Bottom
> Trawl Surveys for 2003 and Beyond (PDF file on Google Drive)

Index standardization is used Kelli Johnson's VAST wrapper has specific examples for each
survey located in the inst\examples folder.

1.6.3 NWFSC Survey Length and Age Compositions

{nwfscSurvey} package is used for comp data and other data explorations.

Scaling from Tow to Stratum Level: Weight normalized length or age comps for each tow by
the numerical CPUE. This is done in the standard data package we get from Beth.

Scaling from Stratum to Coastwide (or Assessment Area) level: Weight strata length or age
comps by numerical index for each strata (from GLMM). This may mean dividing the biomass
index for each stratum by the average weight in that stratum (likely estimated from the length
comp in that stratum).

1.6.3.1 Filtering recorded catches that are fish stuck in net from previous tow

In some cases, fish caught in one tow remain in the net until the next tow and are recorded as
caught in that second tow (despite the attempts of the people on the survey to identify and
exclude such fish from the data). While we plan to come up with a consistent way to deal
with this, it has not been dealt with yet.

One problem arising from this is catch data outside of the depth range of the species. To
identify the depth range, one can start with the deepest/shallowest tow with a positive record
for that species and then look to see if the previous tow conducted by that vessel (likely on
the same date) caught that species. If so, and if a small number or a small relative number
of that fish species were recorded in the second tow, one can assume that those were from

the previous tow. By moving sequentially until one reaches a depth range where a few clearly legitimate tows occurred, one can define a reasonable depth range.

A second phase would be to define a way to filter all the tows to remove likely candidates. A simple way to do this is to look at the range of catch levels that were determined to be not legitimate, and filter the whole data set for that species by removing all tows with catches below some quantile of those catch levels (say 80 or 90%). This will eliminate having a large number of small catches in the database used for the GLMM, which would skew the modeled distribution.

1.6.4 IPHC survey

This survey has been used for Yelloweye Rockfish and Spiny Dogfish. Claude Dykstra (claude@iphc.int) has provided data in the past. The index was calculated using a binomial GLM developed by John Wallace. Talk to John or Ian Taylor to get R code for this analysis.

1.6.5 Oregon recreational observer program data

Troy Buell (troy.v.buell@state.or.us) is still involved with this data source even though he has changed positions.

1.7 Notes and best practices for observer data and discards

Discard mortality by fleet should be accounted for within the assessment. To obtain estimates of total discards based on the fleet structure in the model (gear and/or area) see the Groundfish Expanded Multi-year Mortality (GEMM) report which is a component of the annual Groundfish Mortality Report. The GEMM provides annual estimates of landed and discarded fish by sector off the West Coast starting in 2002 - present. However, the GEMM will not include the most full recent year estimates (example - the GEMM available in 2019 has data through 2017) which will require an assumption regarding the most recent year's discards. Additionally, assumptions will need to be made regarding the total amount of discard prior to the start of the WCGOP data (pre-2002).

The GEMM report is produced by the WGCOP team with Dr. Kayleigh Somers (kayleigh.somers@noaa.gov) as the lead author and is published in the September Council meeting Briefing Book titled the "Groundfish Mortality Report". The GEMM can be found within the associated Excel spreadsheet on the Table 3 tab. Additionally, the GEMM can be accessed via two other methods: 1) the GEMM report is archived on the network under \Assessments\GEMM Report or 2) can be accessed using the {nwfscSurvey} using the `pull_gemm()` function.

There are typically three common methods used within West Coast groundfish stock assessments to incorporate discard mortality.

The first approach is to include discard mortality into the catch data rather than estimating discards within the model. Discard mortality can be included by either adding this total to the catch by fleet or by adding a discard fleet. If using the discard fleet the selectivity of this fleet will need to be mirrored (see the 2017 California Blue/Deacon assessment for an example of this approach).

The second and third alternative approaches to including discard data is to model the process of discarding within SS3. Discards can be modeled either as total discards in mt or through the rate of discarding. Both of these approaches will require discard length data to be included in the model, or if not available a specific assumption regarding the retention curve relative to the estimated selectivity curve.

Estimates of total discards are available in the annual groundfish mortality report (and the GEMM). If a specific breakdown of discard by fleet is required (gear and/or area) speak with Dr. Kayleigh Somers. The data may not be able to be summarized to all fleet structures, so it is best to discuss the options with Kayleigh early in the assessment process. Assumptions regarding the discard total in the most recent year and historical years prior to the start of WCGOP data (2002) will need to be made by the assessor and modeled (often through the use of time blocks). If total discards are modeled, one will need to enter an annual CV into SS3 which is currently not available with the GEMM. The current approach for obtaining discard totals or discard rates with CV is via bootstrapping the available WCGOP observer data. The bootstrap CV will be based on the observer data and may not be entirely consistent with the data available in the groundfish mortality report (and the GEMM), particularly for sectors with limited observer coverage. Please see below for additional information regarding bootstrapping.

Modeling discard rates can be an easier approach since it does not require knowledge about the total discard amounts. However, this approach may not be feasible for stocks with limited observations in the WCGOP data due to high variability in the observed discarded and retained fish. The IFQ trawl fleet currently has near 100% observer coverage starting in 2011, while the non-catch share sectors have a much lower observed percentage (~20% as of last inquiry, but this may change in the future). Historically, it was thought that discard rates could not be calculated for complex managed species. However, this is not the case based on the current data. Discard rates are calculated based on the observed discarded weight relative to the total observed weight of discarded and retained fish. Bootstrapping is done using the data in order to provide a CV to the discard rate. Similar to two previous approaches, assumptions regarding the discard rate in the most recent year and historical years prior to the start of WCGOP data (2002) will need to be made by the assessor and modeled (often through the use of time blocks).

Note, if discard mortality is estimated within the model, it is important to compare the catches (landings + discards) estimated within SS3 to the total mortality estimates from the GEMM.

The GEMM is the official mortality report for West Coast groundfish stocks as is used to determine the ACL and OFL attainment and if overfishing is occurring. The total mortality estimates between SS3 and the GEMM would not be expected to match exactly, however, the should have a reasonable level of similarity. If there are large differences between the mortality estimates across multiple years one may need to reconsider if the model has enough data to appropriately estimate retention reliably for each fleet.

The SSC has specified that the GEMM is the official data source to update recent removals when conducting a catch-only update model. The GMT is currently tasked with allocating removals by modeled fleet using the GEMM. The GMT will provide the removal estimates for year with GEMM data, provide expected removals for the final model year, and removal assumptions to use during the projection period. These data will typically be available between March and April of the assessment year.

Finally, the GEMM includes recreational mortality by state. These values are not estimated by WCGOP but rather are pulled directly from RecFIN since WCGOP does not observe recreational fisheries.

1.7.1 What are the WCGOP data?

The WCGOP database includes only data collected by observers on West Coast vessels. The data available in this database varies fairly dramatically based on the sector. The IFQ vessels essentially have 100% observer coverage, so the database includes a comprehensive view of discards and retained catch from observers for that sector. However, other sectors have a much lower percentage of observer coverage (see the observer coverage). As an example, the nearshore fishery generally has about 20% observer coverage. Only the observations made on that percentage of vessels are going to be available in the WCGOP database. Hence, the observed retained and discard amounts are going to be a significant underestimate of total mortality in that sector. The discard ratio will also be more variable, but could generally be representative of the discarding behavior.

1.7.2 Bootstrapping

The current approach to obtain uncertainty around the data in the WCGOP database, either the total discard or discard rates, is to bootstrap the data. These data are summarized and the observations bootstrapped to obtain uncertainty estimated based on gear and area stratification requested by the assessor. Chantel Wetzel (chantel.wetzel@noaa.gov) currently conducts the bootstrap analysis.

1.7.3 Requesting discard data

There are two types of discard data available using WCGOP data. The first is a summary of the observed discards, discard rates, and bootstrapped uncertainty across years (2002 - present). The second type of data are lengths of discarded fish observed by WCGOP. To request these data please email information regarding data stratification (gear groupings and areas) to Chantel Wetzel (chantel.wetzel@noaa.gov) for observed discards, rates, and uncertainty and Andi Stephens (andi.stephens@noaa.gov) for length composition data for discarded fish.

1.7.4 Discard rates, and length comps, from the Pikitch et al. Discard Study (1985-87) and Mesh Study (1988-90) databases

If enough data exists, discard rates and length comps from the Pikitch et al. Discard Study database (or Mesh Study if no data exists in the Discard Study) may be obtained for a species to be assessed from John Wallace. Optionally, these rates can be expanded out to the surrounding years based on applying the study rates to PacFIN catch from the expanded years. This, of course, is only reasonable when the assumption of no significant changes to the fishery is a good one. For those in NOAA a draft of the methods paper can be downloaded here (for non-NOAA folks that are interested, contact the author at john.wallace@noaa.gov).

2 Modeling choices, notes and best practices

2.1 Selecting maximum age (population and data)

The comments below are based on a team discussion on how to select a population and data maximum age for modeling:

Choice 1, Population length bins: should extend beyond something like the 97.5% quantile of the length at age distribution for the largest age (easy to add more bins to see if it makes any difference).

Choice 2, Max age: should be large enough for growth to be asymptotic, and at least as big as the largest data age bins. It's easy to test the impact of changing to different value, just requires updating ageing error matrices. Look at the stable age-distribution plot and examine the number of fish in the plus group. Additionally, the period of time when data are available (after extensive exploitation), the data plus group may be lower.

Choice 3, Data length bins should probably be big enough that the plus group doesn't have much more in it than the previous bin. We should check to make sure that the selection of length and age bins are consistent with each other. Typically, we often have max length bins where there are only a few fish, but a larger proportion of data in the data age plus group.

Choice 4, Data age bins should probably be big enough that the plus group doesn't have much more in it than the previous bin. In regards to population maximum age, there is no negative repercussions within SS3 for having a larger value, beyond a slower run time. Revising the age bins based on the data, rather than a priori rules about how to set this, may be considered "data mining". Could create a check within the survey and PacFIN comp codes that creates a flag when the data plus group has more than a certain percentage (i.e., 5%). Also, add a warning to {r4ss} about the percentage in the population and data plus groups.

2.2 Determining prior for natural mortality

Owen's Advice on M; July 6, 2022

1. I prefer using age data alone to estimate the natural mortality rate (see accompanying document: M2017_for_Methods_Review_Hamel; Hamel and Cope (in review)), except in cases where getting a reasonable estimate of the maximum age is problematic.

2. The age based prior is simply:

$$\text{lognormal}(\ln(5.4/\text{max age}), 0.31).$$

3. The fixed value for M if not estimating is even more simply the median of that prior:

$$M = 5.4/\text{max age}$$

4. Can explore a range approaches for M estimates and priors here; reference is Cope and Hamel, in press.

2.3 Length-weight relationships

Use the getWLpars() function in {PacFIN.Utilities} which provides estimates for the parameters required by Stock Synthesis. It is common to rely only on data from the WCGBT Survey to get the parameters used in the model under the assumption that this survey is most representative of the population as a whole. These parameters should always be fixed in the model as no data type is available in SS3 to accurately estimate them internally.

2.4 Estimating ageing error

See the {nwfscAgeingError} package.

2.5 Maturity

Talk to Melissa Head about maturity. In 2017, she provided estimated maturity curves based on samples from the NWFSC survey for many species.

Data from the NWFSC survey on maturity includes a column indicating mature or immature and another indicating spawning and not spawning. The latter considers all "mature" fish with over 25% atresia as not spawning (along with all immature fish). The spawning/not spawning column is the one we commonly use to estimate the maturity curve since that is really what we care about. In some cases a simple logistic will fit, but if there is much skip spawning/atresia for older/larger females, a logistic type curve which asymptotes to a lower value or a non-parametric fit is more appropriate. A column with percent atresia is also provided if you with to use a percentage other than 25% for the cutoff. Finally, the mature/immature column can be used instead if the atresia/skip spawning is taken into account in specifying the fecundity relationship.

An additional column has been added to the NWFSC survey table indicating uncertainty in the designation. This can be used to weight or exclude data.

Note: John Field has expressed concern that we are too focused on recent samples from the NWFSC survey, so if you aren't going to include samples from past collections, think about a justification for that choice.

2.6 Fecundity

Dick et al. (2017) has estimates for the a and b parameters in the functional form $F = aL^b$ for many rockfish. The estimates are based on length in mm and predicted number of eggs, fitted in log-space. If you use length in cm (like in SS3), and don't want huge spawning biomass values (eggs), you can convert the values in the paper to units of cm and millions, billions, or trillions of eggs. First, find the values "$\exp(a)$" (referred to as a' below) and "b" from Table 6 in Dick et al. for your species (or subgenus, if no estimate for your species is reported). If your subgenus is not reported, you can use the "*Sebastes*" values.

The correct value of the "a" parameter in Stock Synthesis (using fecundity at length option 2: eggs=a*L^b) with length in cm and spawning output in **millions of eggs** is:

$$a = \frac{a' \cdot 10^b}{1000}$$

The division is by 1 thousand instead of 1 million because recruitment in SS3 is in thousands. The value of b is unchanged, and can be used directly in the assessment.

Other options include spawning output in **billions of eggs** via:

$$a = \frac{a' \cdot 10^b}{10^6}$$

or spawning output in **trillions of eggs** (e.g. 2017 Yellowtail Rockfish):

$$a = \frac{a' \cdot 10^b}{10^9}.$$

The {r4ss} figures in the "Bio" tab show the resulting fecundity relationship as a function of length, weight, and age so you can use that to determine whether your parameter values produce the correct final relationship by comparing to original studies on the relationship between fecundity and length.

2.7 Modeling selectivity

There was a CAPAM workshop on selectivity in 2013. Report, presentations, and recordings are available at here and the associated Fisheries Research special issue is here.

2.7.1 Conceptual reasoning for using different approaches to selectivity

The following set of circumstances might cause selectivity to be dome-shaped:

1. Contact selectivity causing older fish to outswim the trawl, or escape the gillnet/hooks

2. Incomplete spatial coverage in terms of depth or untrawlable habitat

3. Spatial heterogeneity in fishing intensity (see Sampson paper). This probably applies more to fishery selectivity than surveys.

Reasons for justifying asymptotic selectivity

1. It can help estimate L_∞ and variability in growth because the mode of the length comps is often representative of where the oldest fish are piling up.

2. It prevents the estimation of a large amounts of cryptic biomass

2.7.2 General advice on selectivity in SS3

1. Start with a functional form that is commonly used (double normal)

2. Find some initial values using either the Excel spreadsheets or the {r4ss} widgets

3. Put the initial values in the model and run without estimating anything until you get a model that runs. This can be done by setting the maximum phase in the starter file to 0 or (better), by using the command line inputs: `-maxfn 0 -nohess`.

4. Read the output into R using SS_output and plot the selectivity in {r4ss} using either `SS_plots(model, plot=2)` or `SSplotSelex(model, subplot=1)`, where `model` is the object created by `SS_output()`.

5. Set the PHASE for as many parameters to negative values as possible so that you start with estimating relatively few parameters (such as parameters 1 and 3 of the double normal, which control the peak and ascending slope).

2.7.3 Guidelines for SS3 double normal initial setup

- Fix parameters 5 and 6 (negative phase).

  - If selectivity is thought to be zero at the youngest/smallest or the oldest/biggest fish set the value to zero (e.g -15)

  - If selectivity is thought to be larger than zero at the youngest/smallest or the oldest/biggest fish set the value to -999 (does not scale the selectivity for the youngest or oldest age, independently from the normal curve).

- Fix the plateau (parameter 2) to be small values (e.g. -15).

- Set the initial value for the peak (parameter 1) at the age/length equal to the mode of the composition data

- Set the ascending (parameter 3) and descending (parameter 4) slopes at $log(8 \cdot (a_{peak} - a_{min}))$ and $log(8 \cdot (a_{max} - a_{peak}))$ (substitute min and max lengths and length at peak when modeling length-base selectivity).

- Don't estimate selectivity at youngest age/size (parameter 5) unless there are observations of fish in the smallest age- or length-bins, either fix at -5 or -999

- Use the double normal instead of the logistic for asymptotic selectivity to have flexibility of dome shape without major changes to control file. This also provides control over selectivity at the youngest age. To force a logistic shape, you can do one of the following (where parameters 2, 4, and 6 should not be estimated under any of the options):

  - Fix descending slope (parameter 4) at a large number (e.g. 15)

  - Alternative 1: Fix plateau (parameter 2) to a large number (e.g. 15)

  - Alternative 2: Fix selectivity of the oldest age (parameter 6) at a large number (e.g. 15).

2.8 Modeling recruitment deviations

1. Choices to be made:

   a. allow recruitment deviations or not?

   b. range of years?

   c. breaking into "early", "main", "late" vectors?

      i. early and late vectors are intended to add uncertainty to the model for years with little or no data with information about recruitment

2. What was done in the 2011 assessments? Graphical description is here.

3. Guidance on bias adjustment settings

   a. Multiple simulation analyses have shown that applying the bias adjustment settings given by the `r4ss::SS_fitbiasramp()` perform well on average. However, there's no guarantee that this will work well in any given circumstance. User discretion is advised.

4. What to do about σ_R.

   1. Simulation in Methot and Taylor (2011) looked at a few options.

      i. Estimating σ_R. **Performed well under ideal circumstances.**

      ii. Tune σ_R to match the observed variability in recruitment deviations.

      $$\sigma_R{}^2 = \text{sd}(r')^2$$

      Performed less well.

      iii. Tune σ_R so that
      $$\sigma_R{}^2 = \text{sd}(r')^2 + \text{mean}(\text{SE}(r'))^2$$

      where $\text{sd}(r')$ is the standard deviation of the vector of estimated recruitments over a range of years that seem reasonably well informed by the data, and $\text{mean}(\text{SE}(r'))$ is the mean of the estimated variability of those values. **Performed best.**

5. MCMC

   a. If you can get MCMC to work for your model, all the worry about bias adjustment goes away. You would need to either estimate σ_R in the MCMC and hope it converges, or fix it at a value that has been tuned to the MLE.

6. Autocorrelated recruitment deviations

   a. Estimate `# SR_autocorr` (Stock-Recruit parameter in control file)

   b. Here are results from hake in 2019 from the ss_new file: `-1 1 -0.155106 0 99 0 6 0 0 0 0 0 0 0 # SR_autocorr`

   c. Johnson et al. (2016) estimated autocorrelation in a simulation context

2.9 Rockfish steepness profile

Up until the 2019 assessment cycle, a meta-analysis approach was used to develop a prior for steepness for West Coast rockfish species. This method was originally developed to develop this prior by Martin Dorn in 2007, and updated by Dorn in 2009/2011. It was then revised and recoded by James Thorson, who updated it in 2013/2015/2017, with Chantel Wetzel conducting the update in 2019. When the meta-analysis was updated post the 2017 assessment cycle, the estimated mean from the prior distribution was considered unreasonably high, particularly for rockfish species, and the new prior was not approved by the SSC for use in future West Coast rockfish assessments. In the instance that the SSC does not approve a new estimate (or methodology), the approved approach reverts to the previous approved estimate. In this instance that is the prior estimated for use in the 2017 assessment cycle of a mean $= 0.72$ with a standard deviation of 0.158.

Below is detailed information regarding the meta-analysis approach applied between 2007 - 2017:

- The method is fully described in Thorson, Dorn, and Hamel (2018) Fisheries Research

- The method can be replicated for any data set 2007/2009/2011/2013/2015/2017 using R package {SebastesSteepness}

- The rationale for excluding a species when developing a prior for a given focal species (termed "Type-C" meta-analysis) is explained in this paper

    - If you are assessing any of the following species you will need to obtain a Type-C prior: aurora, black, bocaccio, canary, chilipepper, darkblotched, gopher, splitnose, widow, yelloweye, yellowtail north

- The estimated prior by year was as follows:

    - 2007: mean $= 0.58$, sd $= 0.181$

    - 2009: mean $= 0.69$, sd $= 0.218$

    - 2011: mean $= 0.76$, sd $= 0.170$

    - 2013: mean $= 0.78$, sd $= 0.152$

    - 2015: mean $= 0.77$, sd $= 0.147$

    - 2017: mean $= 0.72$, sd $= 0.158$

3 Running Stock Synthesis

3.1 Model setup

1. **Run the model without estimating anything at first.** The best way to do this is to run as `ss -stopph 0 -nohess` where `stopph` (short for "stop phase" is equivalent to setting the maximum phase in the starter file).

2. **Make sure you pay attention to any notes or warnings in "warning.sso".** If you don't understand the warnings, find out, but don't just ignore it.

3. **Debugging models that don't run**. The first place to look is "echoinput.sso". Start at the bottom and scan upwards until things start to look right or start at the top and scan downwards until things start to look wrong. It's often obvious when you have an extra input and things model starts to go awry. Use this information to fix your input files and try again. There are some additional debugging tips in the Stock Synthesis User Manual. Consider also reading the input files into R using `r4ss::SS_read()` which may help you find mismatched columns or bad values in the inputs.

4. **Once the model runs, look at the ".ss_new" files.** These files contain rich comments and often better formatting than your own input files. They are also good for debugging, because sometimes a model will run, but the parameter lines are associated with different fleets, or have different roles than you expected. Check the parameter names on the right hand side of "control.ss_new" to make sure everything looks right. You can then either replace your input files with the ".ss_new" files or just copy and paste elements that you want to keep. Note that if you've estimated any parameters, then the initial values in "control.ss_new" have been updated to these estimates.

5. **Pull in parameter bounds that are way too wide** – if you aren't anywhere near them during minimization, extremely wide bounds (like -15 to 15 on recruit deviations, or 3 to 31 for log-R0) just slow minimization and may result in poorer convergence properties.

3.2 Model tuning

6. **Indices are typically tuned via the extra standard deviation parameter.** There are many reasons to expect that the input uncertainty values on indices of abundance are

underestimates of the true uncertainty. Estimating an extra uncertainty parameter has worked well in a number of west coast groundfish assessments. However, the 2021 best practices document says, "STATs should be cautious to avoid adding variability to an index as a means of resolving model structure issues such as conflicts among data sources. Rather, variability should be added to account for sampling variance underestimating index uncertainty. *STATs should provide a priori reasons for why the index variability input to the model has been underestimated (or underspecified).*" Note that the extra SD parameter should reflect the observed variability in survey indices rather than poor fit to the observed trend in survey indices. Resist adding SD to surveys where there are trends in residuals without evidence of hyperdepletion or hyperstability, in which case a non-linear relationship between indices and stock size is more appropriate.

7. **Composition data is typically tuned by either iterative Francis weighting or estimating Dirichlet-multinomial parameters.** The McAllister-Ianelli method has not performed as well in simulation testing. See the data weighting section of the Stock Synthesis Manual for more info (Dirichlet-multinomial guidance was updated by Jim Thorson in September 2022).

8. **Discard ratios and mean body weight** These data SHOULD be tuned, but we don't typically do so. Kelli Johnson tuned these for Sablefish in 2019 with the following description:

   > Added variances for discard rates and mean body weights were set using values calculated iteratively using the RMSE of differences between input and estimated values derived from SS3. Variances were parameterized in terms of standard deviation and coefficient of variation, respectively.

9. **Think about sigmaR.** This could be an arbitrarily chosen value, freely estimated, or iteratively tuned. Methot and Taylor (2011) suggest a way that the tuning could be done. Whatever you choose, put a little thought into it. SigmaR should be greater than the SD of the estimated recruitment deviations. The table `$sigma_R_info` output by `r4ss::SS_output()` provides information on tuning sigmaR.

4 So you ran an assessment model, more notes and best practices

4.1 Retrospectives

1. Retrospective analysis is a way to assess whether something is inconsistent in data or model assumptions. A retrospective pattern can arise from changes in catch, M, q, selectivity, or growth from that which is in the model. It is primarily an exploratory/diagnostic tool, though see point 4 below.

2. See the 11/17/2021 PEP team meeting presentation for background information and past publications on retrospective analysis

3. PEP's approach is to apply:

   a. 5 years of peels (based on findings from Miller and Legault 2017),

   b. using the alternative Mohn's rho (Mohn's rho averaged over peels - the AFSC_Hurtado term from `r4ss::SSmohnsrho`),

   c. for depletion, biomass, fishing mortality, and recruitment. Often biomass, depletion, and recruitment are provided in assessment reports

4. Although the east coast uses mohn's rho to "correct" status indicators or when setting quotas, our practice is not to. This is based on past precedent, and that our fishing history is not as long as it is on the east coast.

5. Hurtado-Ferro et al. (2015) provide a rule of thumb on the significance of mohn's rho (average over peels) dependent on life history. They suggest a retrospective pattern is not meaningful if $\rho \in (-0.15, 0.2)$ for long lived species and $\rho \in (-0.22, 0.3)$ for short lived species, and note that magnitude of Mohn's rho not related to true bias in assessment. Miller and Legault (2017) argue that variance of Mohn's rho is truly needed to ascertain whether an effect is significant.

4.2 Conducting a rebuilding analysis (aka Puntalyzer)

A rebuilding plan will need to be developed for any species (or stock) that has an GFSC SSC approved stock assessment that estimates the relative spawning biomass to be below the corresponding minimum stock size threshold (0.10 for flatfish and 0.25 for all other groundfish species). A rebuilding analysis is developed using a software program called the "rebuilder" (aka the Puntalyzer) developed and maintained by Andre Punt (aepunt@uw.edu). The program is designed to work with an input rebuilding data file created by Stock Synthesis called "rebuild.dat". The rebuilder software executable then develops numerous future projections and calculates the probability of rebuilding based on alternative harvest strategies. The RES.CSV created by the rebuilder executable contains all of the resulting estimates of rebuilding (although many quantities are not labeled within the CSV file).

The rebuilder github repository (pfmc-assessment/rebuilder) contains the most up-to-date rebuilder executable, the user manual, code tools for processing output, and code examples. This repository should have all the pertinent information to conduct a rebuilding analysis for a species or stock managed by the Pacific Fishery Management Council

4.3 `r4ss`

1. The {r4ss} package is available on CRAN but the most up-to-date version can be installed from GitHub. Installation instructions are available here.

2. See the intro vignette here for info on more advanced topics like scripting Stock Synthesis workflows with r4ss and using the `r4ss::tune_comps()` function.

3. It's good idea to reinstall it on a regular basis to keep up. You can also watch the github repository if you want to get notifications of changes.

4. Look through all the figures that get produced by `r4ss::SS_plots()`. There have been cases where models were put forth with incorrect assumptions about biology, ageing error, etc. that could have been caught if the assessment authors had paid attention to all the plots.

5. Remember that the figures can be modified to look better. For instance, you can replace the fleet names in the model with a less abbreviated set of names that will go in the plot labels.

6. If something is not working right, complain about it on the `r4ss` issues list.

4.4 Writing assessment documents

1. Read the terms of reference and actually follow them.

2. See the {sa4ss} package.

3. If you're using Word, talk to power users of Word about formatting of section headings, links to figures or tables, etc.. These links save much time when document is updated with sections or elements added or removed.

a. See the Assessment Document Template for a pre-made setup that reflects 2017-18 TORs: `\\nwcfile\fram\Assessments\Archives` and shared on the Google Drive

4. Use proper dashes and hyphens for readability: Hyphen, En dash, and Em dash

5. Jason says: "It would be really easy to compare results of every assessment we do with the results of the data-poor methods." He did this for Cabezon in 2009 and thinks we could do it for all our assessments.

6. For Word, consider using Endnote or Zotero to find/organize/insert references. The assessment endnote library is at `\\Nwcfile\fram\Assessment\References`, but please export references you need and do not link a Word document directly to that library.

7. Make sure that labels on Figures are readable. The best way to get figures produced in R into word is to save them as PNG files. The plotting functions in the R4SS package have an input for resolution that can be increased as needed. The default resolution is higher than what you get if you save the images one by one from the RGUI graphics window.

8. Crop out non-informative headings and labels from figures imported from R4SS or other packages.

9. The council website has a useful dashboard for information on recent fishery performance, OFLs, ACLs, etc. Go to the "GMT016 - Stock Summary" table and filter by species and area.

5 Other useful tidbits

5.1 Notes on shared software

5.1.1 Using GitHub

Git is a version control system that can be used to synchronize files between the web and local directories. GitHub is a user-friendly website which hosts files and depends on Git.

5.1.2 Shared code locations

Most of the R packages and code used in NWFSC assessments are listed in the README at (https://github.com/pfmc-assessments). Other sources not included in this github organization include Stock Synthesis and associated packages including {r4ss} and {ss3diags} (not yet used for PFMC assessments).

In addition, NMFS OpenSci has a number of NMFS templates for websites, quarto, Rmd docs, and presentations

6 Cloud computing: jittering a stock assessment

This is the path that I (Kiva) figured out and it worked for me. I am not an expert on computers, cloud computing, or computer security, so if you find yourself thinking "huh, why is she recommending that and not this," there is probably not a very good reason! In other words, please let me know if you think this could be improved.

6.1 Pick a VM

1. You'll need an NMFS Azure account. Contact Christine Stawitz to get one.
2. Log in.
3. Click on Virtual machines -> Create. I think the preset configurations are helpful.
4. I've been using the D-series
5. Give it a name. Other settings I changed from defaults:

    1. Size. Decide how many CPUs (cores) you want. This sets how many stock assessments can be run concurrently.
    2. Under networking, add HTTP (80) and HTTPS (443) to the inbound ports. Ignore the warning.

6. Once you get to the end of all of the options, mostly sticking to defaults, click "Create."
7. You'll need to create a new SSH key for your VM. Once again, just click on the default buttons to keep things advancing, letting the many settings you don't entirely understand wash over you. (You probably created an SSH key at some point for github.)

You're done! It will take a few moments to get going. If after trying it out you don't like it, no worries! Most of these settings can be changed on the fly!

I started out with an 8 core VM. This was twice as many as my laptop, so the gains were not huge. For production purposes, I would probably opt for 16 cores.

6.2 Connect to your VM

There are several ways to do this. This is what I do:

Go to the Azure home portal. Under "Resources" your VM should be there. Click on it. If the "Start" button is blue, click on it. This is sort of like turning on your computer. Creating a new VM will automatically turn it on.

Click on "Connect." I use the Native SSH. Copy your SSH key's file name to step 3 of the Native SSH directions. It is probably something like `[VM name]_key.pem`. It will give you the SSH command to run; copy it.

Open up Powershell, Git Bash, or similar. Change the directory (using `cd`) to wherever you stored your SSH key. If your computer asks if you are sure you want to do this, you bet you are sure.

6.3 Install software

First, install some software you will need for cloud computing by running the following lines in the command line:

```
sudo apt-get update
sudo apt-get upgrade
sudo apt-get install libxml2 libxml2-dev # igraph
sudo apt-get install libcairo2-dev # Graphics packages
sudo apt-get install libssl-dev libcurl4-openssl-dev #httr
sudo apt-get install apache2
```

To make sure everything is working, in your browser window, navigate to your VM's IP address, which you can find in the Azure portal of your browser. You should see:

Now install R:

```
# update indices
sudo apt update -qq
# install two helper packages we need
sudo apt install --no-install-recommends software-properties-common dirmngr
# add the signing key (by Michael Rutter) for these repos
# To verify key, run gpg --show-keys /etc/apt/trusted.gpg.d/cran_ubuntu_key.asc
# Fingerprint: E298A3A825C0D65DFD57CBB651716619E084DAB9
wget -qO- https://cloud.r-project.org/bin/linux/ubuntu/marutter_pubkey.asc | sudo tee -a /etc
# add the R 4.0 repo from CRAN -- adjust 'focal' to 'groovy' or 'bionic' as needed
sudo add-apt-repository "deb https://cloud.r-project.org/bin/linux/ubuntu $(lsb_release -cs)
# install R
sudo apt install --no-install-recommends r-base
```

This installed the latest R version as of 10/30/23 (I ended up with 4.3.1). For up-to-date instructions, go to the R project website.

Install Rstudio Server:

To download the latest version of Rstudio Server, follow the directions here. If you followed the earlier specifications to set up the VM, you should select the operating system "Debian / Ubuntu." The Ubuntu version that is installed shows up when you first SSH into the VM. For me, it was 20. You've already installed R, so scroll down to step 3. It will direct you to run

31

```
sudo apt-get install gdebi-core
```

And then a couple more lines specific to the version.

Christine Stawitz says "If you don't like RStudio as an IDE, there are other options like Code Server (cloud version of VSCode) or Jupyter notebooks."

6.4 Connect to Rstudio

In the Azure portal where you can see the VM settings, in the left bar under "Networking" select "Network settings." Add an inbound port rule. The destination port rule should be 8787 (the default for Rstudio). Keep everything else as a default. As a test, on your browser, navigate to [VM IP address]:8787. You should see an Rstudio login.

I'm not sure what the correct login is, so let's change it. From your VM's Azure portal in your browser, under "Help," click on "Reset password." Click the "reset password" bubble. Pick a username and password.

Now return to that Rstudio login on your browser. Refresh, and enter your username and password you just chose. It should look just like a normal Rstudio window!

Ian: I was actually following the directions here, and then they got really long and I had something working so I stopped. Christine, independently, said she stopped at the same spot. IT may not like accessing it from the public IP address, but she said she is going to do it this way until she gets in trouble.

6.4.1 A note on Rstudio

Rstudio cannot parallel process using a "multicore" strategy, only "multisession." The makes no difference on your Windows laptop, because Windows also does not support multicore parallel processing. However, if you have set up a Linux VM, it is theoretically an option. I do not know if it is faster or how much.

6.5 Install packages

Things should be looking more familiar! From the Rstudio (or your favorite IDE) tab in your browser, run:

```
install.packages('remotes')

remotes::install_github('r4ss/r4ss')

# Plus any others you want, e.g., nwfscDiag, here, tidyverse, etc.
```

6.6 Move files

There are several ways to do this. I am giving you directions for one approach, using Azcopy. To install Azcopy on your VM, run:

```
wget https://aka.ms/downloadazcopy-v10-linux
tar -xvf downloadazcopy-v10-linux
sudo cp ./azcopy_linux_amd64_*/azcopy /usr/bin/
```

Now

1. In the Azure portal of your browser, create a storage account. Title it whatever you want, maybe your name or the name of the assessment. Default settings should be fine.
2. On the left column under "Data storage," click on "Containers." Make a new container. Pick a name. Again, default settings are fine.
3. Navigate to your new container and on the top bar click on "Upload." Upload whatever files you want to transfer.
4. In the same container, click on "Shared access signature" under "Security + networking." I gave it all 7 permissions. Give yourself a little flexibility on the start and expiry date/time. I usually just subtract one day from the start and add one day to the end. You can also enter your VM's IP address if you want.
5. Click "Generate SAS token and URL" and copy the text for the Blob SAS URL.
6. Back in your VM terminal, run

```
sudo azcopy copy "[paste Blob SAS URL]" "." --recursive
```

The general syntax is:

```
sudo azcopy copy "[copy from]" "[copy to]" --recursive
```

The recursive addition is necessary if multiple files are involved. The files should be downloaded into a new folder with the same name as your container!

7. By default, the directory you just created does not have sufficient file permissions to run stock synthesis. To change this type:

```
sudo chmod 777 [model_directory]
```

If you were transferring a stock assessment model, try running stock synthesis (probably using `-nohess`) to make sure it is working. To ensure you have the right executable, you can run `r4ss::get_ss_exe()` from Rstudio (or whatever cloud IDE you are using), and it will automatically download the correct executable to your selected working directory.

6.6.1 Other file transfer methods that you might consider

You could install git and clone your repo. I did not look into that because repos can get large and take a while to clone. You can easily download model files straight from github without git using `wget`, but will eventually need to write the results somewhere.

Another approach is to use the `scp` command from your local computer and avoid the blob storage and azcopy. I think you would have to open up the appropriate port on your VM. Hem, who uses Azure to run Atlantis, recommended the azcopy approach, so that is what I tried. I have used scp in the past on university computing clusters, and it may be fewer steps for each file transfer. I have no idea whether we can run scp on our federal laptops.

6.7 Make sure you log off your VM!!!

Hit "Stop" on the main Azure panel for your VM in your browser. This is akin to shutting down your computer. In general, cloud computing is paid by the minute. The per minute cost is low, but you don't want to keep it on, e.g., overnight, if you are not using it.

6.8 Some thoughts

The strongest use case for this in production stock assessments is running jitters. The first time, this requires more active time on your part than running a jitter on your local computer. However, you should get the jitter results faster once it starts running. I ran 8 jitters all at once and it took X min of processing time! Once you set up your VM, you can get back on it whenever you want and your files and settings will be retained, so it is just a matter of transferring files and hitting run.

Note that {r4ss} is newly set up so that you can run jitters and retrospectives in parallel on your laptop, too! Your laptop just has fewer cores, so you can run fewer models at once.

Profiles are not currently set up to run in parallel because it is often useful for convergence purposes to run them sequentially and then use the previous par file as the starter.

The VM will not run a single stock synthesis model any faster than your laptop. The gains are really in the number of models that you can run simultaneously.

Another use case for this is if you want to rerun all of your sensitivities on a new (e.g., post-STAR) base model. You could do something like `furrr::future_walk(dir_string, r4ss::run)`. For research (e.g., simulations, variable selection, cross validation), the use cases are endless!

I can fumble my way through file management from the command line, but I don't love it. Normally we all probably think of Rstudio as an environment for writing and executing R code, but it does provide a nice graphical file manager that I have been making use of. You can also open and edit any text file, including all of the inputs and outputs for stock synthesis. (Other IDEs should provide this functionality, too.) Your Ubuntu VM does come with Vim.

Until June, 2024, my understanding is this is all free. After that, we may need to pay. Christine Stawitz thinks it will be possible to pay for the credits in advance when funds are available, and use the credits whenever we want. (Cloud computing in general definitely works that way. It is possible the federal bureacracy ruins it, like all nice things.)

A Species seen* in the hake fishery

See note about ASHOP program under data sources. The at-sea hake fishery does not fall under the WCGOP program.

*not a definitive list

ROCKFISH	FLATFISH
COMMON	**COMMON**
aurora	arrowtooth flounder
bank	dover sole
blackspotted	English sole
bocaccio	flathead sole
canary	Pacific halibut
chilipepper	Pacific sanddab
darkblotched	petrale sole
greenstriped	rex sole
POP	slender sole
redstripe	southern rock sole
rougheye	
sharpchin	**UNCOMMON**

shortbelly	California halibut
shortspine	
silvergray	
splitnose	**SHARKS, SKATES, RAYS & RATFISH**
stripetail	
widow	**COMMON**
yellowtail	big skate
	blue shark
UNCOMMON	brown cat shark
black	longnose skate
blackgill	Pacific electric ray
blue	salmon shark
harlequin	sandpaper skate
longspine	six gill shark
quillback	soupfin shark
redbanded	spiny dogfish shark
rosethorn	spotted ratfish
speckled	thresher shark
squarespot	
tiger	
yelloweye	**MISCELLANEOUS**

yellowmouth

SALMON

COMMON

Chinook

chum

coho

pink (odd years)

UNCOMMON

sockeye

steelhead

COMMON

American shad

barracudinas

jack mackeral

king-of-the-salmon

lamprey

lanternfish

lingcod

Pacific cod

Pacific herring

Pacific mackeral

Pacific sardine

pollock

ragfish

sablefish

B Alaska Center CRUISEJOINS for shelf and slope surveys

This list is from AFSC, updated with 2004 info by John Wallace

TRIENNIAL SURVEY CRUISEJOINS

YEAR	CRUISEJOINS
1977	393 (Commando), 421 (Pacific Raider), 423 (Jordan), 500 (Tordenskjold)
1980	394 (Mary Lou), 404 (Pat San Marie)
1983	433 (Warrior II), 434 (Nordfjord)
1986	406 (Pat San Marie), 429 (Alaska)
1989	407 (Pat San Marie), 461 (Golden Fleece)
1992	432 (Alaska), 465 (Green Hope)
1995	852417 (Alaska), 852418 (Vesteraalen)
1998	921326 (Dominator), 929471 (Vesteraalen)
2001	1090096 (Sea Storm), 1090095 (Frosti)
2004	1236675, 1236676 Morning Star Vesteraalen

SLOPE SURVEY CRUISEJOINS

YEAR	CRUISEJOINS
1984	435 (Half Moon Bay)
1988	413 (Freeman)
1989	462 (Golden Fleece)
1990	416 (Freeman)
1991	417 (Freeman)
1992	418 (Freeman)
1993	419 (Freeman)
1995	852455 (Freeman)
1996	869365 (Freeman)
1997	912730 (Freeman)
1999	998132 (Freeman)
2000	1028815 (Freeman)
2001	1105595 (Freeman)