GAP Production Data Documentation

Bering Sea Survey Team

Gulf of Alaska Survey Team

Aleutian Islands Survey Team

Table of contents

# 1. Survey Background

## 1.1 What we do

## 1.2 Who is conducting the research?

Scientists from the Alaska Fisheries Science Center’s Groundfish Assessment Program (GAP) conduct these bottom trawl surveys with participation from the Alaska Department of Fish & Game (ADF&G), the International Pacific Halibut Commission (IPHC), universities, and other organizations. This research is conducted primarily on chartered fishing vessels.

## 1.3 What is the research objective?

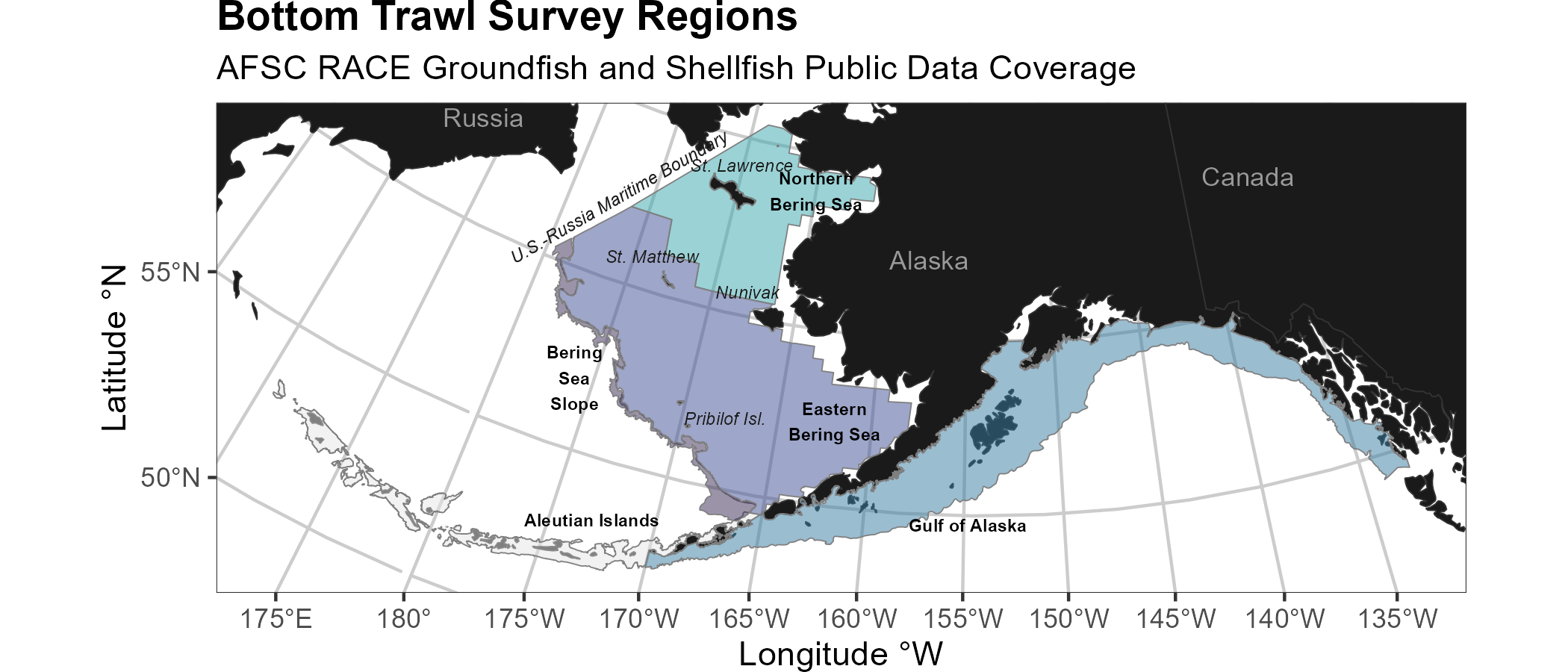
Learn more about the [program](https://www.fisheries.noaa.gov/alaska/science-data/groundfish-assessment-program-bottom-trawl-surveys). The objectives of these surveys are to:

* monitor the population and environmental trends in the marine ecosystem of the Bering Sea, Aleutian Islands, and Gulf of Alaska,
* produce fishery-independent biomass (weight) and abundance (number) estimates for commercially important fish and crab species, and
* collect other biological and environmental data for use in ecosystem-based fishery management.

## 1.4 Who is conducting the research?

Scientists from the Alaska Fisheries Science Center conduct these bottom trawl surveys with participation from the Alaska Department of Fish & Game (ADF&G), the International Pacific Halibut Commission (IPHC), and universities. This research is conducted on chartered fishing vessels.

## 1.5 Bottom trawl surveys and regions



Strata used in the all surveys.

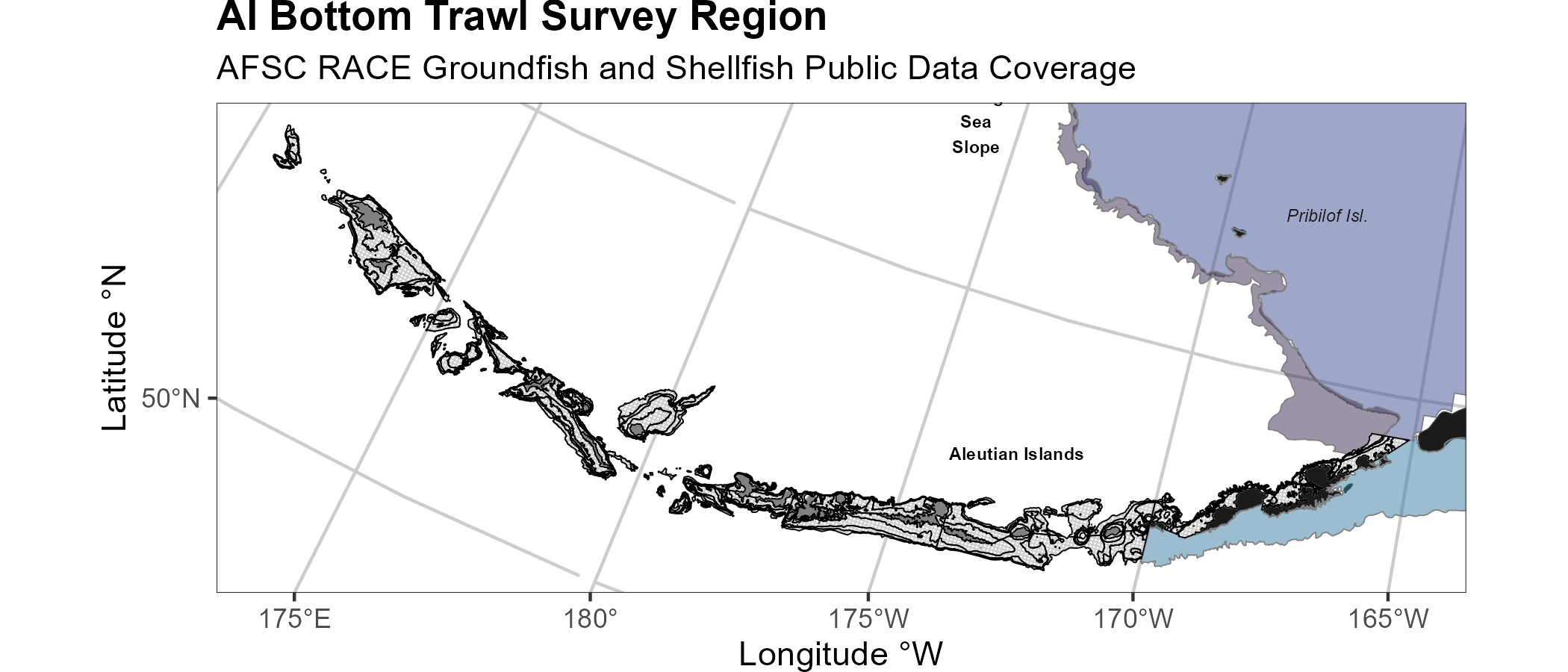
Each survey conducted by the [Groundfish Assessment Program](https://www.fisheries.noaa.gov/alaska/population-assessments/north-pacific-groundfish-stock-assessments-and-fishery-evaluation) are multispecies bottom trawl surveys. We collect environmental and biological data to assess how climate variability and [loss of sea](https://www.fisheries.noaa.gov/alaska/ecosystems/habitat-and-ecological-processes-research-regarding-loss-sea-ice) ice are affecting bottom-dwelling marine life on the Bering Sea shelf. We monitor trends in the distribution (location and movement patterns) and abundance of groundfish and crab species as well as oceanographic data (e.g., water temperature, depth). We collect biological information such as organism weight, length, stomachs to learn about diets, and [otoliths](https://www.fisheries.noaa.gov/alaska/science-data/alaska-age-and-growth-procedures-otolith-examination) to [determine fish ages](https://www.fisheries.noaa.gov/alaska/science-data/fish-otolith-chronologies). We use this information in [annual stock assessments](https://www.fisheries.noaa.gov/alaska/population-assessments/north-pacific-groundfish-stock-assessments-and-fishery-evaluation) and to assess the state of the ecosystem. This research is conducted on fishing industry contract vessels.

| **Survey** | **Survey Definition ID** | **Years** | **Depth (m)** | **Area (km2)** | **# Statistical Areas** | **# Possible Stations** |
| --- | --- | --- | --- | --- | --- | --- |
| Aleutian Islands Bottom Trawl Survey | 52 | 2024 - 1991 (14) | 1 - 500 | 64,415.0 | 80 | 1,312 |
| Eastern Bering Sea Slope Bottom Trawl Survey | 78 | 2016 - 2002 (6) | 201 - 1,200 | 32,861.3 | 37 |  |
| Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 2024 - 1982 (42) | 1 - 200 | 492,989.9 | 28 | 515 |
| Gulf of Alaska Bottom Trawl Survey | 47 | 2023 - 1990 (16) | 1 - 1,000 | 313,287.0 | 37 | 6,939 |
| Northern Bering Sea Crab/Groundfish Survey - Eastern Bering Sea Shelf Survey Extension | 143 | 2023 - 2010 (6) | 1 - 100 | 198,866.8 | 4 | 144 |

### 1.5.1 **Aleutian Islands**

Most recent data report: (Von Szalay et al., 2023)

* Upper Continental Slope of the Aleutian Islands from Unimak Pass to Stalemate Bank
* Triennial (1990s)/Biennial since 2000 in even years, since 1992
* Modified Index-Stratified Random of Successful Stations Survey Design
* Important commercial fish species include Atka mackerel, [Pacific ocean perch](https://www.fisheries.noaa.gov/species/pacific-ocean-perch), [walleye pollock](https://www.fisheries.noaa.gov/species/alaska-pollock), [Pacific cod](https://www.fisheries.noaa.gov/species/pacific-cod), [sablefish](https://www.fisheries.noaa.gov/species/sablefish), and other rockfish species.

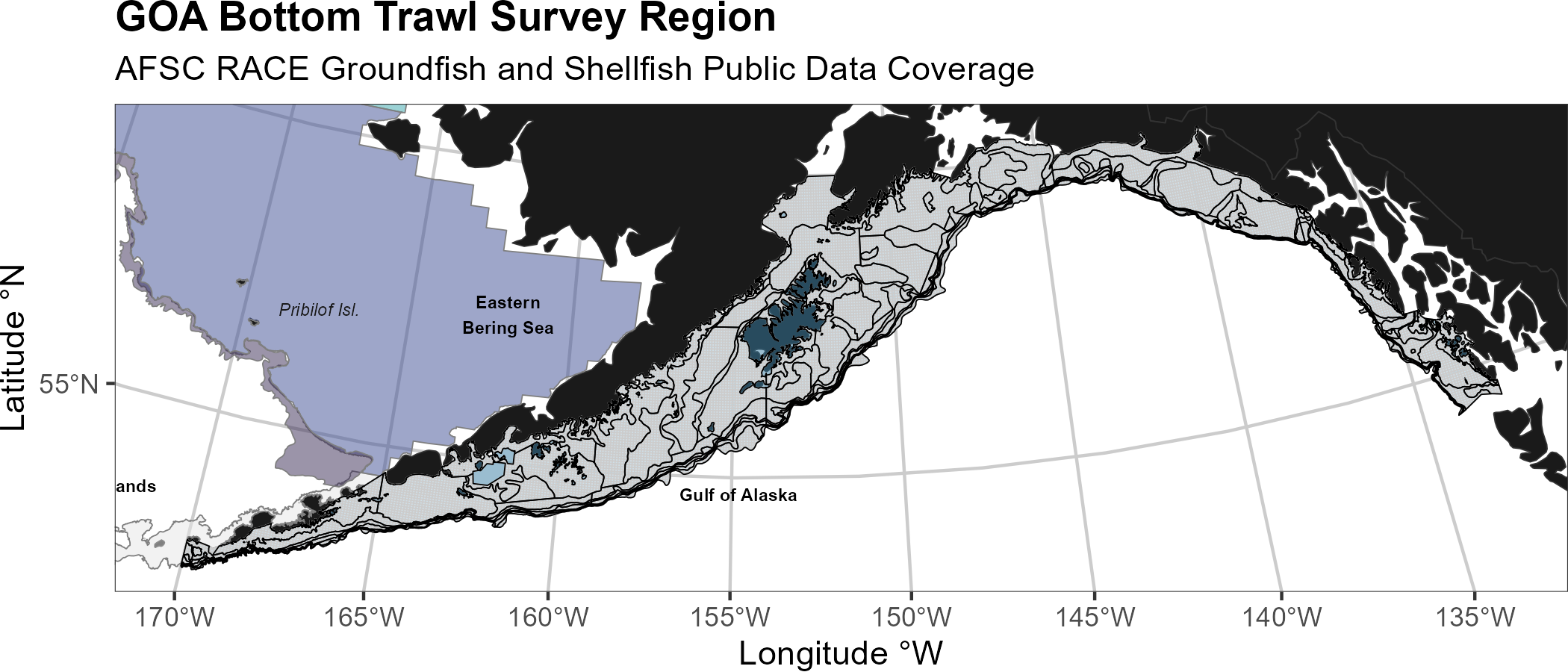


Strata used in the Aleutian Islands bottom trawl survey.

### 1.5.2 **Gulf of Alaska**

Most recent data report: (Siple et al., 2024)

* Continental Shelf and Upper Slope of the Gulf of Alaska extending from the Islands of Four Mountains 2,300 km east to Dixon Entrance
* Triennial (1990s)/Biennial since 2001 in odd years, since 1991
* Stratified Random Survey Design
* Important commercial species in the Gulf of Alaska include [Pacific ocean perch](https://www.fisheries.noaa.gov/species/pacific-ocean-perch), [walleye pollock](https://www.fisheries.noaa.gov/species/alaska-pollock), [Pacific cod](https://www.fisheries.noaa.gov/species/pacific-cod), flatfish, and other rockfish species.

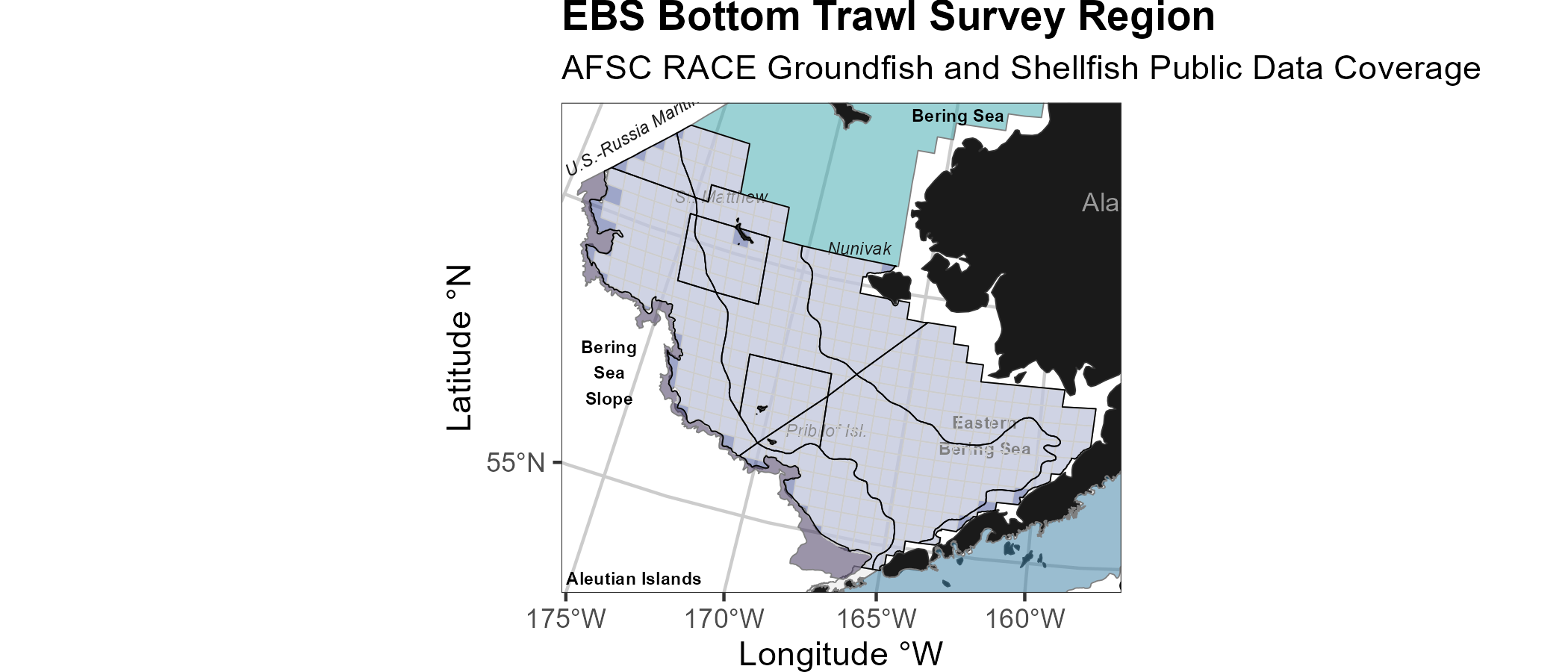


Strata used in the Gulf of Alaska bottom trawl survey.

### 1.5.3 **Eastern Bering Sea Shelf**

Most recent data report: (Markowitz et al., 2024)

* The continental shelf of the eastern Bering Sea from the Aleutian Islands to the Bering Strait
* Conducted annually since 1982.
* Uses a stratified systematic sampling survey design with fixed stations at center of 20 x 20 nm grid.
* Similar in design to the northern Bering Sea shelf bottom trawl survey.
* Focus species for the Bering Sea include [walleye pollock](https://www.fisheries.noaa.gov/species/alaska-pollock), [Pacific cod](https://www.fisheries.noaa.gov/species/pacific-cod), [Greenland turbot](https://www.fisheries.noaa.gov/species/greenland-turbot), [yellowfin sole](https://www.fisheries.noaa.gov/species/yellowfin-sole), [northern rock sole](https://www.fisheries.noaa.gov/species/rock-sole), [red king crab](https://www.fisheries.noaa.gov/species/red-king-crab), and [snow](https://www.fisheries.noaa.gov/species/alaska-snow-crab) and Tanner crabs.



Strata used in the Eastern Bering Sea bottom trawl survey.

### 1.5.4 **Northern Bering Sea**

Most recent data report: (Markowitz et al., 2024)

* The continental shelf of the northern Bering Sea, including the area north of St. Lawrence Island and Norton Sound
* Biennial/Annual; conducted intermittently since 2010
* Uses a stratified systematic sampling survey design with fixed stations at center of 20 x 20 nm grid.
* Similar in design to the eastern Bering Sea shelf bottom trawl survey.



Strata used in the Northern Bering Sea bottom trawl survey.

### 1.5.5 **Eastern Bering Sea Upper Continental Slope**

Most recent data report: (Hoff, 2016)

* The eastern Bering Sea upper continental slope survey area extends from Unalaska and Akutan Islands to the U.S.-Russian Maritime Boundary at 61° N near the International Date Line (166° E to 180° W) at depths from 200 to 1,200 m
* Conducted intermittently since 2002 (funding dependent)
* Modified Index-Stratified Random of Successful Stations Survey Design
* Focus species for the Bering Sea slope include giant grenadier, [Pacific ocean perch](https://www.fisheries.noaa.gov/species/pacific-ocean-perch), popeye grenadier, [walleye pollock](https://www.fisheries.noaa.gov/species/alaska-pollock), and [arrowtooth flounder](https://www.fisheries.noaa.gov/species/arrowtooth-flounder).



Strata used in the Bering Sea Slope bottom trawl survey.

# 2. Workflow

## 2.1 Operational Product Development Timeline

Over the course of the year, the survey team is developing a variety of different data products. Planning and preparation for surveys happens in the late winter and spring, surveys occur in the summer, data validation takes place over the course of the survey and after the survey, and data products are produced through fall and late winter.

|  | January | February | March | April | May | June | July | August | September | October | November | December |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Surveys |  |  |  |  | 1 | 1 | 1 | 1 |  |  |  |  |
| Planning | 1 | 1 | 1 |  |  |  |  |  | 1 | 1 | 1 | 1 |
| Development | 1 | 1 | 1 | 1 | 1 |  |  |  |  | 1 | 1 | 1 |
| Deployment (survey deliverables) |  |  |  |  |  |  |  |  | 1 | 1 | 1 | 1 |
| Deployment (survey operations) |  |  |  |  | 1 | 1 | 1 | 1 |  |  |  |  |
| Triage (fixing bugs and errors) | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| User feedback and brainstorming | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

## 2.2 Data workflow from boat to production

Organisms first need to be collected aboard the vessel before data can be entered into tablets.

|  |
| --- |
| Figure 2.1: Simplified boat deck processing workflow. |

The objective of this process is to take raw data, QA/QC and clean these data, curate standard data products for these survey. Please note, through this process we are not providing “data” (what we consider lower level data material; see the data levels section below) but “data products”, which is intended to facilitate the most fool-proof standard interpretation of the data. These data products only use data from standard and validated hauls, and has undergone careful review.

**Once survey data collected on the vessel has been checked and validated**, the [gap\_products/code/run.R](https://github.com/afsc-gap-products/gap_products/blob/main/code/run.R) script is used to orchestrate a sequence of programs that calculate the standard data products resulting from the NOAA AFSC GAP bottom trawl surveys. Standard data products are the CPUE, BIOMASS, SIZECOMP, and AGECOMP tables in the GAP\_PRODUCTS Oracle schema. The tables are slated to be updated twice a year: once after the survey season following finalization of that summer’s bottom trawl survey data to incorporate the new catch, size, and effort data and once prior to an upcoming survey to incorporate new age data that were processed after the prior summer’s survey season ended. This second pre-survey production run will also incorporate changes in the data due to the specimen voucher process as well as other post-hoc changes in the survey data.

The data from these surveys constitute a **living data set** so we can continue to **provide the best available data to all partners, stakeholders, and fellow scientists**.

|  |
| --- |
| Figure 2.2: Simplified data workflow from boat to production. |

During each data product run cycle:

1. Versions of the tables in GAP\_PRODUCTS are locally imported within the gap\_products repository to compare with the updated production tables. Any changes to a production table will be compared and checked to make sure those changes are intentional and documented.
2. Use the gapindex R package to calculate the four major standard data products: CPUE, BIOMASS, SIZECOMP, AGECOMP. These tables are compared and checked to their respective locally saved copies and any changes to the tables are vetted and documented. These tables are then uploaded to the GAP\_PRODUCTS Oracle schema.
3. Calculate the various materialized views for AKFIN and FOSS purposes. Since these are derivative of the tables in GAP\_PRODUCTS as well as other base tables in RACEBASE and RACE\_DATA, it is not necessary to check these views in addition to the data checks done in the previous steps.

|  |
| --- |
| Figure 2.3: Major end-users of the GAP data product tables. |

## 2.3 Data levels

GAP produces numerous data products that are subjected to different levels of processing, ranging from raw to highly-derived. The suitability of these data products for analysis varies and there is ambiguity about which data products can be used for which purpose. This ambiguity can create challenges in communicating about data products and potentially lead to misunderstanding and misuse of data. One approach to communicating about the level of processing applied to data products and their suitability for analysis is to describe data products using a Data Processing Level system. Data Processing Level systems are widely used in earth system sciences to characterize the extent of processing that has been applied to data products. For example, the NOAA National Centers for Environmental Information (NCEI) Satellite Program uses a Data Processing Level system to describe data on a scale of 0-4, where Level 0 is raw data and Level 4 is model output or results from analysis. Example of how [NASA remote sensing data products](https://ladsweb.modaps.eosdis.nasa.gov/search/) are shared through a public data portal with levels of data processing and documentation.

For more information, see [Sean Rohan’s October 2022 SCRUGS presentation](https://docs.google.com/presentation/d/1rWSZpeghWJqzWMIa5oBc4BCoy-zy1Yue86RoTw58u6M/edit?usp=sharing) on the topic.

* **Level 0**: Raw and unprocessed data. Ex: Data on the G drive, some tables in RACE\_DATA
* **Level 1**: Data products with QA/QC applied that may or may not be expanded to analysis units, but either not georeferenced or does not include full metadata. Ex: Some tables in RACE\_DATA and RACEBASE
* **Level 2**: Analysis-ready data products that are derived for a standardized extent and account for zeros and missing/bad data. Ex: CPUE tables, some data products in public-facing archives and repositories
* **Level 3**: Data products that are synthesized across a standardized extent, often inputs in a higher-level analytical product. Ex: Abundance indices, some data products in public-facing archives and repositories
* **Level 4**: Analytically generated data products that are derived from lower-level data, often to inform management. Ex: Biological reference points from stock assessments, Essential Fish Habitat layers, indicators in Ecosystem Status Reports and Ecosystem and Socioeconomic Profiles

# 3. News

## 3.1 News/change logs

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-12-10) using gapindex v3.0.2](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-12-10.txt): Run completed by: Sean Rooney

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-10-22) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-10-22.txt): Run completed by: Zack Oyafuso

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-10-21) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-10-21.txt): Run completed by: Duane Stevenson, Ned Laman, Zack Oyafuso

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-09-05) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-09-05.txt): Run completed by: Ned Laman, Zack Oyafuso

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-09-03) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-09-03.txt): Run completed by: Ned Laman, Zack Oyafuso

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-08-29) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-08-29.txt): The additions of previous years’ age data and 2024 EBS catch, effort, and size data

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-08-20) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-08-20.txt): Initial 2024 post-survey run with new ages since last run and all of EBS Shelf 2024 survey data but none of AI 2024 survey data. While trying to update the records in the GAP\_PRODUCTS table, the connection was terminated, partially uploading records in the agecomp tables and outputting NA to the N\_HAUL and N\_LENGTH fields in the biomass tables. At this point, the GAP\_PRODUCTS tables are incomplete. The AKFIN and FOSS tables were NOT updated in this run.

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-05-04) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-05-04.txt): A development branch version of gapindex called [using\_datatable](https://github.com/afsc-gap-products/gap_products/tree/using_datatable) uses the data.table package for many dataframe manipulations, which greatly decreased the computation time of many of the functions. There were no major changes in the calculations in this version of the gapindex package and thus the major changes listed below are not related to the gapindex package. The only major change from this run was the addition of GOA 2023 Pacific Ocean perch read otolith data.

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-04-09) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-04-09.txt): A development branch version of gapindex called [using\_datatable](https://github.com/afsc-gap-products/gap_products/tree/using_datatable) uses the data.table package for many dataframe manipulations, which greatly decreased the computation time of many of the functions. There were no major changes in the calculations in this version of the gapindex package and thus the major changes listed below are not related to the gapindex package.

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-02-29) using gapindex v2.2.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-02-29.txt): A new version of gapindex [2.2.0](https://github.com/afsc-gap-products/gapindex/releases/tag/v2.2.0) was used for this production run and now accesses taxonomic information from RACEBASE.SPECIES instead of GAP\_PRODUCTS.TAXONOMIC\_CLASSIFICATION. As a result, there will be some SPECIES\_CODE values that are supported due to slight differences between the two tables. Discussion in this [github issue #54](https://github.com/afsc-gap-products/gapindex/issues/54). As a result there are new cpue records for SPECIES\_CODE values 22290 and 22292 and removed cpue records for SPECIES\_CODE values 21345, 22200 and 69326.

– [GAP\_PRODUCTS ChangeLog (last produced on 2024-01-09) using gapindex v2.1.3](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2024-01-09.txt): A new version of gapindex ([v2.1.3](https://github.com/afsc-gap-products/gapindex/releases/tag/v2.1.3)) was used to produced these data. Data for SPECIES\_CODE 68590 (Chionoecetes hybrids) are now removed, per this issue (https://github.com/afsc-gap-products/gap\_products/issues/3). New read otolith data were incorporated into the age compositions. GOA depth subareas are now included in the size comps, and there were some modifications with EBS skate length data that are now incorporated into the length compositions.

– [GAP\_PRODUCTS ChangeLog (last produced on 2023-11-17) using gapindex v2.1.2](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2023-11-17.txt): A new version of gapindex ([v2.1.2](https://github.com/afsc-gap-products/gapindex/releases/tag/v2.1.2)) was used to produced these data. There was a slight change to how subarea biomass totals are calculated that was not fully addressed in v2.1.1. The modified biomass records reflect this change.

– [GAP\_PRODUCTS ChangeLog (last produced on 2023-11-14) using gapindex v2.1.1](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2023-11-14_v2-1-1.txt): A new version of gapindex (v2.1.1) was used to produced these data. There was a slight change to how subarea biomass totals are calculated. The modified biomass records reflect this change. New 2022 otolith data were available since the last iteration of the GAP\_PRODUCTS for Aleutian Island Pacific ocean perch and northern rockifsh and Eastern Bering Sea northern rock sole. Zero-filled CPUE records for four GOA species codes (SPECIES\_CODE: 21210, 30010, 30360, 77102, 98101) were added due to how the 1990 data were integrated in the last production run of GAP\_PRODUCTS. Two Arctic cod (SPECIES\_CODE: 21725) and one plain sculpin (SPECIES\_CODE: 21371) count records were modified in the NBS data, which changes the numerical CPUE estimates for those hauls which changes the estimated population abundance and size composition for those species.

– [Groundfish Assessment Program Survey Data Serving and Data Improvements](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2023-06-20_datachangesbreif): Initial data changes brief distributed to SSMA and other partners by Ned Laman, Zack Oyafuso, and Emily Markowitz

– [Run 2023-06-01 gapindex v2.1.0](https://raw.githubusercontent.com/afsc-gap-products/gap_products/main/content/intro-news/2023-06-01_v2-1-0.txt): Initial compiling and planning notes

# 4. Code of Conduct

## 4.1 What are Codes of Conduct?

Codes of Conduct are voluntary sets of rules that assist creators, developers, and users of code and data with data protection compliance and accountability in specific sectors or relating to particular processing operations.

Codes can help organizations to ensure all participants follow best practices and rules designed specifically for their sector or processing operations, thus enhancing compliance and collaboration. They are developed and managed by an association or other body (the ‘Code Owner’) which is representative of a sector (or category of data controllers or processors), with the expert and sectoral knowledge of how to enhance data protection in their area.

### 4.1.1 [Code of Conduct](https://github.com/nmfs-opensci/.github/blob/main/CODE_OF_CONDUCT.md) from the [nmfs-opensci GitHub](https://nmfs-opensci.github.io/).

# 5. NOAA Fisheries Open Science Code of Conduct

This code of conduct was developed and adapted from the Atom code of conduct in October 2021.

## 5.1 Our Pledge

In the interest of fostering an open and welcoming environment, we as contributors and maintainers pledge to making participation in our project and our community a harassment-free experience for everyone, regardless of age, body size, disability, ethnicity, gender identity and expression, level of experience, nationality, personal appearance, race, religion, or sexual identity and orientation.

## 5.2 Our Standards

Examples of behavior that contributes to creating a positive environment include:

* Using welcoming and inclusive language
* Being respectful of differing viewpoints and experiences
* Gracefully accepting constructive criticism
* Focusing on what is best for the community
* Showing empathy towards other community members

Examples of unacceptable behavior by participants include:

* The use of sexualized language or imagery and unwelcome sexual attention or advances
* Trolling, insulting/derogatory comments, and personal or political attacks
* Public or private harassment
* Publishing others’ private information, such as a physical or electronic address, without explicit permission
* Other conduct which could reasonably be considered inappropriate in a professional setting

## 5.3 Our Responsibilities

Project maintainers are responsible for clarifying the standards of acceptable behavior and are expected to take appropriate and fair corrective action in response to any instances of unacceptable behavior.

Project maintainers have the right and responsibility to remove, edit, or reject comments, commits, code, wiki edits, issues, and other contributions that are not aligned to this Code of Conduct, or to ban temporarily or permanently any contributor for other behaviors that they deem inappropriate, threatening, offensive, or harmful.

## 5.4 Scope

This Code of Conduct applies both within project spaces and in public spaces when an individual is representing the project or its community. Examples of representing a project or community include using an official project e-mail address, posting via an official social media account, or acting as an appointed representative at an online or offline event. Representation of a project may be further defined and clarified by project maintainers.

## 5.5 Enforcement

Instances of abusive, harassing, or otherwise unacceptable behavior may be reported by contacting the project team. All complaints will be reviewed and investigated and will result in a response that is deemed necessary and appropriate to the circumstances. Further details of specific enforcement policies may be posted separately.

## 5.6 Attribution

This Code of Conduct is adapted from the [Contributor Covenant](https://contributor-covenant.org), version 1.4, available at [https://contributor-covenant.org/version/1/4](https://contributor-covenant.org/version/1/4/)

# 6. Data description

## 6.1 Data tables

### 6.1.1 AGECOMP

Stratum- and region-level age compositions by sex. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 680,094

Number of columns: 10

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SEX

Sex of a specimen

ID key code

NUMBER(38,0)

Sex of a specimen where “1” = “Male”, “2” = “Female”, “3” = Unsexed.

AGE

Taxon age bin (yrs)

integer

NUMBER(38,0)

Age bin of taxon. Age bin of a taxon in years estimated by the age comp estimate. Age -9 indicates unaged lengths for a particular sex because no otoliths were collected for that sex/length combination. Age -99 indicates a case where no lengths were collected within a stratum for a species/year even though catch numbers were recorded.

POPULATION\_COUNT

Estimated population

numeric

NUMBER(38,0)

The estimated population caught in the survey for a species, group, or total for a given survey.

LENGTH\_MM\_MEAN

Mean length at age weighted by numbers at length

numeric

NUMBER(38,3)

Mean length (millimeters)

LENGTH\_MM\_SD

Standard deviation of length at age weighted by numbers at length

numeric

NUMBER(38,3)

Variance of mean length.

AREA\_ID\_FOOTPRINT

Survey Footprint

text

VARCHAR2(4000 BYTE)

Survey footprint, usually equivalent to the SURVEY\_DEFINITION\_ID with the exception of the Standard and Standard +NW survey footprints in the Eastern Bering Sea shelf bottom trawl survey

### 6.1.2 AREA

Information related to the various strata, subareas, INPFC and NMFS management areas, and regions for the Aleutian Islands, Gulf of Alaska, and Bering Sea shelf and slope bottom trawl surveys. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 395

Number of columns: 9

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

DESIGN\_YEAR

Design year

year

NUMBER(10,0)

Year ID associated with a given value AREA\_ID. This field describes the changes in the survey design over time.

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

AREA\_TYPE

Area ID type description

category

VARCHAR2(255 BYTE)

The type of stratum that AREA\_ID represents. Types include: STRATUM (the smallest building-block unit of area in these surveys), REGION, DEPTH, SUBAREA, INPFC BY DEPTH, INPFC, SUBAREA BY DEPTH, REGULATORY AREA, NMFS STATISTICAL AREA.

AREA\_NAME

Area ID name

text

VARCHAR2(4000 BYTE)

Descriptive name of each AREA\_ID. These names often identify the region, depth ranges, or other regional information for the area ID.

DESCRIPTION

Description

text

VARCHAR2(4000 BYTE)

Description of row observation.

AREA\_KM2

Area (km2)

kilometers squared

NUMBER(38,3)

Area in square kilometers.

DEPTH\_MIN\_M

Area ID minimum depth (m)

meters

NUMBER(38,3)

Minimum depth (meters).

DEPTH\_MAX\_M

Area ID maximum depth (m)

meters

NUMBER(38,3)

Maximum depth (meters).

### 6.1.3 BIOMASS

Stratum/subarea/region-level mean CPUE (weight and numbers), total biomass, and total abundance with associated variances. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 2,656,482

Number of columns: 16

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

CPUE\_KGKM2\_MEAN

Mean weight CPUE

kilograms per kilometers squared

NUMBER(38,6)

The mean catch weight (kilograms) per unit effort (area swept by the net, units squared kilometers).

CPUE\_NOKM2\_MEAN

Mean numeric CPUE

count per kilometers squared

NUMBER(38,6)

The mean of numerical catch per unit effort (area swept by the net, units square kilometers).

N\_HAUL

Valid hauls

count

NUMBER(38,0)

Total number of hauls.

N\_WEIGHT

Hauls with catch

count

NUMBER(38,0)

Total number of hauls with positive catch biomass.

N\_COUNT

Hauls with taxon counts

numeric

NUMBER(38,0)

Total number of hauls with positive count data.

N\_LENGTH

Hauls with taxon lengths

count

NUMBER(38,0)

Total number of hauls with length data.

BIOMASS\_MT

Estimated biomass

numeric

NUMBER(38,6)

The estimated total biomass.

BIOMASS\_VAR

Estimated biomass variance

numeric

NUMBER(38,6)

The estimated variance associated with the total biomass.

POPULATION\_COUNT

Estimated population

numeric

NUMBER(38,0)

The estimated population caught in the survey for a species, group, or total for a given survey.

POPULATION\_VAR

Estimated population variance

numeric

NUMBER(38,6)

The estimated population variance caught in the survey for a species, group, or total for a given survey.

CPUE\_KGKM2\_VAR

Variance of the mean weight CPUE

kilograms per kilometers squared

NUMBER(38,6)

The variance of mean catch weight (kilograms) per unit effort (area swept by the net, units squared kilometers).

CPUE\_NOKM2\_VAR

Variance of the mean numeric CPUE

count per kilometers squared

NUMBER(38,6)

The variance of mean numerical catch per unit effort (area swept by the net, units square kilometers).

### 6.1.4 CPUE

Haul-level zero-filled weight and numerical catch-per-unit-effort. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 21,558,257

Number of columns: 7

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

WEIGHT\_KG

Sample or taxon weight (kg)

kilograms

NUMBER(38,3)

Weight (thousandths of a kilogram) of individuals in a haul by taxon.

COUNT

Taxon count

count, whole number resolution

NUMBER(38,0)

Total whole number of individuals caught in haul or samples collected.

AREA\_SWEPT\_KM2

Area swept (km)

kilometers

NUMBER(38,6)

The area the net covered while the net was fishing (kilometers squared), defined as the distance fished times the net width.

CPUE\_KGKM2

Weight CPUE (kg/km2)

kilograms per kilometers squared

NUMBER(38,6)

Catch weight (kilograms) per unit effort (area swept by the net, units square kilometers).

CPUE\_NOKM2

Number CPUE (no/km2)

count per kilometers squared

NUMBER(38,6)

Numerical catch per unit effort (area swept by the net, units square kilometers).

### 6.1.5 SIZECOMP

Stratum/subarea/region-level size compositions by sex. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 3,239,488

Number of columns: 7

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

LENGTH\_MM

Length of a specimen

millimeters

NUMBER(10,0)

Length bin in millimeters. A length of -9 indicates cases where no lengths were collected within a stratum for a species/year, even though catch numbers were recorded.

SEX

Sex of a specimen

ID key code

NUMBER(38,0)

Sex of a specimen where “1” = “Male”, “2” = “Female”, “3” = Unsexed.

POPULATION\_COUNT

Estimated population

numeric

NUMBER(38,0)

The estimated population caught in the survey for a species, group, or total for a given survey.

### 6.1.6 SPECIES\_YEAR

This is a table

Number of rows: 18

Number of columns: 2

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

### 6.1.7 STRATUM\_GROUPS

Lookup table for which strata are contained within a given subarea, INPFC or NMFS management area, or region for the Aleutian Islands, Gulf of Alaska, and Bering Sea shelf and slope bottom trawl surveys. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 768

Number of columns: 4

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

DESIGN\_YEAR

Design year

year

NUMBER(10,0)

Year ID associated with a given value AREA\_ID. This field describes the changes in the survey design over time.

STRATUM

Stratum ID

ID key code

NUMBER(10,0)

RACE database statistical area for analyzing data. Strata were designed using bathymetry and other geographic and habitat-related elements. The strata are unique to each survey region. Stratum of value 0 indicates experimental tows.

### 6.1.8 SURVEY\_DESIGN

This table contains for a given survey (via SURVEY\_DEFINITION\_ID) and survey year (YEAR), which version (DESIGN\_YEAR) of the AREA\_IDs that were used to calculate the various standard data products. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 87

Number of columns: 3

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

DESIGN\_YEAR

Design year

year

NUMBER(10,0)

Year ID associated with a given value AREA\_ID. This field describes the changes in the survey design over time.

### 6.1.9 TAXON\_GROUPS

GAP\_PRODUCTS.TAXONOMIC\_CLASSIFICATION subsetted for taxonomic classifications accepted by the GAP bottom trawl survey and added GROUP\_CODE to denote taxonomic aggregations. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 25 October 2024.

Number of rows: 2,777

Number of columns: 22

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SPECIES\_NAME

Scientific name of species

text

VARCHAR2(255 BYTE)

Scientific name of species.

COMMON\_NAME

Taxon common name

text

VARCHAR2(255 BYTE)

The common name of the marine organism associated with the scientific\_name and species\_code columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

ID\_RANK

Lowest taxonomic rank

text

VARCHAR2(255 BYTE)

Lowest taxonomic rank of a given species entry.

DATABASE

Database source

category

VARCHAR2(255 BYTE)

Taxonomic database source, either ITIS or WoRMS.

DATABASE\_ID

Species ID in database

ID key code

VARCHAR2(255 BYTE)

Species ID key code of a species in the taxonomic “DATABASE” source.

GENUS\_TAXON

Genus phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of genus of a given species.

SUBFAMILY\_TAXON

Subfamily phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subfamily of a given species.

FAMILY\_TAXON

Family phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of family of a given species.

SUPERFAMILY\_TAXON

Superfamily phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superfamily of a given species.

INFRAORDER\_TAXON

Infraorder phylogenetic rank

category

VARCHAR2(255 BYTE)

Infraorder phylogenetic rank. Phylogenetic latin rank of infraorder of a given speices.

SUBORDER\_TAXON

Suborder phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of suborder of a given species.

ORDER\_TAXON

Order phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of order of a given species.

SUPERORDER\_TAXON

Superorder phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superorder of a given species.

INFRACLASS\_TAXON

Infraclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Infraclass phylogenetic rank. Phylogenetic latin rank of infraclass of a given speices.

SUBCLASS\_TAXON

Subclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subclass of a given species.

CLASS\_TAXON

Class phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of class of a given species.

SUPERCLASS\_TAXON

Superclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superclass of a given species.

SUBPHYLUM\_TAXON

Subphylum phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subphylum of a given species.

PHYLUM\_TAXON

Phylum phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of phylum of a given species.

KINGDOM\_TAXON

Kingdom phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of kingdom of a given species.

GROUP\_CODE

Species or Complex ID

ID key code

NUMBER(38,0)

Equivalent to the SPECIES\_CODE if the taxon is reported as a single taxon in GAP\_PRODUCTS, otherwise denotes a SPECIES\_CODE of a higher taxonomic group to which the taxon is aggregated in the GAP\_PRODUCTS CPUE and BIOMASS tables.

# 7. Universal Column Metadata

This table is used to string together the various field comments for the tables in GAP\_PRODUCTS. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

| **Column name from data** | **Descriptive column Name** | **Units** | **Oracle data type** | **Column description** |
| --- | --- | --- | --- | --- |
| ABUNDANCE\_HAUL | Design-based index approved haul | logical | VARCHAR2(255 BYTE) | Logical, describing if this haul was conducted in a standard manner and thus used for design-based index estimates (TRUE) or not (FALSE). |
| ACCESSORIES | Type of gear accessories used on the net | ID key code | NUMBER(38,0) | Type of accessories used on net. For a complete list of accessories ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| ACTION | Database action | text | VARCHAR2(255 BYTE) | Standard action taken to alter current database record |
| ACTIVE | Vessel active/inactive | logical | VARCHAR2(255 BYTE) | Logical, describing if a vessel is active (TRUE) or not (FALSE). |
| AGE | Taxon age bin (yrs) | integer | NUMBER(38,0) | Age bin of taxon. Age bin of a taxon in years estimated by the age comp estimate. Age -9 indicates unaged lengths for a particular sex because no otoliths were collected for that sex/length combination. Age -99 indicates a case where no lengths were collected within a stratum for a species/year even though catch numbers were recorded. |
| AGENCY\_ACRONYM | Acronym of listed Agency | text abbreviated | VARCHAR2(255 BYTE) | Abbreviated agencies that are affiliated with the Alaska bottom trawl survey. The column agency\_acronym is associated with the agency\_short and agency\_long columns. |
| AGENCY\_JOIN | Agency ID | ID key code | NUMBER(38,0) | Affiliated agency ID key code. |
| AGENCY\_LONG | Official name of agency | text | VARCHAR2(255 BYTE) | Full official name of affiliated agencies to the Alaska bottom trawl survey. The column agency\_long is associated with the agency\_acronym and agency\_short columns. |
| AGENCY\_SHORT | Agency shorthand name | text | VARCHAR2(255 BYTE) | A sort version of the full official name of affiliated agencies to the Alaska bottom trawl survey. The column agency\_short is associated with the agency\_acronym and agency\_long columns. |
| AGE\_DETERMINATION\_METHOD | Aging method | ID key code | NUMBER(10,0) | Numeric code corresponding to the method of age determination. For a complete list of age determination codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| AGE\_DETERMINATION\_METHODS | Age determination method | ID key code | NUMBER(38,0) | A unique ID used to identify this age determination method. |
| AGE\_YEAR | Age bin of taxon | year | NUMBER(38,0) | Age bin of a taxon in years estimated by the age comp estimate. |
| AREAJOIN | Area polygon ID | ID key code | NUMBER(38,0) | A call sign is a designated sequence of letters and numbers that are assigned when a vessel, whether it be a sailing yacht, motor yacht, rib or commercial vessel, receives its Ship Radio Licence. The vessel also receives its MMSI number, so that each vessel is uniquely identified. |
| AREA\_ID | Area ID | ID key code | NUMBER(38,0) | Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey. |
| AREA\_ID\_FOOTPRINT | Survey Footprint | text | VARCHAR2(4000 BYTE) | Survey footprint, usually equivalent to the SURVEY\_DEFINITION\_ID with the exception of the Standard and Standard +NW survey footprints in the Eastern Bering Sea shelf bottom trawl survey |
| AREA\_KM2 | Area (km2) | kilometers squared | NUMBER(38,3) | Area in square kilometers. |
| AREA\_NAME | Area ID name | text | VARCHAR2(4000 BYTE) | Descriptive name of each AREA\_ID. These names often identify the region, depth ranges, or other regional information for the area ID. |
| AREA\_SWEPT\_KM2 | Area swept (km) | kilometers | NUMBER(38,6) | The area the net covered while the net was fishing (kilometers squared), defined as the distance fished times the net width. |
| AREA\_TYPE | Area ID type description | category | VARCHAR2(255 BYTE) | The type of stratum that AREA\_ID represents. Types include: STRATUM (the smallest building-block unit of area in these surveys), REGION, DEPTH, SUBAREA, INPFC BY DEPTH, INPFC, SUBAREA BY DEPTH, REGULATORY AREA, NMFS STATISTICAL AREA. |
| BIOMASS\_MT | Estimated biomass | numeric | NUMBER(38,6) | The estimated total biomass. |
| BIOMASS\_VAR | Estimated biomass variance | numeric | NUMBER(38,6) | The estimated variance associated with the total biomass. |
| BOTTOM\_TEMPERATURE\_C | Bottom temperature (degrees Celsius) | degrees Celsius | NUMBER(38,1) | Bottom temperature (tenths of a degree Celsius); NA indicates removed or missing values. |
| BOTTOM\_TYPE | Seafloor bottom type code | ID key code | NUMBER(38,0) | Bottom type on sea floor at haul location. For a complete list of bottom type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| CATALOG\_NUM | Catalog number | text | VARCHAR2(255 BYTE) | Museum catalog number associated with record |
| CATCHJOIN | Catch observation ID | ID key code | NUMBER(38,0) | Unique integer ID assigned to each survey, vessel, year, and catch observation combination. |
| CLASSIFICATION | Taxonomic classification rank group | category | VARCHAR2(255 BYTE) | Phylogenetic classification group rank for a given species. |
| CLASS\_TAXON | Class phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of class of a given species. |
| COLLECTED\_BY | Person who collected specimen | text | VARCHAR2(255 BYTE) | Initials of person who collected specimen in the field |
| COMMENTS | Comments | text | VARCHAR2(4000 BYTE) | Comments regarding row observation. |
| COMMON\_NAME | Taxon common name | text | VARCHAR2(255 BYTE) | The common name of the marine organism associated with the scientific\_name and species\_code columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| COUNT | Taxon count | count, whole number resolution | NUMBER(38,0) | Total whole number of individuals caught in haul or samples collected. |
| COUNTRY\_ID | Country code | ID key code | NUMBER(38,0) | Country ID key code of where a vessel, for example, may be from. For a complete list of country ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| CPUE\_KGHA | Weight CPUE (kg/ha) | kilograms per hectare | NUMBER(38,6) | Catch weight (kilograms) per unit effort (area swept by the net, units hectares). |
| CPUE\_KGKM2 | Weight CPUE (kg/km2) | kilograms per kilometers squared | NUMBER(38,6) | Catch weight (kilograms) per unit effort (area swept by the net, units square kilometers). |
| CPUE\_KGKM2\_MEAN | Mean weight CPUE | kilograms per kilometers squared | NUMBER(38,6) | The mean catch weight (kilograms) per unit effort (area swept by the net, units squared kilometers). |
| CPUE\_KGKM2\_VAR | Variance of the mean weight CPUE | kilograms per kilometers squared | NUMBER(38,6) | The variance of mean catch weight (kilograms) per unit effort (area swept by the net, units squared kilometers). |
| CPUE\_NOHA | Number CPUE (no/ha) | count per hectare | NUMBER(38,6) | Numerical catch per unit effort (area swept by the net, units hectares). |
| CPUE\_NOKM2 | Number CPUE (no/km2) | count per kilometers squared | NUMBER(38,6) | Numerical catch per unit effort (area swept by the net, units square kilometers). |
| CPUE\_NOKM2\_MEAN | Mean numeric CPUE | count per kilometers squared | NUMBER(38,6) | The mean of numerical catch per unit effort (area swept by the net, units square kilometers). |
| CPUE\_NOKM2\_VAR | Variance of the mean numeric CPUE | count per kilometers squared | NUMBER(38,6) | The variance of mean numerical catch per unit effort (area swept by the net, units square kilometers). |
| CRS | Coordinate reference system | ID key code | VARCHAR2(255 BYTE) | The coordinate reference system (CRS) that shapefiles were created in or areas (like AREA\_KM2) are calculated in, as defined by https://spatialreference.org/ (e.g., "+proj=longlat", "EPSG:3338"). |
| CRUISE | Cruise Name | ID key code | NUMBER(38,0) | This is a six-digit integer identifying the cruise number of the form: YYYY99 (where YYYY = year of the cruise; 99 = 2-digit number and is sequential; 01 denotes the first cruise that vessel made in this year, 02 is the second, etc.). |
| CRUISEJOIN | Cruise ID | ID key code | NUMBER(38,0) | Unique integer ID assigned to each survey, vessel, and year combination. |
| DATABASE | Database source | category | VARCHAR2(255 BYTE) | Taxonomic database source, either ITIS or WoRMS. |
| DATABASE\_ID | Species ID in database | ID key code | VARCHAR2(255 BYTE) | Species ID key code of a species in the taxonomic "DATABASE" source. |
| DATE | Date | YYYY-MM-DD | DATE | The date (YYYY-MM-DD) of the event (e.g., cruise). |
| DATE\_END | End date | YYYY-MM-DD | DATE | The date (YYYY-MM-DD) of the end of the event (e.g., cruise). |
| DATE\_START | Start date | YYYY-MM-DD | DATE | The date (YYYY-MM-DD) of the beginning of the event (e.g., cruise). |
| DATE\_TIME | Date and time | MM/DD/YYYY HH::MM | DATE | The date (MM/DD/YYYY) and time (HH:MM) of the haul. All dates and times are in Alaska time (AKDT) of Anchorage, AK, USA (UTC/GMT -8 hours). |
| DATE\_TIME\_END | End date and time | MM/DD/YYYY HH::MM | TIMESTAMP | The date (MM/DD/YYYY) and time (HH:MM) of the end of the haul. All dates and times are in Alaska time (AKDT) of Anchorage, AK, USA (UTC/GMT -8 hours). |
| DATE\_TIME\_START | Start date and time | MM/DD/YYYY HH::MM | TIMESTAMP | The date (MM/DD/YYYY) and time (HH:MM) of the beginning of the haul. All dates and times are in Alaska time (AKDT) of Anchorage, AK, USA (UTC/GMT -8 hours). |
| DEPTH\_GEAR\_M | Depth of gear (m) | degrees Celsius | NUMBER(38,1) | Depth of gear (meters). |
| DEPTH\_M | Depth (m) | degrees Celsius | NUMBER(38,1) | Bottom depth (meters). |
| DEPTH\_MAX\_M | Area ID maximum depth (m) | meters | NUMBER(38,3) | Maximum depth (meters). |
| DEPTH\_MIN\_M | Area ID minimum depth (m) | meters | NUMBER(38,3) | Minimum depth (meters). |
| DESCRIPTION | Description | text | VARCHAR2(4000 BYTE) | Description of row observation. |
| DESIGN\_YEAR | Design year | year | NUMBER(10,0) | Year ID associated with a given value AREA\_ID. This field describes the changes in the survey design over time. |
| DISTANCE\_FISHED\_KM | Distance fished (km) | kilometers | NUMBER(38,3) | Distance the net fished (kilometers). |
| DUMMY | dummy | dummy | VARCHAR2(255 BYTE) | dummy |
| DURATION\_HR | Tow duration (decimal hr) | hours | NUMBER(38,1) | This is the elapsed time between start and end of a haul (decimal hours). |
| FAMILY\_TAXON | Family phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of family of a given species. |
| FIELD\_ID | Field specimen identification | text | VARCHAR2(255 BYTE) | Field identification for the vouchered specimen |
| FREQUENCY | Count of observation | count | NUMBER(38,0) | Frequency, or count, of an observation. |
| GEAR | Type of gear used on the net | ID key code | NUMBER(38,0) | Type of gear used on net. For a complete list of gear ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| GEAR\_DEPTH\_M | Gear depth | meters | NUMBER(38,1) | Depth gear was deployed at (tenths of a meter). Gear depth plus net height equals bottom depth. |
| GEAR\_ID | Gear ID | ID key code | NUMBER(38,0) | Type of trawl or gear deployed. For a complete list of vessel gear type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| GEAR\_TEMPERATURE\_C | Gear temperature (degrees Celsius) | degrees Celsius | NUMBER(38,1) | Temperature recorded by net gear (tenths of a degree Celsius); NA indicates removed or missing values. |
| GENUS\_TAXON | Genus phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of genus of a given species. |
| GONAD\_G | Weight of gonads (g) | grams | NUMBER(38,1) | Weight of specimen gonads (grams). |
| GROUP\_CODE | Species or Complex ID | ID key code | NUMBER(38,0) | Equivalent to the SPECIES\_CODE if the taxon is reported as a single taxon in GAP\_PRODUCTS, otherwise denotes a SPECIES\_CODE of a higher taxonomic group to which the taxon is aggregated in the GAP\_PRODUCTS CPUE and BIOMASS tables. |
| HAUL | Haul number | ID key code | NUMBER(38,0) | This number uniquely identifies a sampling event (haul) within a cruise. It is a sequential number, in chronological order of occurrence. |
| HAULJOIN | Haul ID | ID key code | NUMBER(38,0) | This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination. |
| HAUL\_TYPE | Haul sampling type | ID key code | NUMBER(38,0) | Type of haul sampling method. For a complete list of haul type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| ID\_RANK | Lowest taxonomic rank | text | VARCHAR2(255 BYTE) | Lowest taxonomic rank of a given species entry. |
| INFRACLASS\_TAXON | Infraclass phylogenetic rank | category | VARCHAR2(255 BYTE) | Infraclass phylogenetic rank. Phylogenetic latin rank of infraclass of a given speices. |
| INFRAORDER\_TAXON | Infraorder phylogenetic rank | category | VARCHAR2(255 BYTE) | Infraorder phylogenetic rank. Phylogenetic latin rank of infraorder of a given speices. |
| ITIS | Integrated taxonomic information system (ITIS) serial number | ID key code | NUMBER(38,0) | Species code as identified in the Integrated Taxonomic Information System (https://itis.gov/). |
| KINGDOM\_TAXON | Kingdom phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of kingdom of a given species. |
| LATITUDE\_DD | Latitude (decimal degrees) | decimal degrees | NUMBER(38,6) | Latitude (one hundred thousandth of a decimal degree). |
| LATITUDE\_DD\_END | End latitude (decimal degrees) | decimal degrees | NUMBER(38,6) | Latitude (one hundred thousandth of a decimal degree) of the end of the haul. |
| LATITUDE\_DD\_START | Start latitude (decimal degrees) | decimal degrees | NUMBER(38,6) | Latitude (one hundred thousandth of a decimal degree) of the start of the haul. |
| LENGTH\_MM | Length of a specimen | millimeters | NUMBER(10,0) | Length bin in millimeters. A length of -9 indicates cases where no lengths were collected within a stratum for a species/year, even though catch numbers were recorded. |
| LENGTH\_MM\_MEAN | Mean length at age weighted by numbers at length | numeric | NUMBER(38,3) | Mean length (millimeters) |
| LENGTH\_MM\_SD | Standard deviation of length at age weighted by numbers at length | numeric | NUMBER(38,3) | Variance of mean length. |
| LENGTH\_TYPE | Length type | ID key code | NUMBER(38,0) | How the taxon was measured (e.g., fork length, carapace width). For a complete list of length\_type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| LONGITUDE\_DD | Longitude (decimal degrees) | decimal degrees | NUMBER(38,6) | Longitude (one hundred thousandth of a decimal degree). |
| LONGITUDE\_DD\_END | End longitude (decimal degrees) | decimal degrees | NUMBER(38,6) | Longitude (one hundred thousandth of a decimal degree) of the end of the haul. |
| LONGITUDE\_DD\_START | Start longitude (decimal degrees) | decimal degrees | NUMBER(38,6) | Longitude (one hundred thousandth of a decimal degree) of the start of the haul. |
| MATURITY | Specimen maturity code | ID key code | NUMBER(38,0) | The maturity code or the condition identified by the maturity code. |
| METADATA\_COLNAME | Column name | text | VARCHAR2(4000 BYTE) | Name of the column in a table. |
| METADATA\_COLNAME\_DESC | Column description | text | VARCHAR2(4000 BYTE) | Description of the column. |
| METADATA\_COLNAME\_LONG | Column name spelled out | text | VARCHAR2(4000 BYTE) | Long name for the column. |
| METADATA\_DATATYPE | Oracle datatype code | text | VARCHAR2(4000 BYTE) | Oracle data type of data column. |
| METADATA\_SENTENCE | Sentence | text | VARCHAR2(4000 BYTE) | Table metadata sentence. |
| METADATA\_SENTENCE\_NAME | Metadata sentence name | text | VARCHAR2(4000 BYTE) | Name of table metadata sentence. |
| METADATA\_SENTENCE\_TYPE | Sentence type | text | VARCHAR2(4000 BYTE) | Type of sentence to have in table metadata. |
| METADATA\_UNITS | Units | category | VARCHAR2(4000 BYTE) | Units of the column. |
| NET\_HEIGHT\_M | Net height (m) | meters | NUMBER(38,1) | Measured or estimated distance (meters) between footrope and headrope of the trawl. |
| NET\_MEASURED | Net measured during haul | logical | BINARY\_DOUBLE | Logical, describing if the net was measured (TRUE) or not (FALSE) by wheelhouse and marport programs during the haul. |
| NET\_WIDTH\_M | Net width (m) | meters | NUMBER(38,1) | Measured or estimated distance (meters) between wingtips of the trawl. |
| NEW\_ID | New specimen identification | text | VARCHAR2(255 BYTE) | Confirmed taxonomist identification of the vouchered specimen |
| NEW\_SPECIES\_CODE | New species code | ID key code | NUMBER(10,0) | Species code associated with new species name |
| NEW\_SPECIES\_NAME | New species name | text | VARCHAR2(255 BYTE) | Updated taxonomic name |
| N\_COUNT | Hauls with taxon counts | numeric | NUMBER(38,0) | Total number of hauls with positive count data. |
| N\_HAUL | Valid hauls | count | NUMBER(38,0) | Total number of hauls. |
| N\_LENGTH | Hauls with taxon lengths | count | NUMBER(38,0) | Total number of hauls with length data. |
| N\_SAMPLE | Hauls with sample | count | NUMBER(38,0) | Total number of hauls with positive sample collection. |
| N\_SPECIMENS | Number of specimens in the lot | count | NUMBER(38,0) | Number of specimens in the voucher lot |
| N\_WEIGHT | Hauls with catch | count | NUMBER(38,0) | Total number of hauls with positive catch biomass. |
| OLD\_SPECIES\_CODE | Old species code | ID key code | NUMBER(10,0) | Species code associated with old species name |
| OLD\_SPECIES\_NAME | Old species name | text | VARCHAR2(255 BYTE) | Taxonomic name previously used in the database |
| ORDER\_TAXON | Order phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of order of a given species. |
| PERFORMANCE | Haul performance code | category | NUMBER(38,0) | This denotes what, if any, issues arose during the haul. For more information, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| PHYLUM\_TAXON | Phylum phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of phylum of a given species. |
| POLYGON\_WKB | Polygon binary string | code string | VARCHAR2(255 BYTE) | Well-known binary (WKB) representation of geometry for a AREA\_JOIN polygon. WKB is used to transfer and store the same information in a more compact form convenient for computer processing but that is not human-readable. |
| POLYGON\_WKT | Polygon well known text | code string | VARCHAR2(255 BYTE) | Well-known text (WKT) representation of geometry for a AREA\_JOIN polygon. WKT is a text markup language for representing vector geometry objects. |
| POPULATION\_COUNT | Estimated population | numeric | NUMBER(38,0) | The estimated population caught in the survey for a species, group, or total for a given survey. |
| POPULATION\_VAR | Estimated population variance | numeric | NUMBER(38,6) | The estimated population variance caught in the survey for a species, group, or total for a given survey. |
| PRESERVATIVE | Chemical specimen stored in | text | VARCHAR2(255 BYTE) | Chemical specimen currently stored in |
| PRINCIPAL\_INVESTIGATOR | Principle investigator | text | VARCHAR2(255 BYTE) | First and last name of principal investigator for a project. |
| PROJECT\_TITLE | Title of special project | text | VARCHAR2(255 BYTE) | Special project title. |
| PROJECT\_TITLE\_SHORT | Short title of special project | text | VARCHAR2(255 BYTE) | Special project short title (short version of PROJECT\_TITLE). |
| RANK\_ID | Taxonomic rank | category | VARCHAR2(255 BYTE) | The taxonomic rank of a taxon identification. |
| REASON | Reason for taxonomic change | text | VARCHAR2(255 BYTE) | Reason for taxonomic change; pulled directly from online database (i.e. WoRMS or ITIS) |
| SAMPLE\_TYPE | Sample type | ID key code | NUMBER(38,0) | Sampling information on how the taxon was sampled. For a complete list of length\_type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| SCIENTIFIC\_NAME | Taxon scientific name | text | VARCHAR2(255 BYTE) | The scientific name of the organism associated with the common\_name and species\_code columns. For a complete taxon list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| SEX | Sex of a specimen | ID key code | NUMBER(38,0) | Sex of a specimen where "1" = "Male", "2" = "Female", "3" = Unsexed. |
| SPECIES\_CODE | Taxon code | ID key code | NUMBER(38,0) | The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| SPECIES\_NAME | Scientific name of species | text | VARCHAR2(255 BYTE) | Scientific name of species. |
| SPECIES\_NAME\_ACCEPTED | Scientific name used in taxonomic database | text | VARCHAR2(255 BYTE) | Scientific name of species used in taxonomic "DATABASE" column. |
| SPECIES\_NAME\_SURVEY | Scientific name used in survey data | text | VARCHAR2(255 BYTE) | Scientific name of species historically or currently used in the survey. |
| SPECIMEN\_ID | Specimen unique ID | ID key code | NUMBER(38,0) | Each individual examined must have a number assigned to it that is unique within each haul (0001 to 9999), though specimen numbers may be repeated between hauls |
| SPECIMEN\_SAMPLE\_TYPE | Specimen sample type | ID key code | NUMBER(38,0) | The specimen sample type ID key code as defined in the RACE\_DATA.SPECIMEN\_SAMPLE\_TYPES table. For a complete list of Specimen sample type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| SPECIMEN\_SUBSAMPLE\_METHOD | Specimen subsample method | ID key code | NUMBER(38,0) | For a complete list of specimen subsample method ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| SRVY | Survey abbreviation | text abbreviated | VARCHAR2(255 BYTE) | Abbreviated survey names. The column srvy is associated with the survey and survey\_definition\_id columns. Northern Bering Sea (NBS), Southeastern Bering Sea (EBS), Bering Sea Slope (BSS), Gulf of Alaska (GOA), Aleutian Islands (AI). |
| STANDARD\_LENGTH\_MM | Standard length of specimens (mm) | numeric | VARCHAR2(255 BYTE) | Standard length of specimen or range of lengths if multiple specimens in lot; measured by taxonomists in lab |
| STATION | Station ID | ID key code | VARCHAR2(255 BYTE) | Alpha-numeric designation for the station established in the design of a survey. |
| STRATUM | Stratum ID | ID key code | NUMBER(10,0) | RACE database statistical area for analyzing data. Strata were designed using bathymetry and other geographic and habitat-related elements. The strata are unique to each survey region. Stratum of value 0 indicates experimental tows. |
| SUBCLASS\_TAXON | Subclass phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of subclass of a given species. |
| SUBFAMILY\_TAXON | Subfamily phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of subfamily of a given species. |
| SUBMISSION\_DATE | Date | YYYY-MM-DD | DATE | Date special projects were due to be submitted for the upcoming survey season. |
| SUBORDER\_TAXON | Suborder phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of suborder of a given species. |
| SUBPHYLUM\_TAXON | Subphylum phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of subphylum of a given species. |
| SUPERCLASS\_TAXON | Superclass phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of superclass of a given species. |
| SUPERFAMILY\_TAXON | Superfamily phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of superfamily of a given species. |
| SUPERORDER\_TAXON | Superorder phylogenetic rank | category | VARCHAR2(255 BYTE) | Phylogenetic latin rank of superorder of a given species. |
| SURFACE\_TEMPERATURE\_C | Surface temperature (degrees Celsius) | degrees Celsius | NUMBER(38,1) | Surface temperature (tenths of a degree Celsius); NA indicates removed or missing values. |
| SURVEY | Survey name | text | VARCHAR2(255 BYTE) | Name and description of survey. The column survey is associated with the srvy and survey\_definition\_id columns. |
| SURVEY\_DEFINITION\_ID | Survey ID | ID key code | NUMBER(38,0) | The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| SURVEY\_ID | Survey ID raw | ID key code | NUMBER(38,0) | The survey ID uniquely identifies a survey instance. |
| SURVEY\_NAME | Survey name official | text | VARCHAR2(255 BYTE) | Long name of the survey conducted |
| SURVEY\_SPECIES | Species used in survey | logical | BINARY\_DOUBLE | Designates whether or not species name is accepted/actively used in the RACE surveys |
| TAXONOMIST | Taxonomist | text | VARCHAR2(255 BYTE) | Taxonomist(s) who re-identified specimen(s) |
| TAXON\_CONFIDENCE | Taxon confidence rating | category | VARCHAR2(255 BYTE) | Confidence in the ability of the survey team to correctly identify the taxon to the specified level, based solely on identification skill (e.g., not likelihood of a taxon being caught at that station on a location-by-location basis). Quality codes follow: \*\*High\*\*: High confidence and consistency. Taxonomy is stable and reliable at this level, and field identification characteristics are well known and reliable. \*\*Moderate\*\*: Moderate confidence. Taxonomy may be questionable at this level, or field identification characteristics may be variable and difficult to assess consistently. \*\*Low\*\*: Low confidence. Taxonomy is incompletely known, or reliable field identification characteristics are unknown. Documentation: [Species identification confidence in the eastern Bering Sea shelf survey (1982-2008)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2009-04.pdf), [Species identification confidence in the eastern Bering Sea slope survey (1976-2010)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2014-05.pdf), and [Species identification confidence in the Gulf of Alaska and Aleutian Islands surveys (1980-2011)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2014-01.pdf). |
| TAXON\_CONFIDENCE\_CODE | Taxon confidence rating | category | NUMBER(38,0) | Confidence in the ability of the survey team to correctly identify the taxon to the specified level, based solely on identification skill (e.g., not likelihood of a taxon being caught at that station on a location-by-location basis). Quality codes follow: \*\*High\*\*: High confidence and consistency. Taxonomy is stable and reliable at this level, and field identification characteristics are well known and reliable. \*\*Moderate\*\*: Moderate confidence. Taxonomy may be questionable at this level, or field identification characteristics may be variable and difficult to assess consistently. \*\*Low\*\*: Low confidence. Taxonomy is incompletely known, or reliable field identification characteristics are unknown. Documentation: [Species identification confidence in the eastern Bering Sea shelf survey (1982-2008)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2009-04.pdf), [Species identification confidence in the eastern Bering Sea slope survey (1976-2010)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2014-05.pdf), and [Species identification confidence in the Gulf of Alaska and Aleutian Islands surveys (1980-2011)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2014-01.pdf). |
| TRAWLABLE | Trawlable stations | logical | BINARY\_DOUBLE | Logical, describing if stations are trawlable (TRUE) or not (FALSE). |
| VESSEL\_CALLSIGN | Vessel call sign | ID key code | NUMBER(38,0) | A call sign is a designated sequence of letters and numbers that are assigned when a vessel, whether it be a sailing yacht, motor yacht, rib or commercial vessel, receives its Ship Radio Licence. The vessel also receives its MMSI number, so that each vessel is uniquely identified. |
| VESSEL\_COAST\_GUARD\_NUMBER | Vessel coast guard number | ID key code | NUMBER(38,0) | Official Identification number as defined by www.dco.uscg.mil. The Official Number (O/N) is the 6 or 7 digit number awarded to the vessel at the time it is first documented with the US Coast Guard. This number remains with the vessel indefinitely and should be marked in accordance with 46 CFR 67.121. |
| VESSEL\_ID | Vessel ID | ID key code | NUMBER(38,0) | ID number of the vessel used to collect data for that haul. The column vessel\_id is associated with the vessel\_name column. Note that it is possible for a vessel to have a new name but the same vessel id number. For a complete list of vessel ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| VESSEL\_IMO | Vessel international maritime organization number | ID key code | NUMBER(38,0) | The International Maritime Organization (IMO) number consists of the letters "IMO" followed by a unique, seven-digit number: the pattern is "NNNNNNN", where N is a single-digit number, e.g., "1234567" |
| VESSEL\_LENGTH\_M | Vessel length (m) | meters | NUMBER(38,0) | The length of vessel in meters. |
| VESSEL\_MMSI | Vessel maritime mobile service identities | ID key code | NUMBER(38,0) | Maritime Mobile Service Identities (MMSIs) are nine-digit numbers used by maritime digital selective calling (DSC), automatic identification systems (AIS) and certain other equipment to uniquely identify a ship or a coast radio station. |
| VESSEL\_NAME | Vessel name | text | VARCHAR2(255 BYTE) | Name of the vessel used to collect data for that haul. The column vessel\_name is associated with the vessel\_id column. Note that it is possible for a vessel to have a new name but the same vessel id number. For a complete list of vessel ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual). |
| VESSEL\_OWNER | Vessel owner | text | VARCHAR2(255 BYTE) | Name of vessel owner or company. |
| VESSEL\_TONNAGE | Vessel tonnage | metric tons | NUMBER(38,0) | The tonnage of vessel in metric tons. |
| VOUCHER | Voucher number | numeric | NUMBER(38,0) | The voucher number of the specimen within a single haul |
| WEIGHT\_G | Specimen weight (g) | grams | NUMBER(38,1) | Weight of specimen (grams). |
| WEIGHT\_KG | Sample or taxon weight (kg) | kilograms | NUMBER(38,3) | Weight (thousandths of a kilogram) of individuals in a haul by taxon. |
| WIRE\_LENGTH\_M | Trawl wire length | meters | NUMBER(38,0) | Length of wire deployed during a given haul in meters. |
| WORMS | World register of marine species (WoRMS) taxonomic serial number | ID key code | NUMBER(38,0) | Species code as identified in the World Register of Marine Species (WoRMS) (https://www.marinespecies.org/). |
| YEAR | Survey year | year | NUMBER(10,0) | Year the observation (survey) was collected. |
| YEAR\_CHANGED | Year changed | numeric | DATE | Year change implemented in database |

# 8. Data description

[AKFIN Answers](https://akfin.psmfc.org/akfin-answers/) is an Oracle BI tool used for distributing data to stock assessors and other users. Usernames and passwords are distinct from direct AKFIN database credentials.

## 8.1 Data tables

### 8.1.1 AKFIN\_AGECOMP

Mirror of GAP\_PRODUCTS.AGECOMP. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 683,178

Number of columns: 10

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SEX

Sex of a specimen

ID key code

NUMBER(38,0)

Sex of a specimen where “1” = “Male”, “2” = “Female”, “3” = Unsexed.

AGE

Taxon age bin (yrs)

integer

NUMBER(38,0)

Age bin of taxon. Age bin of a taxon in years estimated by the age comp estimate. Age -9 indicates unaged lengths for a particular sex because no otoliths were collected for that sex/length combination. Age -99 indicates a case where no lengths were collected within a stratum for a species/year even though catch numbers were recorded.

POPULATION\_COUNT

Estimated population

numeric

NUMBER(38,0)

The estimated population caught in the survey for a species, group, or total for a given survey.

LENGTH\_MM\_MEAN

Mean length at age weighted by numbers at length

numeric

NUMBER(38,3)

Mean length (millimeters)

LENGTH\_MM\_SD

Standard deviation of length at age weighted by numbers at length

numeric

NUMBER(38,3)

Variance of mean length.

AREA\_ID\_FOOTPRINT

Survey Footprint

text

VARCHAR2(4000 BYTE)

Survey footprint, usually equivalent to the SURVEY\_DEFINITION\_ID with the exception of the Standard and Standard +NW survey footprints in the Eastern Bering Sea shelf bottom trawl survey

### 8.1.2 AKFIN\_AREA

Mirror of GAP\_PRODUCTS.AREA. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 395

Number of columns: 9

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

DESIGN\_YEAR

Design year

year

NUMBER(10,0)

Year ID associated with a given value AREA\_ID. This field describes the changes in the survey design over time.

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

AREA\_TYPE

Area ID type description

category

VARCHAR2(255 BYTE)

The type of stratum that AREA\_ID represents. Types include: STRATUM (the smallest building-block unit of area in these surveys), REGION, DEPTH, SUBAREA, INPFC BY DEPTH, INPFC, SUBAREA BY DEPTH, REGULATORY AREA, NMFS STATISTICAL AREA.

AREA\_NAME

Area ID name

text

VARCHAR2(4000 BYTE)

Descriptive name of each AREA\_ID. These names often identify the region, depth ranges, or other regional information for the area ID.

DESCRIPTION

Description

text

VARCHAR2(4000 BYTE)

Description of row observation.

AREA\_KM2

Area (km2)

kilometers squared

NUMBER(38,3)

Area in square kilometers.

DEPTH\_MIN\_M

Area ID minimum depth (m)

meters

NUMBER(38,3)

Minimum depth (meters).

DEPTH\_MAX\_M

Area ID maximum depth (m)

meters

NUMBER(38,3)

Maximum depth (meters).

### 8.1.3 AKFIN\_BIOMASS

Mirror of GAP\_PRODUCTS.BIOMASS. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 2,623,956

Number of columns: 16

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

CPUE\_KGKM2\_MEAN

Mean weight CPUE

kilograms per kilometers squared

NUMBER(38,6)

The mean catch weight (kilograms) per unit effort (area swept by the net, units squared kilometers).

CPUE\_NOKM2\_MEAN

Mean numeric CPUE

count per kilometers squared

NUMBER(38,6)

The mean of numerical catch per unit effort (area swept by the net, units square kilometers).

N\_HAUL

Valid hauls

count

NUMBER(38,0)

Total number of hauls.

N\_WEIGHT

Hauls with catch

count

NUMBER(38,0)

Total number of hauls with positive catch biomass.

N\_COUNT

Hauls with taxon counts

numeric

NUMBER(38,0)

Total number of hauls with positive count data.

N\_LENGTH

Hauls with taxon lengths

count

NUMBER(38,0)

Total number of hauls with length data.

BIOMASS\_MT

Estimated biomass

numeric

NUMBER(38,6)

The estimated total biomass.

BIOMASS\_VAR

Estimated biomass variance

numeric

NUMBER(38,6)

The estimated variance associated with the total biomass.

POPULATION\_COUNT

Estimated population

numeric

NUMBER(38,0)

The estimated population caught in the survey for a species, group, or total for a given survey.

POPULATION\_VAR

Estimated population variance

numeric

NUMBER(38,6)

The estimated population variance caught in the survey for a species, group, or total for a given survey.

CPUE\_KGKM2\_VAR

Variance of the mean weight CPUE

kilograms per kilometers squared

NUMBER(38,6)

The variance of mean catch weight (kilograms) per unit effort (area swept by the net, units squared kilometers).

CPUE\_NOKM2\_VAR

Variance of the mean numeric CPUE

count per kilometers squared

NUMBER(38,6)

The variance of mean numerical catch per unit effort (area swept by the net, units square kilometers).

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

### 8.1.4 AKFIN\_CATCH

Non-zero catch records from RACEBASE.CATCH subsetted for standard GAP bottom trawl stations (i.e., HAULJOIN values associated with ABUNDANCE\_HAUL = Y in RACEBASE.HAUL). This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 973,538

Number of columns: 6

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

CRUISEJOIN

Cruise ID

ID key code

NUMBER(38,0)

Unique integer ID assigned to each survey, vessel, and year combination.

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

CATCHJOIN

Catch observation ID

ID key code

NUMBER(38,0)

Unique integer ID assigned to each survey, vessel, year, and catch observation combination.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

WEIGHT\_KG

Sample or taxon weight (kg)

kilograms

NUMBER(38,3)

Weight (thousandths of a kilogram) of individuals in a haul by taxon.

COUNT

Taxon count

count, whole number resolution

NUMBER(38,0)

Total whole number of individuals caught in haul or samples collected.

### 8.1.5 AKFIN\_CPUE

Mirror of GAP\_PRODUCTS.CPUE. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 21,558,257

Number of columns: 7

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

WEIGHT\_KG

Sample or taxon weight (kg)

kilograms

NUMBER(38,3)

Weight (thousandths of a kilogram) of individuals in a haul by taxon.

COUNT

Taxon count

count, whole number resolution

NUMBER(38,0)

Total whole number of individuals caught in haul or samples collected.

AREA\_SWEPT\_KM2

Area swept (km)

kilometers

NUMBER(38,6)

The area the net covered while the net was fishing (kilometers squared), defined as the distance fished times the net width.

CPUE\_KGKM2

Weight CPUE (kg/km2)

kilograms per kilometers squared

NUMBER(38,6)

Catch weight (kilograms) per unit effort (area swept by the net, units square kilometers).

CPUE\_NOKM2

Number CPUE (no/km2)

count per kilometers squared

NUMBER(38,6)

Numerical catch per unit effort (area swept by the net, units square kilometers).

### 8.1.6 AKFIN\_CRUISE

Cruise data for the five standard GAP bottom trawl regions. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 174

Number of columns: 10

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

CRUISEJOIN

Cruise ID

ID key code

NUMBER(38,0)

Unique integer ID assigned to each survey, vessel, and year combination.

CRUISE

Cruise Name

ID key code

NUMBER(38,0)

This is a six-digit integer identifying the cruise number of the form: YYYY99 (where YYYY = year of the cruise; 99 = 2-digit number and is sequential; 01 denotes the first cruise that vessel made in this year, 02 is the second, etc.).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SURVEY\_NAME

Survey name official

text

VARCHAR2(255 BYTE)

Long name of the survey conducted

VESSEL\_ID

Vessel ID

ID key code

NUMBER(38,0)

ID number of the vessel used to collect data for that haul. The column vessel\_id is associated with the vessel\_name column. Note that it is possible for a vessel to have a new name but the same vessel id number. For a complete list of vessel ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

VESSEL\_NAME

Vessel name

text

VARCHAR2(255 BYTE)

Name of the vessel used to collect data for that haul. The column vessel\_name is associated with the vessel\_id column. Note that it is possible for a vessel to have a new name but the same vessel id number. For a complete list of vessel ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

DATE\_START

Start date

YYYY-MM-DD

DATE

The date (YYYY-MM-DD) of the beginning of the event (e.g., cruise).

DATE\_END

End date

YYYY-MM-DD

DATE

The date (YYYY-MM-DD) of the end of the event (e.g., cruise).

### 8.1.7 AKFIN\_HAUL

Standard GAP bottom trawl haul (station) data. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 34,263

Number of columns: 25

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

CRUISEJOIN

Cruise ID

ID key code

NUMBER(38,0)

Unique integer ID assigned to each survey, vessel, and year combination.

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

HAUL

Haul number

ID key code

NUMBER(38,0)

This number uniquely identifies a sampling event (haul) within a cruise. It is a sequential number, in chronological order of occurrence.

HAUL\_TYPE

Haul sampling type

ID key code

NUMBER(38,0)

Type of haul sampling method. For a complete list of haul type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

PERFORMANCE

Haul performance code

category

NUMBER(38,0)

This denotes what, if any, issues arose during the haul. For more information, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

DATE\_TIME\_START

Start date and time

MM/DD/YYYY HH::MM

TIMESTAMP

The date (MM/DD/YYYY) and time (HH:MM) of the beginning of the haul. All dates and times are in Alaska time (AKDT) of Anchorage, AK, USA (UTC/GMT -8 hours).

DURATION\_HR

Tow duration (decimal hr)

hours

NUMBER(38,1)

This is the elapsed time between start and end of a haul (decimal hours).

DISTANCE\_FISHED\_KM

Distance fished (km)

kilometers

NUMBER(38,3)

Distance the net fished (kilometers).

NET\_WIDTH\_M

Net width (m)

meters

NUMBER(38,1)

Measured or estimated distance (meters) between wingtips of the trawl.

NET\_MEASURED

Net measured during haul

logical

BINARY\_DOUBLE

Logical, describing if the net was measured (TRUE) or not (FALSE) by wheelhouse and marport programs during the haul.

NET\_HEIGHT\_M

Net height (m)

meters

NUMBER(38,1)

Measured or estimated distance (meters) between footrope and headrope of the trawl.

STRATUM

Stratum ID

ID key code

NUMBER(10,0)

RACE database statistical area for analyzing data. Strata were designed using bathymetry and other geographic and habitat-related elements. The strata are unique to each survey region. Stratum of value 0 indicates experimental tows.

LATITUDE\_DD\_START

Start latitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Latitude (one hundred thousandth of a decimal degree) of the start of the haul.

LATITUDE\_DD\_END

End latitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Latitude (one hundred thousandth of a decimal degree) of the end of the haul.

LONGITUDE\_DD\_START

Start longitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Longitude (one hundred thousandth of a decimal degree) of the start of the haul.

LONGITUDE\_DD\_END

End longitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Longitude (one hundred thousandth of a decimal degree) of the end of the haul.

STATION

Station ID

ID key code

VARCHAR2(255 BYTE)

Alpha-numeric designation for the station established in the design of a survey.

DEPTH\_GEAR\_M

Depth of gear (m)

degrees Celsius

NUMBER(38,1)

Depth of gear (meters).

DEPTH\_M

Depth (m)

degrees Celsius

NUMBER(38,1)

Bottom depth (meters).

BOTTOM\_TYPE

Seafloor bottom type code

ID key code

NUMBER(38,0)

Bottom type on sea floor at haul location. For a complete list of bottom type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SURFACE\_TEMPERATURE\_C

Surface temperature (degrees Celsius)

degrees Celsius

NUMBER(38,1)

Surface temperature (tenths of a degree Celsius); NA indicates removed or missing values.

GEAR\_TEMPERATURE\_C

Gear temperature (degrees Celsius)

degrees Celsius

NUMBER(38,1)

Temperature recorded by net gear (tenths of a degree Celsius); NA indicates removed or missing values.

WIRE\_LENGTH\_M

Trawl wire length

meters

NUMBER(38,0)

Length of wire deployed during a given haul in meters.

GEAR

Type of gear used on the net

ID key code

NUMBER(38,0)

Type of gear used on net. For a complete list of gear ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

ACCESSORIES

Type of gear accessories used on the net

ID key code

NUMBER(38,0)

Type of accessories used on net. For a complete list of accessories ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

### 8.1.8 AKFIN\_LENGTH

Length data subsetted for standard GAP bottom trawl stations (i.e., HAULJOIN values associated with ABUNDANCE\_HAUL = Y in RACEBASE.HAUL). This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 4,456,380

Number of columns: 7

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SEX

Sex of a specimen

ID key code

NUMBER(38,0)

Sex of a specimen where “1” = “Male”, “2” = “Female”, “3” = Unsexed.

FREQUENCY

Count of observation

count

NUMBER(38,0)

Frequency, or count, of an observation.

LENGTH\_MM

Length of a specimen

millimeters

NUMBER(10,0)

Length bin in millimeters. A length of -9 indicates cases where no lengths were collected within a stratum for a species/year, even though catch numbers were recorded.

LENGTH\_TYPE

Length type

ID key code

NUMBER(38,0)

How the taxon was measured (e.g., fork length, carapace width). For a complete list of length\_type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SAMPLE\_TYPE

Sample type

ID key code

NUMBER(38,0)

Sampling information on how the taxon was sampled. For a complete list of length\_type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

### 8.1.9 AKFIN\_METADATA\_COLUMN

snapshot table for snapshot GAP\_PRODUCTS.AKFIN\_METADATA\_COLUMN

Number of rows: 172

Number of columns: 5

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

METADATA\_COLNAME

Column name

text

VARCHAR2(4000 BYTE)

Name of the column in a table.

METADATA\_COLNAME\_LONG

Column name spelled out

text

VARCHAR2(4000 BYTE)

Long name for the column.

METADATA\_UNITS

Units

category

VARCHAR2(4000 BYTE)

Units of the column.

METADATA\_DATATYPE

Oracle datatype code

text

VARCHAR2(4000 BYTE)

Oracle data type of data column.

METADATA\_COLNAME\_DESC

Column description

text

VARCHAR2(4000 BYTE)

Description of the column.

### 8.1.10 AKFIN\_SIZECOMP

Mirror of GAP\_PRODUCTS.SIZECOMP. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 3,284,629

Number of columns: 7

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

LENGTH\_MM

Length of a specimen

millimeters

NUMBER(10,0)

Length bin in millimeters. A length of -9 indicates cases where no lengths were collected within a stratum for a species/year, even though catch numbers were recorded.

SEX

Sex of a specimen

ID key code

NUMBER(38,0)

Sex of a specimen where “1” = “Male”, “2” = “Female”, “3” = Unsexed.

POPULATION\_COUNT

Estimated population

numeric

NUMBER(38,0)

The estimated population caught in the survey for a species, group, or total for a given survey.

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

### 8.1.11 AKFIN\_SPECIMEN

Specimen data subsetted for standard GAP bottom trawl stations (i.e., HAULJOIN values associated with ABUNDANCE\_HAUL = Y in RACEBASE.HAUL). This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 589,317

Number of columns: 12

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

SPECIMEN\_ID

Specimen unique ID

ID key code

NUMBER(38,0)

Each individual examined must have a number assigned to it that is unique within each haul (0001 to 9999), though specimen numbers may be repeated between hauls

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

LENGTH\_MM

Length of a specimen

millimeters

NUMBER(10,0)

Length bin in millimeters. A length of -9 indicates cases where no lengths were collected within a stratum for a species/year, even though catch numbers were recorded.

SEX

Sex of a specimen

ID key code

NUMBER(38,0)

Sex of a specimen where “1” = “Male”, “2” = “Female”, “3” = Unsexed.

WEIGHT\_G

Specimen weight (g)

grams

NUMBER(38,1)

Weight of specimen (grams).

AGE

Taxon age bin (yrs)

integer

NUMBER(38,0)

Age bin of taxon. Age bin of a taxon in years estimated by the age comp estimate. Age -9 indicates unaged lengths for a particular sex because no otoliths were collected for that sex/length combination. Age -99 indicates a case where no lengths were collected within a stratum for a species/year even though catch numbers were recorded.

MATURITY

Specimen maturity code

ID key code

NUMBER(38,0)

The maturity code or the condition identified by the maturity code.

GONAD\_G

Weight of gonads (g)

grams

NUMBER(38,1)

Weight of specimen gonads (grams).

SPECIMEN\_SUBSAMPLE\_METHOD

Specimen subsample method

ID key code

NUMBER(38,0)

For a complete list of specimen subsample method ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SPECIMEN\_SAMPLE\_TYPE

Specimen sample type

ID key code

NUMBER(38,0)

The specimen sample type ID key code as defined in the RACE\_DATA.SPECIMEN\_SAMPLE\_TYPES table. For a complete list of Specimen sample type ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

AGE\_DETERMINATION\_METHOD

Aging method

ID key code

NUMBER(10,0)

Numeric code corresponding to the method of age determination. For a complete list of age determination codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

### 8.1.12 AKFIN\_STRATUM\_GROUPS

Mirror of GAP\_PRODUCTS.STRATUM\_GROUPS. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 768

Number of columns: 4

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

AREA\_ID

Area ID

ID key code

NUMBER(38,0)

Area ID key code for each statistical area used to produce production estimates (e.g., biomass, population, age comps, length comps). Each area ID is unique within each survey.

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

DESIGN\_YEAR

Design year

year

NUMBER(10,0)

Year ID associated with a given value AREA\_ID. This field describes the changes in the survey design over time.

STRATUM

Stratum ID

ID key code

NUMBER(10,0)

RACE database statistical area for analyzing data. Strata were designed using bathymetry and other geographic and habitat-related elements. The strata are unique to each survey region. Stratum of value 0 indicates experimental tows.

### 8.1.13 AKFIN\_SURVEY\_DESIGN

Mirror of GAP\_PRODUCTS.SURVEY\_DESIGN. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 87

Number of columns: 3

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

DESIGN\_YEAR

Design year

year

NUMBER(10,0)

Year ID associated with a given value AREA\_ID. This field describes the changes in the survey design over time.

### 8.1.14 AKFIN\_TAXONOMIC\_CLASSIFICATION

Mirror of GAP\_PRODUCTS.TAXONOMIC\_CLASSIFICATION, subsetting for SURVEY\_SPECIES = 1 includes taxonomic classification information accepted by the AFSC GAP bottom trawl survey. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 2,718

Number of columns: 19

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SPECIES\_NAME

Scientific name of species

text

VARCHAR2(255 BYTE)

Scientific name of species.

COMMON\_NAME

Taxon common name

text

VARCHAR2(255 BYTE)

The common name of the marine organism associated with the scientific\_name and species\_code columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

ID\_RANK

Lowest taxonomic rank

text

VARCHAR2(255 BYTE)

Lowest taxonomic rank of a given species entry.

DATABASE\_ID

Species ID in database

ID key code

VARCHAR2(255 BYTE)

Species ID key code of a species in the taxonomic “DATABASE” source.

DATABASE

Database source

category

VARCHAR2(255 BYTE)

Taxonomic database source, either ITIS or WoRMS.

GENUS\_TAXON

Genus phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of genus of a given species.

SUBFAMILY\_TAXON

Subfamily phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subfamily of a given species.

FAMILY\_TAXON

Family phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of family of a given species.

SUPERFAMILY\_TAXON

Superfamily phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superfamily of a given species.

SUBORDER\_TAXON

Suborder phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of suborder of a given species.

ORDER\_TAXON

Order phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of order of a given species.

SUPERORDER\_TAXON

Superorder phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superorder of a given species.

SUBCLASS\_TAXON

Subclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subclass of a given species.

CLASS\_TAXON

Class phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of class of a given species.

SUPERCLASS\_TAXON

Superclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superclass of a given species.

SUBPHYLUM\_TAXON

Subphylum phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subphylum of a given species.

PHYLUM\_TAXON

Phylum phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of phylum of a given species.

KINGDOM\_TAXON

Kingdom phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of kingdom of a given species.

### 8.1.15 AKFIN\_TAXONOMIC\_GROUPS

Mirror of GAP\_PRODUCTS.TAXON\_GROUPS. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 2,777

Number of columns: 22

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SPECIES\_NAME

Scientific name of species

text

VARCHAR2(255 BYTE)

Scientific name of species.

COMMON\_NAME

Taxon common name

text

VARCHAR2(255 BYTE)

The common name of the marine organism associated with the scientific\_name and species\_code columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

ID\_RANK

Lowest taxonomic rank

text

VARCHAR2(255 BYTE)

Lowest taxonomic rank of a given species entry.

DATABASE

Database source

category

VARCHAR2(255 BYTE)

Taxonomic database source, either ITIS or WoRMS.

DATABASE\_ID

Species ID in database

ID key code

VARCHAR2(255 BYTE)

Species ID key code of a species in the taxonomic “DATABASE” source.

GENUS\_TAXON

Genus phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of genus of a given species.

SUBFAMILY\_TAXON

Subfamily phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subfamily of a given species.

FAMILY\_TAXON

Family phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of family of a given species.

SUPERFAMILY\_TAXON

Superfamily phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superfamily of a given species.

INFRAORDER\_TAXON

Infraorder phylogenetic rank

category

VARCHAR2(255 BYTE)

Infraorder phylogenetic rank. Phylogenetic latin rank of infraorder of a given speices.

SUBORDER\_TAXON

Suborder phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of suborder of a given species.

ORDER\_TAXON

Order phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of order of a given species.

SUPERORDER\_TAXON

Superorder phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superorder of a given species.

INFRACLASS\_TAXON

Infraclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Infraclass phylogenetic rank. Phylogenetic latin rank of infraclass of a given speices.

SUBCLASS\_TAXON

Subclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subclass of a given species.

CLASS\_TAXON

Class phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of class of a given species.

SUPERCLASS\_TAXON

Superclass phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of superclass of a given species.

SUBPHYLUM\_TAXON

Subphylum phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of subphylum of a given species.

PHYLUM\_TAXON

Phylum phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of phylum of a given species.

KINGDOM\_TAXON

Kingdom phylogenetic rank

category

VARCHAR2(255 BYTE)

Phylogenetic latin rank of kingdom of a given species.

GROUP\_CODE

Species or Complex ID

ID key code

NUMBER(38,0)

Equivalent to the SPECIES\_CODE if the taxon is reported as a single taxon in GAP\_PRODUCTS, otherwise denotes a SPECIES\_CODE of a higher taxonomic group to which the taxon is aggregated in the GAP\_PRODUCTS CPUE and BIOMASS tables.

# 9. Access data via Oracle and R

## Access data via Oracle (AFSC only)

AFSC Oracle users can access the database via SQL developer to view and pull the production data directly from the GAP\_PRODUCTS Oracle schema. The user can also use SQL developer to view and pull the GAP Products data directly from the GAP\_PRODUCTS Oracle schema.

### 9.0.1 Connect to Oracle from R

Many users will want to access the data from Oracle using R. The user will need to install the RODBC R package and ask OFIS (IT) connect R to Oracle. Then, use the following code in R to establish a connection from R to Oracle:

Here, the user can establish the oracle connection by entering their username and password in the channel <- gapindex::oracle\_connect() function. Never save usernames or passwords in scripts that may be intentionally or unintentionally shared with others. If no username and password is entered in the function, pop-ups will appear on the screen asking for the username and password.

After you connect to VPN, you’ll be able to log into Oracle.

library(RODBC)  
channel <- gapindex::get\_connected()

## Data SQL Query Examples:

library(gapindex)  
library(RODBC)  
library(flextable)  
library(ggplot2)  
library(magrittr)  
library(dplyr)

### 9.0.2 Ex. Select all data from tables

You can download all of the tables locally using a variation of the code below. Once connected, pull and save the tables of interest into the R environment.

locations <- c(  
 "GAP\_PRODUCTS.AKFIN\_AGECOMP",   
 "GAP\_PRODUCTS.AKFIN\_AREA",   
 "GAP\_PRODUCTS.AKFIN\_BIOMASS",   
 "GAP\_PRODUCTS.AKFIN\_CATCH",   
 "GAP\_PRODUCTS.AKFIN\_CPUE",   
 "GAP\_PRODUCTS.AKFIN\_CRUISE",   
 "GAP\_PRODUCTS.AKFIN\_HAUL",   
 "GAP\_PRODUCTS.AKFIN\_LENGTH",   
 "GAP\_PRODUCTS.AKFIN\_METADATA\_COLUMN",   
 "GAP\_PRODUCTS.AKFIN\_SIZECOMP",   
 "GAP\_PRODUCTS.AKFIN\_SPECIMEN",   
 "GAP\_PRODUCTS.AKFIN\_STRATUM\_GROUPS",   
 "GAP\_PRODUCTS.AKFIN\_SURVEY\_DESIGN",   
 "GAP\_PRODUCTS.AKFIN\_TAXONOMIC\_CLASSIFICATION"  
)  
  
for (i in 1:length(locations)) {  
 print(locations[i])  
 a <- RODBC::sqlQuery(channel, paste0("SELECT \* FROM ", locations[i]))  
 write.csv(x = a, file = here::here("data", paste0(locations[i], ".csv")))  
}

library(odbc)  
library(RODBC)  
library(dbplyr)  
  
my\_spp\_codes <- c(  
 30010, # Sebastolobus sp. thornyhead unid.  
 30020, # Sebastolobus alascanus shortspine thornyhead  
 30025, # Sebastolobus macrochir broadfin thornyhead  
 30330, # Sebastes melanops black rockfish  
 30430, # Sebastes proriger redstripe rockfish  
 30470, # Sebastes ruberrimus yelloweye rockfish  
 30475, # Sebastes babcocki redbanded rockfish  
 30535, # Sebastes variegatus harlequin rockfish  
 30560, # Sebastes zacentrus sharpchin rockfish  
 30600, # Sebastes reedi yellowmouth rockfish  
 30030, # Sebastolobus altivelis longspine thornyhead  
 30040, # Sebastes sp. rockfish unid.  
 30100, # Sebastes brevispinis silvergray rockfish  
 30150, # NA dusky and dark rockfishes unid.  
 30152, # Sebastes variabilis dusky rockfish  
 30170, # Sebastes crameri darkblotched rockfish  
 30270) # Sebastes helvomaculatus rosethorn rockfish  
  
a <- dplyr::tbl(channel, dplyr::sql('gap\_products.akfin\_biomass')) %>%   
 dplyr::rename\_all(tolower) %>%   
 dplyr::select(survey\_definition\_id, area\_id, species\_code, year, biomass\_mt, biomass\_var) %>%   
 dplyr::filter(species\_code %in% my\_spp\_codes &   
 area\_id %in% 99904 &   
 year >= 1991) %>%   
 dplyr::collect()   
  
flextable::flextable(head(a)) %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra()

### 9.0.3 Ex. CPUE for all EBS and NBS stations with associated haul, cruise, and species information.

a <- RODBC::sqlQuery(channel = channel, # NOT RACEBASE.HAUL  
 query = paste0(  
 "  
-- Select columns for output data  
SELECT  
cr.CRUISEJOIN,  
cr.CRUISE,  
cr.YEAR,  
cr.SURVEY\_DEFINITION\_ID,  
cr.SURVEY\_NAME,  
cr.VESSEL\_ID,  
cr.VESSEL\_NAME,  
cp.HAULJOIN,  
cp.SPECIES\_CODE,  
tt.SPECIES\_NAME,  
tt.COMMON\_NAME,  
cp.WEIGHT\_KG,  
cp.COUNT,  
cp.AREA\_SWEPT\_KM2,  
cp.CPUE\_KGKM2,  
cp.CPUE\_NOKM2,  
hh.HAUL,  
hh.STATION  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_HAUL hh  
LEFT JOIN GAP\_PRODUCTS.AKFIN\_CRUISE cr  
ON hh.CRUISEJOIN = cr.CRUISEJOIN  
LEFT JOIN GAP\_PRODUCTS.AKFIN\_CPUE cp  
ON hh.HAULJOIN = cp.HAULJOIN  
LEFT JOIN GAP\_PRODUCTS.TAXONOMIC\_CLASSIFICATION tt  
ON cp.SPECIES\_CODE = tt.SPECIES\_CODE  
  
-- Filter for EBS and NBS observations  
WHERE SURVEY\_DEFINITION\_ID IN (143, 98) -- 143 NBS, 98 EBS  
AND tt.SURVEY\_SPECIES = 1  
  
-- Only return the first 3 rows because otherwise this would be a huge table!  
FETCH FIRST 3 ROWS ONLY;"))   
  
flextable::flextable(head(a[,2:8])) %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra()

| **CRUISE** | **YEAR** | **SURVEY\_DEFINITION\_ID** | **SURVEY\_NAME** | **VESSEL\_ID** | **VESSEL\_NAME** | **HAULJOIN** |
| --- | --- | --- | --- | --- | --- | --- |
| 198,203 | 1,982 | 98 | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 1 | CHAPMAN | 877 |
| 198,203 | 1,982 | 98 | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 1 | CHAPMAN | 877 |
| 198,203 | 1,982 | 98 | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 1 | CHAPMAN | 877 |

### 9.0.4 Ex. CPUE for all stations contained in the INPFC Shumagin region (AREA\_ID = 919) for Pacific cod.

dat <- RODBC::sqlQuery(channel = channel,  
 query =  
 "  
-- Select columns for output data  
SELECT   
HAULJOIN,   
SPECIES\_CODE,   
STRATUM,   
LATITUDE\_DD\_START,   
LONGITUDE\_DD\_START,  
CPUE\_KGKM2,   
GEAR\_TEMPERATURE\_C  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_CPUE cpue  
LEFT JOIN GAP\_PRODUCTS.AKFIN\_HAUL haul  
USING (HAULJOIN)   
  
-- Filter for P. Cod observations  
WHERE SPECIES\_CODE IN (21720)  
  
-- Select all stratum within the area\_id 919 (INPFC Shumagin region)  
AND haul.STRATUM IN  
(  
SELECT   
STRATUM  
FROM GAP\_PRODUCTS.AKFIN\_STRATUM\_GROUPS   
WHERE AREA\_ID = 919  
);")

dat <- dat %>%   
 dplyr::select(HAULJOIN, STRATUM, SPECIES\_CODE, LATITUDE\_DD\_START, LONGITUDE\_DD\_START, CPUE\_KGKM2, GEAR\_TEMPERATURE\_C) %>%   
 dplyr::mutate(SPECIES\_CODE = as.character(SPECIES\_CODE),   
 STRATUM = as.character(STRATUM)) %>%   
 dplyr::arrange(SPECIES\_CODE)  
  
flextable::flextable(head(dat)) %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra()

| **HAULJOIN** | **STRATUM** | **SPECIES\_CODE** | **LATITUDE\_DD\_START** | **LONGITUDE\_DD\_START** | **CPUE\_KGKM2** | **GEAR\_TEMPERATURE\_C** |
| --- | --- | --- | --- | --- | --- | --- |
| -12,880 | 210 | 21720 | 52.55793 | -169.7829 | 6,863.3672 |  |
| -12,881 | 10 | 21720 | 52.63840 | -169.7815 | 1,536.8594 | 4.9 |
| -12,882 | 111 | 21720 | 52.67131 | -169.4279 | 10,044.8409 | 4.7 |
| -12,883 | 10 | 21720 | 53.24099 | -168.0725 | 1,937.7294 | 5.2 |
| -12,884 | 10 | 21720 | 53.16771 | -167.9810 | 830.2039 | 5.1 |
| -12,885 | 111 | 21720 | 53.06838 | -167.6713 | 2,891.8092 | 4.9 |

### 9.0.5 Ex. EBS Pacific Ocean perch CPUE and [akgfmaps](https://github.com/afsc-gap-products/akgfmaps) map

Pacific Ocean perch catch-per-unit-effort estimates for EBS in 2021 from GAP\_PRODUCTS.AKFIN\_CPUE and map constructed using [akgfmaps](https://github.com/afsc-gap-products/akgfmaps). Here, we’ll use AKFIN HAUL and CRUISES data also included in this repo, for convenience, though they are very similar to their RACEBASE analogs.

dat <- RODBC::sqlQuery(channel = channel,   
 query =   
 "  
-- Select columns for output data  
SELECT   
(cp.CPUE\_KGKM2/100) CPUE\_KGHA, -- akgfmaps is expecting hectares, but can take any units  
hh.LATITUDE\_DD\_START LATITUDE,  
hh.LONGITUDE\_DD\_START LONGITUDE  
  
-- Use HAUL data to obtain LATITUDE & LONGITUDE and connect to cruisejoin  
FROM GAP\_PRODUCTS.AKFIN\_CPUE cp  
LEFT JOIN GAP\_PRODUCTS.AKFIN\_HAUL hh  
ON cp.HAULJOIN = hh.HAULJOIN  
  
-- Use CRUISES data to obtain YEAR and SURVEY\_DEFINITION\_ID  
LEFT JOIN GAP\_PRODUCTS.AKFIN\_CRUISE cc  
ON hh.CRUISEJOIN = cc.CRUISEJOIN  
  
-- Filter data  
WHERE cp.SPECIES\_CODE = 30060   
AND cc.SURVEY\_DEFINITION\_ID = 98   
AND cc.YEAR = 2021;")

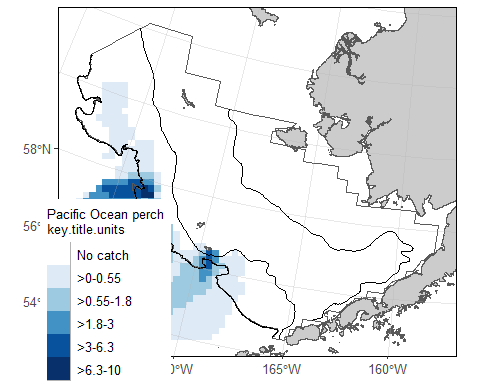
dat %>%   
 dplyr::arrange(desc(CPUE\_KGHA)) %>%   
 head() %>%   
 flextable::flextable() %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra()

| **CPUE\_KGHA** | **LATITUDE** | **LONGITUDE** |
| --- | --- | --- |
| 10.1768965 | 57.64871 | -173.3735 |
| 6.2734470 | 56.36952 | -169.4604 |
| 3.0252034 | 56.66253 | -171.9549 |
| 1.8214628 | 57.98912 | -173.4816 |
| 0.5535672 | 55.65865 | -168.1804 |
| 0.2813533 | 57.32545 | -173.3217 |

# devtools::install\_github("afsc-gap-products/akgfmaps", build\_vignettes = TRUE)  
library(akgfmaps)  
  
figure <- akgfmaps::make\_idw\_map(  
 x = dat, # Pass data as a data frame  
 region = "bs.south", # Predefined EBS area  
 set.breaks = "jenks", # Gets Jenks breaks from classint::classIntervals()  
 in.crs = "+proj=longlat", # Set input coordinate reference system  
 out.crs = "EPSG:3338", # Set output coordinate reference system  
 grid.cell = c(20000, 20000), # 20x20km grid  
 key.title = "Pacific Ocean perch") # Include in the legend title

[inverse distance weighted interpolation]  
[inverse distance weighted interpolation]

figure$plot



EBS Pacific Ocean perch CPUE and [akgfmaps](https://github.com/afsc-gap-products/akgfmaps) map.

### 9.0.6 Ex. GOA Pacific Ocean perch biomass and abundance

Biomass and abundance for Pacific Ocean perch from 1990 – 2023 for the western/central/eastern GOA management areas as well as for the entire region.

dat <- RODBC::sqlQuery(channel = channel,   
 query =   
 "  
-- Manipulate data to join to  
WITH FILTERED\_STRATA AS (  
SELECT AREA\_ID, DESCRIPTION FROM GAP\_PRODUCTS.AKFIN\_AREA  
WHERE AREA\_TYPE in ('REGULATORY AREA', 'REGION')   
AND SURVEY\_DEFINITION\_ID = 47  
-- Use the AREA records associated with the GOA stratification prior to 2025  
AND DESIGN\_YEAR = 1984)  
  
-- Select columns for output data  
SELECT   
BIOMASS\_MT,  
POPULATION\_COUNT,   
YEAR,   
DESCRIPTION  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_BIOMASS BIOMASS  
JOIN FILTERED\_STRATA STRATA   
ON STRATA.AREA\_ID = BIOMASS.AREA\_ID  
  
-- Filter data results  
WHERE BIOMASS.SPECIES\_CODE = 30060  
AND BIOMASS.YEAR BETWEEN 1990 AND 2023")

dat0 <- dat %>%   
 janitor::clean\_names() %>%   
 dplyr::select(biomass\_mt, population\_count, year, area = description) %>%  
 pivot\_longer(cols = c("biomass\_mt", "population\_count"),   
 names\_to = "var",   
 values\_to = "val") %>%   
 dplyr::mutate(  
 val = ifelse(var == "biomass\_mt", val/1e6, val/1e9),   
 var = ifelse(var == "biomass\_mt", "Biomass (Mmt)", "Population (B)"),   
 area = gsub(x = area, pattern = " - ", replacement = "\n"),   
 area = gsub(x = area, pattern = ": ", replacement = "\n"),   
 type = sapply(X = strsplit(x = area, split = "\n", fixed = TRUE), `[[`, 2)) %>%   
 dplyr::arrange(type) %>%   
 dplyr::mutate(  
 area = factor(area, levels = unique(area), labels = unique(area), ordered = TRUE))  
  
flextable::flextable(head(dat)) %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra() %>%  
 flextable::colformat\_num(x = ., j = "YEAR", big.mark = "")

| **BIOMASS\_MT** | **POPULATION\_COUNT** | **YEAR** | **DESCRIPTION** |
| --- | --- | --- | --- |
| 31,074.24 | 60,111,107 | 1990 | CENTRAL GOA - INPFC |
| 101,678.29 | 177,314,827 | 1990 | EASTERN GOA - INPFC |
| 24,542.58 | 79,703,473 | 1990 | WESTERN GOA - INPFC |
| 157,295.11 | 317,129,408 | 1990 | GOA Region: All Strata |
| 256,485.83 | 454,379,678 | 1993 | CENTRAL GOA - INPFC |
| 151,580.88 | 235,121,936 | 1993 | EASTERN GOA - INPFC |

# install.packages("scales")  
library(scales)  
figure <- ggplot2::ggplot(  
 dat = dat0,   
 mapping = aes(x = year, y = val, color = type)) +  
 ggplot2::geom\_point(size = 3) +   
 ggplot2::facet\_grid(cols = vars(area), rows = vars(var), scales = "free\_y") +   
 ggplot2::scale\_x\_continuous(name = "Year", n.breaks = 3) +  
 ggplot2::scale\_y\_continuous(name = "Estimate", labels = comma) +  
 ggplot2::labs(title = 'GOA Pacific Ocean perch biomass and abundance 1990 – 2023') +   
 ggplot2::guides(color=guide\_legend(title = "Region Type"))+  
 ggplot2::scale\_color\_grey() +  
 ggplot2::theme\_bw() +  
 ggplot2::theme(legend.direction = "horizontal",   
 legend.position = "bottom")  
  
figure



GOA Pacific Ocean perch biomass and abundance.

### 9.0.7 Ex. AI rock sole size compositions and ridge plot

Northern and Southern rock sole size composition data from 1991 – 2022 for the Aleutian Islands, with Ridge plot from [ggridges](https://cran.r-project.org/web/packages/ggridges/vignettes/introduction.html).

dat <- RODBC::sqlQuery(channel = channel,   
 query = "  
SELECT   
YEAR,  
LENGTH\_MM / 10 AS LENGTH\_CM,   
SUM(POPULATION\_COUNT) AS POPULATION\_COUNT  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_SIZECOMP   
  
-- 99904 is the AREA\_ID that codes for the whole AI survey region  
WHERE AREA\_ID = 99904  
-- including northern rock sole, southern rock sole, and rock sole unid.  
AND SPECIES\_CODE IN (10260, 10261, 10262)  
-- remove the -9 LENGTH\_MM code  
AND LENGTH\_MM > 0  
-- sum over species\_codes and sexes  
GROUP BY (YEAR, LENGTH\_MM)")

dat0 <- dat %>%   
 janitor::clean\_names() %>%   
 head() %>%   
 flextable::flextable() %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra() %>%  
 flextable::colformat\_num(x = ., j = "year", big.mark = "")  
dat0

| **year** | **length\_cm** | **population\_count** |
| --- | --- | --- |
| 1991 | 23 | 4,625,236 |
| 1991 | 38 | 2,254,964 |
| 1991 | 42 | 820,614 |
| 1991 | 52 | 11,225 |
| 1994 | 16 | 741,246 |
| 1994 | 26 | 9,762,322 |

# install.packages("ggridges")  
library(ggridges)  
figure <- ggplot(dat,   
 mapping = aes(x = LENGTH\_CM,   
 y = YEAR,   
 height = POPULATION\_COUNT,   
 group = YEAR)) +  
 ggridges::geom\_density\_ridges(stat = "identity", scale = 1) +  
 ggplot2::ylab(label = "Year") +  
 ggplot2::scale\_x\_continuous(name = "Length (cm)") +  
 ggplot2::labs(title = paste0('Aleutian Islands Rock sole Size Compositions'),   
 subtitle = paste0(min(dat$YEAR), ' – ', max(dat$YEAR))) +  
 ggplot2::theme\_bw()  
  
figure



AI Rock sole size compositions and ridge plot.

### 9.0.8 Ex. 2023 EBS Walleye Pollock Age Compositions and Age Pyramid

Walleye pollock age composition for the EBS standard + NW Area from 2023, with age pyramid plot.

dat <- RODBC::sqlQuery(channel = channel,   
 query = "  
-- Manipulate data to join to  
WITH FILTERED\_STRATA AS (  
SELECT   
AREA\_ID,   
DESCRIPTION   
FROM GAP\_PRODUCTS.AKFIN\_AREA  
-- Filter for EBS Standard + NW Area   
WHERE AREA\_ID = 99900)  
  
-- Select columns for output data  
SELECT   
AGECOMP.AGE,   
AGECOMP.POPULATION\_COUNT,   
AGECOMP.SEX  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_AGECOMP AGECOMP  
JOIN FILTERED\_STRATA STRATA   
ON STRATA.AREA\_ID = AGECOMP.AREA\_ID  
  
-- Filter data results  
WHERE SPECIES\_CODE = 21740  
AND YEAR = 2023  
AND AGE >= 0")

dat0 <- dat %>%   
 janitor::clean\_names() %>%   
 dplyr::filter(sex %in% c(1,2)) %>%  
 dplyr::mutate(  
 sex = ifelse(sex == 1, "M", "F"),  
 population\_count = # change male population to negative  
 ifelse(sex=="M", population\_count\*(-1), population\_count\*1)/1e9)   
  
flextable::flextable(head(dat)) %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra()

| **AGE** | **POPULATION\_COUNT** | **SEX** |
| --- | --- | --- |
| 1 | 22,060,172 | 1 |
| 2 | 123,165,369 | 1 |
| 3 | 136,542,625 | 1 |
| 4 | 252,538,747 | 1 |
| 5 | 964,790,939 | 1 |
| 6 | 242,135,720 | 1 |

figure <- ggplot2::ggplot(  
 data = dat0,   
 mapping =   
 aes(x = age,  
 y = population\_count,   
 fill = sex)) +  
 ggplot2::scale\_fill\_grey() +  
 ggplot2::geom\_bar(stat = "identity") +  
 ggplot2::coord\_flip() +  
 ggplot2::scale\_x\_continuous(name = "Age") +  
 ggplot2::scale\_y\_continuous(name = "Population (billions)", labels = abs) +  
 ggplot2::ggtitle(label = "2023 EBS (Standard Area + NW) walleye pollock Age Composition") +   
 ggplot2::guides(fill = guide\_legend(title = "Sex"))+  
 ggplot2::theme\_bw()  
  
figure



2023 EBS Walleye Pollock Age Compositions and Age Pyramid.

### 9.0.9 Ex. NBS Pacific cod biomass and abundance

Pacific cod biomass and abundance data for the NBS by stratum.

dat <- RODBC::sqlQuery(channel = channel,   
 query =   
 "  
SELECT YEAR, AREA\_ID AS STRATUM, AREA\_NAME, BIOMASS\_MT, POPULATION\_COUNT   
FROM GAP\_PRODUCTS.AKFIN\_BIOMASS  
  
JOIN ( -- join with area table  
SELECT AREA\_ID, AREA\_NAME  
FROM GAP\_PRODUCTS.AKFIN\_AREA  
WHERE AREA\_TYPE = 'STRATUM'  
AND SURVEY\_DEFINITION\_ID = 143  
AND DESIGN\_YEAR = 2022)  
  
USING (AREA\_ID)  
  
-- Filter data results to NBS Pacific cod  
WHERE SURVEY\_DEFINITION\_ID IN 143   
AND SPECIES\_CODE = 21720  
ORDER BY YEAR, STRATUM")

dat0 <- dat %>%   
 janitor::clean\_names() %>%   
 dplyr::select(year, area\_name, biomass\_mt, population\_count) %>%  
 pivot\_longer(cols = c("biomass\_mt", "population\_count"),   
 names\_to = "var",   
 values\_to = "val") %>%   
 dplyr::mutate(  
 val = ifelse(var == "biomass\_mt", val/1e6, val/1e9),   
 var = ifelse(var == "biomass\_mt", "Biomass (Mmt)", "Population (B)"),   
 area = factor(area\_name, levels = unique(area\_name), labels = unique(area\_name), ordered = TRUE))  
flextable::flextable(dat) %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra() %>%  
 flextable::colformat\_num(x = ., j = "YEAR", big.mark = "")

| **YEAR** | **STRATUM** | **AREA\_NAME** | **BIOMASS\_MT** | **POPULATION\_COUNT** |
| --- | --- | --- | --- | --- |
| 2010 | 70 | Inner Domain | 7,462.5586 | 4,724,153 |
| 2010 | 71 | Inner Domain | 20,983.3757 | 3,928,600 |
| 2010 | 81 | Middle Domain | 680.4357 | 250,837 |
| 2017 | 70 | Inner Domain | 132,490.1518 | 66,187,245 |
| 2017 | 71 | Inner Domain | 147,971.4542 | 65,078,489 |
| 2017 | 81 | Middle Domain | 7,089.8740 | 4,191,118 |
| 2019 | 70 | Inner Domain | 107,096.7296 | 102,734,142 |
| 2019 | 71 | Inner Domain | 194,846.7230 | 73,495,085 |
| 2019 | 81 | Middle Domain | 63,061.2786 | 25,926,805 |
| 2021 | 70 | Inner Domain | 95,849.9833 | 68,767,498 |
| 2021 | 71 | Inner Domain | 53,814.6332 | 17,941,471 |
| 2021 | 81 | Middle Domain | 77,917.1083 | 42,991,939 |
| 2022 | 70 | Inner Domain | 96,500.6975 | 60,433,135 |
| 2022 | 71 | Inner Domain | 26,747.0747 | 10,447,602 |
| 2022 | 81 | Middle Domain | 30,487.2782 | 15,157,597 |
| 2023 | 70 | Inner Domain | 76,708.4327 | 39,605,860 |
| 2023 | 71 | Inner Domain | 19,130.0046 | 8,459,469 |
| 2023 | 81 | Middle Domain | 12,507.8566 | 4,128,368 |

figure <- ggplot2::ggplot(  
 dat = dat0,   
 mapping = aes(y = val, x = year, fill = area)) +   
 ggplot2::geom\_bar(position="stack", stat="identity") +   
 ggplot2::facet\_grid(rows = vars(var), scales = "free\_y") +  
 ggplot2::scale\_y\_continuous(name = "Estimate", labels = comma) +  
 ggplot2::scale\_x\_continuous(name = "Year", breaks = unique(dat0$year)) +  
 ggplot2::labs(title = 'NBS Pacific cod biomass and abundance by stratum') +   
 ggplot2::guides(fill=guide\_legend(title = "Domain Type "))+  
 ggplot2::scale\_fill\_grey() +  
 ggplot2::theme\_bw() +  
 ggplot2::theme(legend.direction = "horizontal",   
 legend.position = "bottom")  
  
figure



NBS Pacific cod biomass and abundance.

### 9.0.10 Ex. GOA Pacific Ocean perch biomass and line plot

Pacific Ocean perch biomass totals for GOA between 1984-2021 from GAP\_PRODUCTS.AKFIN\_BIOMASS

dat <- RODBC::sqlQuery(channel = channel,  
 query = "  
-- Select columns for output data  
SELECT  
SURVEY\_DEFINITION\_ID,  
BIOMASS\_MT / 1000000 AS BIOMASS\_MMT,  
(BIOMASS\_MT - 2 \* SQRT(BIOMASS\_VAR)) / 1000000 AS BIOMASS\_CI\_DW,  
(BIOMASS\_MT + 2 \* SQRT(BIOMASS\_VAR)) / 1000000 AS BIOMASS\_CI\_UP,  
YEAR  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_BIOMASS  
  
-- Filter data results  
WHERE SPECIES\_CODE = 30060  
AND SURVEY\_DEFINITION\_ID = 47  
AND AREA\_ID = 99903  
AND YEAR BETWEEN 1990 AND 2023" ) %>%   
 janitor::clean\_names()

flextable::flextable(head(dat)) %>%  
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra() %>%  
 flextable::colformat\_num(x = ., j = "year", big.mark = "")

| **survey\_definition\_id** | **biomass\_mmt** | **biomass\_ci\_dw** | **biomass\_ci\_up** | **year** |
| --- | --- | --- | --- | --- |
| 47 | 0.1572951 | 0.06303638 | 0.2515538 | 1990 |
| 47 | 0.4836226 | 0.26633581 | 0.7009093 | 1993 |
| 47 | 0.7714128 | 0.36430515 | 1.1785204 | 1996 |
| 47 | 0.7270635 | -0.05006854 | 1.5041955 | 1999 |
| 47 | 0.6731551 | 0.22914901 | 1.1171611 | 2001 |
| 47 | 0.4574216 | 0.31339204 | 0.6014511 | 2003 |

a\_mean <- dat %>%   
 dplyr::group\_by(survey\_definition\_id) %>%   
 dplyr::summarise(biomass\_mmt = mean(biomass\_mmt, na.rm = TRUE),   
 minyr = min(year, na.rm = TRUE),   
 maxyr = max(year, na.rm = TRUE))   
  
figure <-  
 ggplot(data = dat,   
 mapping = aes(x = year,   
 y = biomass\_mmt)) +  
 ggplot2::geom\_point(size = 2.5, color = "grey40") +   
 ggplot2::scale\_x\_continuous(  
 name = "Year",   
 labels = scales::label\_number(  
 accuracy = 1,   
 big.mark = "")) +  
 ggplot2::scale\_y\_continuous(  
 name = "Biomass (Mmt)",   
 labels = comma) +  
 ggplot2::geom\_segment(  
 data = a\_mean,  
 mapping = aes(x = minyr,   
 xend = maxyr,   
 y = biomass\_mmt,   
 yend = biomass\_mmt),  
 linetype = "dashed",   
 linewidth = 2) +  
 ggplot2::geom\_errorbar(  
 mapping = aes(ymin = biomass\_ci\_dw, ymax = biomass\_ci\_up),  
 position = position\_dodge(.9),  
 alpha = 0.5, width=.2) +  
 ggplot2::ggtitle(  
 label = "GOA Pacific Ocean Perch Biomass 1984-2021",   
 subtitle = paste0("Mean = ",   
 formatC(x = a\_mean$biomass\_mmt,   
 digits = 2,   
 big.mark = ",",   
 format = "f"),   
 " Mmt")) +  
 ggplot2::theme\_bw()  
  
figure



GOA Pacific Ocean perch biomass and line plot.

### 9.0.11 Ex. 2022 AI Atka mackerel age specimen summary

#### 9.0.11.1 All ages determined:

dat <- RODBC::sqlQuery(channel = channel,  
 query = "  
-- Select columns for output data  
SELECT SURVEY\_DEFINITION\_ID, YEAR, SPECIES\_CODE, AGE  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_SPECIMEN  
JOIN (SELECT HAULJOIN, CRUISEJOIN FROM GAP\_PRODUCTS.AKFIN\_HAUL)  
USING (HAULJOIN)  
JOIN (SELECT CRUISEJOIN, YEAR, SURVEY\_DEFINITION\_ID FROM GAP\_PRODUCTS.AKFIN\_CRUISE)  
USING (CRUISEJOIN)  
  
-- Filter data results  
WHERE GAP\_PRODUCTS.AKFIN\_SPECIMEN.SPECIMEN\_SAMPLE\_TYPE = 1  
AND SPECIES\_CODE = 21921  
AND YEAR = 2022  
AND SURVEY\_DEFINITION\_ID = 52") %>%   
 janitor::clean\_names()

flextable::flextable(head(dat) %>%   
 dplyr::arrange(age)) %>%  
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra() %>%  
 flextable::colformat\_num(x = ., j = c("year", "species\_code"), big.mark = "")

| **survey\_definition\_id** | **year** | **species\_code** | **age** |
| --- | --- | --- | --- |
| 52 | 2022 | 21921 | 3 |
| 52 | 2022 | 21921 | 3 |
| 52 | 2022 | 21921 | 4 |
| 52 | 2022 | 21921 | 4 |
| 52 | 2022 | 21921 | 4 |
| 52 | 2022 | 21921 | 7 |

#### 9.0.11.2 How many of each age was found:

dat <- RODBC::sqlQuery(channel = channel,  
 query = "  
-- Select columns for output data  
SELECT SURVEY\_DEFINITION\_ID, YEAR, SPECIES\_CODE, AGE,   
COUNT(AGE) AS COUNTAGE  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_SPECIMEN  
JOIN (SELECT HAULJOIN, CRUISEJOIN FROM GAP\_PRODUCTS.AKFIN\_HAUL)  
USING (HAULJOIN)  
JOIN (SELECT CRUISEJOIN, YEAR, SURVEY\_DEFINITION\_ID FROM GAP\_PRODUCTS.AKFIN\_CRUISE)  
USING (CRUISEJOIN)  
  
-- Filter data results  
WHERE AGE >= 0  
AND SPECIES\_CODE = 21921  
AND YEAR = 2022  
AND SURVEY\_DEFINITION\_ID = 52  
GROUP BY (YEAR, SURVEY\_DEFINITION\_ID, SPECIES\_CODE, AGE)  
  
ORDER BY AGE") %>%   
 janitor::clean\_names()

flextable::flextable(dat) %>%   
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra() %>%  
 flextable::colformat\_num(x = ., j = c("year", "species\_code"), big.mark = "")

| **survey\_definition\_id** | **year** | **species\_code** | **age** | **countage** |
| --- | --- | --- | --- | --- |
| 52 | 2022 | 21921 | 1 | 1 |
| 52 | 2022 | 21921 | 2 | 40 |
| 52 | 2022 | 21921 | 3 | 295 |
| 52 | 2022 | 21921 | 4 | 119 |
| 52 | 2022 | 21921 | 5 | 130 |
| 52 | 2022 | 21921 | 6 | 116 |
| 52 | 2022 | 21921 | 7 | 108 |
| 52 | 2022 | 21921 | 8 | 61 |
| 52 | 2022 | 21921 | 9 | 88 |
| 52 | 2022 | 21921 | 10 | 73 |
| 52 | 2022 | 21921 | 11 | 20 |
| 52 | 2022 | 21921 | 12 | 9 |
| 52 | 2022 | 21921 | 13 | 1 |

#### 9.0.11.3 How many otoliths were aged:

Using SQL

dat <- RODBC::sqlQuery(channel = channel,  
 query = "  
-- Select columns for output data  
SELECT SURVEY\_DEFINITION\_ID, YEAR, SPECIES\_CODE,   
COUNT(AGE) AS COUNTAGE  
  
-- Identify what tables to pull data from  
FROM GAP\_PRODUCTS.AKFIN\_SPECIMEN  
JOIN (SELECT HAULJOIN, CRUISEJOIN FROM GAP\_PRODUCTS.AKFIN\_HAUL)  
USING (HAULJOIN)  
JOIN (SELECT CRUISEJOIN, YEAR, SURVEY\_DEFINITION\_ID FROM GAP\_PRODUCTS.AKFIN\_CRUISE)  
USING (CRUISEJOIN)  
  
-- Filter data results  
WHERE GAP\_PRODUCTS.AKFIN\_SPECIMEN.SPECIMEN\_SAMPLE\_TYPE = 1  
AND SPECIES\_CODE = 21921  
AND YEAR = 2022  
AND SURVEY\_DEFINITION\_ID = 52  
GROUP BY (YEAR, SURVEY\_DEFINITION\_ID, SPECIES\_CODE)") %>%   
 janitor::clean\_names()

Using dbplyr:

library(odbc)  
library(keyring)  
library(dplyr)  
library(dbplyr)  
  
channel <- DBI::dbConnect(odbc::odbc(), "akfin", uid = keyring::key\_list("akfin")$username,  
 pwd = keyring::key\_get("akfin", keyring::key\_list("akfin")$username))  
  
dat <- dplyr::tbl(src = channel, dplyr::sql('gap\_products.akfin\_specimen')) %>%   
 dplyr::rename\_all(tolower) %>%   
 dplyr::select(hauljoin, specimen = specimen\_id, species\_code, length = length\_mm,   
 weight = weight\_g, age, sex, age\_method = age\_determination\_method) %>%   
 dplyr::left\_join(dplyr::tbl(akfin, dplyr::sql('gap\_products.akfin\_haul')) %>%  
 dplyr::rename\_all(tolower) %>%   
 dplyr::select(cruisejoin, hauljoin, haul, date\_collected = date\_time\_start,   
 latitude = latitude\_dd\_start, longitude = longitude\_dd\_start),  
 by = join\_by(hauljoin)) %>%   
 dplyr::left\_join(dplyr::tbl(akfin, dplyr::sql('gap\_products.akfin\_cruise')) %>%  
 dplyr::rename\_all(tolower) %>%   
 dplyr::select(cruisejoin, year, vessel = vessel\_id, survey\_definition\_id),  
 by = join\_by(cruisejoin)) %>%   
 dplyr::filter(year == YEAR &  
 survey\_definition\_id == 52 &   
 species\_code %in% spp\_codes &  
 !is.na(age)) %>%   
 dplyr::collect()

Both scripts will produce this table:

flextable::flextable(head(dat)) %>%  
 flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra() %>%  
 flextable::colformat\_num(x = ., j = c("year", "species\_code"), big.mark = "")

| **survey\_definition\_id** | **year** | **species\_code** | **countage** |
| --- | --- | --- | --- |
| 52 | 2022 | 21921 | 1,061 |

# 10. Access API data via R

AKFIN has developed web services (apis) to distribute GAP data. Like the GAP\_PRODUCTS schema, these are under active development. These do not require VPN or an oracle connection but they are protected by Oracle authentication, please contact matt.callahan@noaa.gov for information on how to get an api token to use this option.

The url structure is “https://apex.psmfc.org/akfin/data\_marts/gap\_products/gap\_[base table name]” . For example “https://apex.psmfc.org/akfin/data\_marts/gap\_products/gap\_biomass” is the base url to get data from the akfin\_biomass table. Web services linked to large tables have mandatory parameters to reduce data download size. For example to get agecomp data for Bering Sea pollock in area\_id 10 in 2022 you would use “https://apex.psmfc.org/akfin/data\_marts/gap\_products/gap\_biomass?survey\_definition\_id=98&area\_id=10&species\_code=21740&start\_year=2022&end\_year=2022”.

If you’re using R to pull data through web services you might find the [akfingapdata](https://github.com/MattCallahan-NOAA/akfingapdata/tree/main) (pronounced **akfin-gap-data** not **ak-eff-ing-app-data**) R package helpful.

### 10.0.1 Load packages and helpful functions

## 10.1 Ex. Direct database query in R using the [akfingapdata R package README](https://github.com/MattCallahan-NOAA/akfingapdata/blob/main/README.Rmd):

Sign into akfin with token (need to request token from AKFIN)

akfingapdata::get\_gap\_catch()[,1:6] %>%   
 head() %>%   
 flextable::flextable() %>%  
 flextable::theme\_zebra()

# 11. Data description

The Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC) conducts fisheries-independent bottom trawl surveys to monitor the condition of the demersal fish and crab stocks of Alaska. These data are developed to describe the temporal distribution and abundance of commercially and ecologically important groundfish species, examine the changes in the species composition of the fauna over time and space, and describe the physical environment of the groundfish habitat.

There are no legal restrictions on access to the data. They reside in the public domain and can be freely distributed. Users must read and fully comprehend the metadata prior to use. Data should not be used beyond the limits of the source scale. Acknowledgement of NOAA, as the source from which these data were obtained, in any publications and/or other representations of these data, is suggested. These data are compiled and approved annually after each summer survey season. The data from previous years are unlikely to change substantially once published.

These data are zero-filled (presence and absence) observations from surveys conducted on fishing vessels. These surveys monitor trends in distribution and abundance of groundfish, crab, and bottom-dwelling species in Alaska’s marine ecosystems. These data include estimates of catch-per-unit-effort (CPUE) for all identified species for index stations. Some survey data are excluded, such as non-standard stations, surveys completed in earlier years using different/non-standard gear, and special tows and non-standard data collections.

Though not included in the public data, these surveys also collect oceanographic and environmental data, and biological data such as length, weight, stomach contents (to learn more about diet), otoliths (fish ear bones to learn about age), and tissue samples for genetic analysis, all of which can be shared upon special request. Also not included in the public data are estimated biomass (average total weight of all fish and crabs sampled) of crabs and groundfish that support the creation of annual stock assessments.

## 11.1 Data tables

### 11.1.1 FOSS\_CATCH

Positive catch and effort from GAP\_PRODUCTS.CPUE with associated taxonomic confidence. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 891,144

Number of columns: 7

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

CPUE\_KGKM2

Weight CPUE (kg/km2)

kilograms per kilometers squared

NUMBER(38,6)

Catch weight (kilograms) per unit effort (area swept by the net, units square kilometers).

CPUE\_NOKM2

Number CPUE (no/km2)

count per kilometers squared

NUMBER(38,6)

Numerical catch per unit effort (area swept by the net, units square kilometers).

COUNT

Taxon count

count, whole number resolution

NUMBER(38,0)

Total whole number of individuals caught in haul or samples collected.

WEIGHT\_KG

Sample or taxon weight (kg)

kilograms

NUMBER(38,3)

Weight (thousandths of a kilogram) of individuals in a haul by taxon.

TAXON\_CONFIDENCE

Taxon confidence rating

category

VARCHAR2(255 BYTE)

Confidence in the ability of the survey team to correctly identify the taxon to the specified level, based solely on identification skill (e.g., not likelihood of a taxon being caught at that station on a location-by-location basis). Quality codes follow: **High**: High confidence and consistency. Taxonomy is stable and reliable at this level, and field identification characteristics are well known and reliable. **Moderate**: Moderate confidence. Taxonomy may be questionable at this level, or field identification characteristics may be variable and difficult to assess consistently. **Low**: Low confidence. Taxonomy is incompletely known, or reliable field identification characteristics are unknown. Documentation: [Species identification confidence in the eastern Bering Sea shelf survey (1982-2008)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2009-04.pdf), [Species identification confidence in the eastern Bering Sea slope survey (1976-2010)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2014-05.pdf), and [Species identification confidence in the Gulf of Alaska and Aleutian Islands surveys (1980-2011)](http://apps-afsc.fisheries.noaa.gov/Publications/ProcRpt/PR2014-01.pdf).

### 11.1.2 FOSS\_HAUL

Mirror of GAP\_PRODUCTS.HAUL with additional year and survey data. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 33,991

Number of columns: 27

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

YEAR

Survey year

year

NUMBER(10,0)

Year the observation (survey) was collected.

SRVY

Survey abbreviation

text abbreviated

VARCHAR2(255 BYTE)

Abbreviated survey names. The column srvy is associated with the survey and survey\_definition\_id columns. Northern Bering Sea (NBS), Southeastern Bering Sea (EBS), Bering Sea Slope (BSS), Gulf of Alaska (GOA), Aleutian Islands (AI).

SURVEY

Survey name

text

VARCHAR2(255 BYTE)

Name and description of survey. The column survey is associated with the srvy and survey\_definition\_id columns.

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SURVEY\_NAME

Survey name official

text

VARCHAR2(255 BYTE)

Long name of the survey conducted

CRUISE

Cruise Name

ID key code

NUMBER(38,0)

This is a six-digit integer identifying the cruise number of the form: YYYY99 (where YYYY = year of the cruise; 99 = 2-digit number and is sequential; 01 denotes the first cruise that vessel made in this year, 02 is the second, etc.).

CRUISEJOIN

Cruise ID

ID key code

NUMBER(38,0)

Unique integer ID assigned to each survey, vessel, and year combination.

HAULJOIN

Haul ID

ID key code

NUMBER(38,0)

This is a unique numeric identifier assigned to each (vessel, cruise, and haul) combination.

HAUL

Haul number

ID key code

NUMBER(38,0)

This number uniquely identifies a sampling event (haul) within a cruise. It is a sequential number, in chronological order of occurrence.

STRATUM

Stratum ID

ID key code

NUMBER(10,0)

RACE database statistical area for analyzing data. Strata were designed using bathymetry and other geographic and habitat-related elements. The strata are unique to each survey region. Stratum of value 0 indicates experimental tows.

STATION

Station ID

ID key code

VARCHAR2(255 BYTE)

Alpha-numeric designation for the station established in the design of a survey.

VESSEL\_ID

Vessel ID

ID key code

NUMBER(38,0)

ID number of the vessel used to collect data for that haul. The column vessel\_id is associated with the vessel\_name column. Note that it is possible for a vessel to have a new name but the same vessel id number. For a complete list of vessel ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

VESSEL\_NAME

Vessel name

text

VARCHAR2(255 BYTE)

Name of the vessel used to collect data for that haul. The column vessel\_name is associated with the vessel\_id column. Note that it is possible for a vessel to have a new name but the same vessel id number. For a complete list of vessel ID key codes, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

DATE\_TIME

Date and time

MM/DD/YYYY HH::MM

DATE

The date (MM/DD/YYYY) and time (HH:MM) of the haul. All dates and times are in Alaska time (AKDT) of Anchorage, AK, USA (UTC/GMT -8 hours).

LATITUDE\_DD\_START

Start latitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Latitude (one hundred thousandth of a decimal degree) of the start of the haul.

LONGITUDE\_DD\_START

Start longitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Longitude (one hundred thousandth of a decimal degree) of the start of the haul.

LATITUDE\_DD\_END

End latitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Latitude (one hundred thousandth of a decimal degree) of the end of the haul.

LONGITUDE\_DD\_END

End longitude (decimal degrees)

decimal degrees

NUMBER(38,6)

Longitude (one hundred thousandth of a decimal degree) of the end of the haul.

BOTTOM\_TEMPERATURE\_C

Bottom temperature (degrees Celsius)

degrees Celsius

NUMBER(38,1)

Bottom temperature (tenths of a degree Celsius); NA indicates removed or missing values.

SURFACE\_TEMPERATURE\_C

Surface temperature (degrees Celsius)

degrees Celsius

NUMBER(38,1)

Surface temperature (tenths of a degree Celsius); NA indicates removed or missing values.

DEPTH\_M

Depth (m)

degrees Celsius

NUMBER(38,1)

Bottom depth (meters).

DISTANCE\_FISHED\_KM

Distance fished (km)

kilometers

NUMBER(38,3)

Distance the net fished (kilometers).

DURATION\_HR

Tow duration (decimal hr)

hours

NUMBER(38,1)

This is the elapsed time between start and end of a haul (decimal hours).

NET\_WIDTH\_M

Net width (m)

meters

NUMBER(38,1)

Measured or estimated distance (meters) between wingtips of the trawl.

NET\_HEIGHT\_M

Net height (m)

meters

NUMBER(38,1)

Measured or estimated distance (meters) between footrope and headrope of the trawl.

AREA\_SWEPT\_KM2

Area swept (km)

kilometers

NUMBER(38,6)

The area the net covered while the net was fishing (kilometers squared), defined as the distance fished times the net width.

PERFORMANCE

Haul performance code

category

NUMBER(38,0)

This denotes what, if any, issues arose during the haul. For more information, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

### 11.1.3 FOSS\_SPECIES

List of GAP SPECIES\_CODE values with associated WORMS and ITIS database values. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 1,014

Number of columns: 6

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SCIENTIFIC\_NAME

Taxon scientific name

text

VARCHAR2(255 BYTE)

The scientific name of the organism associated with the common\_name and species\_code columns. For a complete taxon list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

COMMON\_NAME

Taxon common name

text

VARCHAR2(255 BYTE)

The common name of the marine organism associated with the scientific\_name and species\_code columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

ID\_RANK

Lowest taxonomic rank

text

VARCHAR2(255 BYTE)

Lowest taxonomic rank of a given species entry.

WORMS

World register of marine species (WoRMS) taxonomic serial number

ID key code

NUMBER(38,0)

Species code as identified in the World Register of Marine Species (WoRMS) (https://www.marinespecies.org/).

ITIS

Integrated taxonomic information system (ITIS) serial number

ID key code

NUMBER(38,0)

Species code as identified in the Integrated Taxonomic Information System (https://itis.gov/).

### 11.1.4 FOSS\_SURVEY\_SPECIES

List of observed SPECIES\_CODE values for each survey region. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 2,754

Number of columns: 2

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

SURVEY\_DEFINITION\_ID

Survey ID

ID key code

NUMBER(38,0)

The survey definition ID key code is an integer that uniquely identifies a survey region/survey design. The column survey\_definition\_id is associated with the srvy and survey columns. Full list of survey definition IDs are in RACE\_DATA.SURVEY\_DEFINITIONS and in the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

### 11.1.5 FOSS\_TAXON\_GROUP

This reference table will allow for easier searching and sorting of species in FOSS. This table was created by the Resource Assessment and Conservation Engineering Division (RACE) Groundfish Assessment Program (GAP) of the Alaska Fisheries Science Center (AFSC). The GitHub repository for the scripts that created this code can be found at (https://github.com/afsc-gap-products/gap\_products). There are no legal restrictions on access to the data. Last updated on 10 January 2025.

Number of rows: 10,309

Number of columns: 3

Column name from data

Descriptive column Name

Units

Oracle data type

Column description

RANK\_ID

Taxonomic rank

category

VARCHAR2(255 BYTE)

The taxonomic rank of a taxon identification.

CLASSIFICATION

Taxonomic classification rank group

category

VARCHAR2(255 BYTE)

Phylogenetic classification group rank for a given species.

SPECIES\_CODE

Taxon code

ID key code

NUMBER(38,0)

The species code of the organism associated with the common\_name and scientific\_name columns. For a complete species list, review the [code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

# 12. Using the FOSS platform

## 12.1 Select and filter



AFSC Groundfish and Crab Assessment Program Bottom Trawl Survey data interface on the Fisheries One Stop Shop platform.

Select, filter, and download this and other NOAA Fisheries data from the [Fisheries One Stop Shop (FOSS)](https://www.fisheries.noaa.gov/foss) platform. A user guide for the FOSS platform can be found [here](https://www.fisheries.noaa.gov/foss/f?p=215:7:7542600605674:::::). To begin a report, select the kind of data you need: Haul and catch data, Haul data only, All observed species.

In this example, we’ll select for 2023 eastern Bering Sea Arctic cod data. Here, we used the Search Species box to search for species with the term “cod” in their common names and selected “Pacific cod” from that shortened list.

### 12.1.1 Catch and haul



Catch data on the AFSC Groundfish and Crab Assessment Program Bottom Trawl Survey data interface on the Fisheries One Stop Shop platform.

### 12.1.2 Haul



Haul data on the AFSC Groundfish and Crab Assessment Program Bottom Trawl Survey data interface on the Fisheries One Stop Shop platform.

### 12.1.3 Species



All species observed by survey on the AFSC Groundfish and Crab Assessment Program Bottom Trawl Survey data interface on the Fisheries One Stop Shop platform.

## 12.2 Search options

The user must select a option in each of the three option boxes as they appear for catch, haul, and species:

* Survey: Each survey has different in design, time series, and history. More information on each survey and their designs can be found in our [annual data reports](https://www.fisheries.noaa.gov/alaska/science-data/groundfish-assessment-program-bottom-trawl-surveys#data-products).
* Year: Surveys are not conducted in all years, so only data from the years for which the survey was conducted will be returned.
* Species: Common name of all species ever encountered in the survey. Find more information about these species in our [survey code books](https://www.fisheries.noaa.gov/resource/document/groundfish-survey-species-code-manual-and-data-codes-manual).

For a given box, select one or a few options from the options box (list on the left) to query. To select multiple options, hold down the CTRL key while clicking on the options of interest, or click and drag down the list. Once the options you wish to be included in your query are highlighted, click the right-pointing arrow (>) to move them into the “selection box” (list on the right). This can also be achieved by double clicking the option item of interest. If you accidentally select an option that you do not want to query, simply select the unwanted option from the selection box and click the left-pointing arrow (<).

If you wish to select all options from the options box and send them to the selection box, simply click the double right-pointing arrow (>>). If you want to unselect all options from the selection box, use the double left-pointing arrow (<<) or the reset icon.

To find a specific species or group more quickly you can use the Search Species option to quickly narrow the options. Search for parts of species common names in the Search Species box by entering a term and clicking the search button. The platform will return a shorter list in the Speices options box of only species that contain a match to that search term.

Use the Reset All Parameters button to reset all parameters for entire form.



Diagram of selection and search tools available on the FOSS platfrom.

## 12.3 Run report

Click the RUN REPORT button. Below the select and filter area, the results of your query will appear below the page in the format you selected. To change the format, make a different selection and run the report again. Further modifications to your results can be made by clicking on the Actions button above your data. Here you can download your data, select columns included in your results, and apply a variety of filters and mathematical tools.



Example data returned from running the report.

## 12.4 API

APIs, or Application Programming Interfaces, allows users to pull data through a IDE, or integrated development environment, like RStudio or VS Code. Explore the API pages for each of the data pages (Haul and catch data, Haul data only, All observed species).

# 13. Use data

Learn how to pull and use this data through the

* [API and R programming language](https://afsc-gap-products.github.io/gap_products/content/foss-api-r.html)
* [API and python programming language using the afscgap python package](https://afsc-gap-products.github.io/gap_products/content/foss-api-py.html)
* [Oracle and R programming language (AFSC scientists only)](https://afsc-gap-products.github.io/gap_products/content/foss-oracle-r.html)

# 14. Access via API and R

**An application programming interface (API) is a way for two or more computer programs to communicate with each other.** More information about how to amend API links can be found [here](https://docs.oracle.com/en/database/oracle/oracle-rest-data-services/22.3/books.html#AELIG90103/). Useful introductions to using APIs in R can be found [here](https://www.dataquest.io/blog/r-api-tutorial/).

There are three tables the user can pull from the API. Learn more about them on the [FOSS data description page](https://afsc-gap-products.github.io/gap_products/content/foss-metadata.html). Here, you can see them in their raw JSON format:

* haul: <https://apps-st.fisheries.noaa.gov/ods/foss/afsc_groundfish_survey_haul/>
* catch: <https://apps-st.fisheries.noaa.gov/ods/foss/afsc_groundfish_survey_catch/>
* species: <https://apps-st.fisheries.noaa.gov/ods/foss/afsc_groundfish_survey_species/>

Here are some examples of how to use the data with R:

## 14.1 Ex. Load all rows of the catch, haul, and species data tables

Note that without specifying, a basic query to the API will only return 25 entries.

### 14.1.1 Load haul data

# link to the API  
api\_link\_haul <- 'https://apps-st.fisheries.noaa.gov/ods/foss/afsc\_groundfish\_survey\_haul/'

#### 14.1.1.1 Load first 25 rows of data

res <- httr::GET(url = api\_link\_haul)  
# res ## Test connection  
  
## convert from JSON format  
dat <- jsonlite::fromJSON(base::rawToChar(res$content))$items  
  
# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 25; cols: 28"

#### 14.1.1.2 Load all data:

Since the maxim number of rows a user can pull is 10,000 rows in a query, the user needs to cycle through by offsetting to the next 10,000 rows (as is shown here).

dat <- data.frame()  
for (i in seq(0, 500000, 10000)){  
 ## find how many iterations it takes to cycle through the data  
 print(i)  
 ## query the API link  
 res <- httr::GET(url = paste0(api\_link\_haul, "?offset=",i,"&limit=10000"))  
 ## convert from JSON format  
 data <- jsonlite::fromJSON(base::rawToChar(res$content))   
   
 ## if there are no data, stop the loop  
 if (is.null(nrow(data$items))) {  
 break  
 }  
   
 ## bind sub-pull to dat data.frame  
 dat <- dplyr::bind\_rows(dat,   
 data$items %>%  
 dplyr::select(-links)) # necessary for API accounting, but not part of the dataset)  
}

[1] 0  
[1] 10000  
[1] 20000  
[1] 30000  
[1] 40000

Explore the data contents:

# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 33991; cols: 27"

# learn about the structure of the data  
summary(dat)

year srvy survey survey\_name   
 Min. :1982 Length:33991 Length:33991 Length:33991   
 1st Qu.:1997 Class :character Class :character Class :character   
 Median :2006 Mode :character Mode :character Mode :character   
 Mean :2005   
 3rd Qu.:2015   
 Max. :2024   
   
 survey\_definition\_id cruise cruisejoin hauljoin   
 Min. : 47.00 Min. :198201 Min. : -770 Min. : -23911   
 1st Qu.: 47.00 1st Qu.:199701 1st Qu.: -697 1st Qu.: -14104   
 Median : 78.00 Median :200601 Median : -616 Median : -4314   
 Mean : 74.55 Mean :200543 Mean : 294616 Mean : 289722   
 3rd Qu.: 98.00 3rd Qu.:201501 3rd Qu.: 837799 3rd Qu.: 816124   
 Max. :143.00 Max. :202401 Max. :1225395 Max. :1225635   
   
 haul stratum station vessel\_id   
 Min. : 1.0 Min. : 10.0 Length:33991 Min. : 1.0   
 1st Qu.: 56.0 1st Qu.: 31.0 Class :character 1st Qu.: 88.0   
 Median :112.0 Median : 50.0 Mode :character Median : 94.0   
 Mean :117.3 Mean :130.9 Mean :107.8   
 3rd Qu.:170.0 3rd Qu.:142.0 3rd Qu.:147.0   
 Max. :355.0 Max. :794.0 Max. :178.0   
   
 vessel\_name date\_time latitude\_dd\_start longitude\_dd\_start  
 Length:33991 Length:33991 Min. :51.19 Min. :-180.0   
 Class :character Class :character 1st Qu.:55.00 1st Qu.:-170.7   
 Mode :character Mode :character Median :57.16 Median :-165.3   
 Mean :56.86 Mean :-139.6   
 3rd Qu.:58.97 3rd Qu.:-154.4   
 Max. :65.34 Max. : 180.0   
   
 latitude\_dd\_end longitude\_dd\_end bottom\_temperature\_c surface\_temperature\_c  
 Min. :51.19 Min. :-180.0 Min. :-2.100 Min. :-1.100   
 1st Qu.:55.00 1st Qu.:-170.7 1st Qu.: 2.700 1st Qu.: 5.800   
 Median :57.16 Median :-165.3 Median : 4.100 Median : 7.400   
 Mean :56.86 Mean :-139.6 Mean : 3.829 Mean : 7.794   
 3rd Qu.:58.96 3rd Qu.:-154.4 3rd Qu.: 5.200 3rd Qu.: 9.300   
 Max. :65.35 Max. : 180.0 Max. :15.300 Max. :18.100   
 NA's :4 NA's :4 NA's :1601 NA's :852   
 depth\_m distance\_fished\_km duration\_hr net\_width\_m   
 Min. : 9.0 Min. :0.135 Min. :0.0250 Min. : 7.51   
 1st Qu.: 68.0 1st Qu.:1.497 1st Qu.:0.2710 1st Qu.:15.58   
 Median : 102.0 Median :2.528 Median :0.4900 Median :16.40   
 Mean : 137.8 Mean :2.206 Mean :0.4006 Mean :16.42   
 3rd Qu.: 156.0 3rd Qu.:2.833 3rd Qu.:0.5090 3rd Qu.:17.21   
 Max. :1200.0 Max. :4.334 Max. :0.9800 Max. :23.82   
   
 net\_height\_m area\_swept\_km2 performance   
 Min. : 0.000 Min. :0.002314 Min. :0.0000   
 1st Qu.: 2.383 1st Qu.:0.024261 1st Qu.:0.0000   
 Median : 5.865 Median :0.039562 Median :0.0000   
 Mean : 4.822 Mean :0.036378 Mean :0.2779   
 3rd Qu.: 6.788 3rd Qu.:0.047281 3rd Qu.:0.0000   
 Max. :11.038 Max. :0.077795 Max. :7.0000   
 NA's :3269

# Print the first few lines of the data   
dat %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("year", "cruise", "cruisejoin"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **year** | **srvy** | **survey** | **survey\_name** | **survey\_definition\_id** | **cruise** | **cruisejoin** | **hauljoin** | **haul** | **stratum** | **station** | **vessel\_id** | **vessel\_name** | **date\_time** | **latitude\_dd\_start** | **longitude\_dd\_start** | **latitude\_dd\_end** | **longitude\_dd\_end** | **bottom\_temperature\_c** | **surface\_temperature\_c** | **depth\_m** | **distance\_fished\_km** | **duration\_hr** | **net\_width\_m** | **net\_height\_m** | **area\_swept\_km2** | **performance** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 2004 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 200401 | 1195616 | 1,195,895 | 110 | 42 | HG2019 | 89 | ALDEBARAN | 2004-06-30T16:19:47Z | 57.17397 | -169.3162 | 57.14825 | -169.3204 | 3.8 | 9.1 | 72 | 2.869 | 0.51 | 17.532 | 2.219 | 0.050299 | 0 |
| 2004 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 200401 | 1195616 | 1,195,896 | 111 | 42 | G-21 | 89 | ALDEBARAN | 2004-07-02T08:09:22Z | 56.99756 | -170.1878 | 56.99808 | -170.1400 | 4.7 | 7.9 | 70 | 2.912 | 0.51 | 17.500 | 2.290 | 0.050960 | 0 |
| 2004 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 200401 | 1195616 | 1,195,897 | 113 | 42 | HG2120 | 89 | ALDEBARAN | 2004-07-02T13:36:10Z | 57.15147 | -169.9100 | 57.17434 | -169.8874 | 5.0 | 7.7 | 50 | 2.891 | 0.51 | 16.999 | 2.366 | 0.049144 | 0 |

# save outputs for later comparison  
dat\_haul\_api <- dat

### 14.1.2 Load catch data

# link to the API  
api\_link\_catch <- 'https://apps-st.fisheries.noaa.gov/ods/foss/afsc\_groundfish\_survey\_catch/'

#### 14.1.2.1 Load first 25 rows of data

res <- httr::GET(url = api\_link\_catch)  
# res ## Test connection  
  
## convert from JSON format  
dat <- jsonlite::fromJSON(base::rawToChar(res$content))$items  
  
# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 25; cols: 8"

#### 14.1.2.2 Load all data

Since the maxim number of rows a user can pull is 10,000 rows in a query, the user needs to cycle through by offsetting to the next 10,000 rows (as is shown here).

dat <- data.frame()  
# for (i in seq(0, 100000, 10000)){  
for (i in seq(0, 1000000, 10000)){  
 ## find how many iterations it takes to cycle through the data  
 # print(i)  
 ## query the API link  
 res <- httr::GET(url = paste0(api\_link\_catch, "?offset=",i,"&limit=10000"))  
 ## convert from JSON format  
 data <- jsonlite::fromJSON(base::rawToChar(res$content))   
   
 ## if there are no data, stop the loop  
 if (is.null(nrow(data$items))) {  
 break  
 }  
   
 ## bind sub-pull to dat data.frame  
 dat <- dplyr::bind\_rows(dat,   
 data$items %>%  
 dplyr::select(-links)) # necessary for API accounting, but not part of the dataset)  
}

Explore the data contents:

# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 891144; cols: 7"

# learn about the structure of the data  
summary(dat)

hauljoin species\_code cpue\_kgkm2 cpue\_nokm2   
 Min. : -23911 Min. : 1 Min. : 0 Min. : 13   
 1st Qu.: -14439 1st Qu.:20510 1st Qu.: 6 1st Qu.: 58   
 Median : -5267 Median :40500 Median : 49 Median : 214   
 Mean : 280338 Mean :45195 Mean : 1250 Mean : 4605   
 3rd Qu.: 802426 3rd Qu.:71800 3rd Qu.: 372 3rd Qu.: 1137   
 Max. :1225635 Max. :99999 Max. :3226235 Max. :21780780   
 NA's :87811   
 count weight\_kg taxon\_confidence   
 Min. : 1.0 Min. : 0.001 Length:891144   
 1st Qu.: 2.0 1st Qu.: 0.199 Class :character   
 Median : 8.0 Median : 1.814 Mode :character   
 Mean : 180.5 Mean : 41.720   
 3rd Qu.: 43.0 3rd Qu.: 13.780   
 Max. :867119.0 Max. :18187.700   
 NA's :87811

# Print the first few lines of the data   
dat %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("species\_code"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **hauljoin** | **species\_code** | **cpue\_kgkm2** | **cpue\_nokm2** | **count** | **weight\_kg** | **taxon\_confidence** |
| --- | --- | --- | --- | --- | --- | --- |
| -7,235 | 20510 | 1,904.036558 | 594.6202 | 19 | 60.840 | High |
| -7,235 | 20622 | 0.688508 | 62.5916 | 2 | 0.022 | High |
| -7,235 | 21230 | 769.876715 | 219.0706 | 7 | 24.600 | High |

# save outputs for later comparison  
dat\_catch\_api <- dat

### 14.1.3 Load species data

Since there are less than 10,000 rows of species data (and the maxim number of rows a user can pull from this API is 10,000 rows in a query), we can simply call ?offset=0&limit=10000 in our query call.

# link to the API  
api\_link\_species <- 'https://apps-st.fisheries.noaa.gov/ods/foss/afsc\_groundfish\_survey\_species/'

res <- httr::GET(url = paste0(api\_link\_species, "?offset=0&limit=10000"))  
  
## convert from JSON format  
data <- jsonlite::fromJSON(base::rawToChar(res$content))  
dat <- data$items %>%  
 dplyr::select(-links) # necessary for API accounting, but not part of the dataset

Explore the data contents:

# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 1014; cols: 6"

# learn about the structure of the data  
summary(dat)

species\_code scientific\_name common\_name id\_rank   
 Min. : 1 Length:1014 Length:1014 Length:1014   
 1st Qu.:22177 Class :character Class :character Class :character   
 Median :66868 Mode :character Mode :character Mode :character   
 Mean :50653   
 3rd Qu.:75077   
 Max. :99999   
   
 worms itis   
 Min. : 51 Min. : 46861   
 1st Qu.: 127206 1st Qu.: 97781   
 Median : 254573 Median : 162045   
 Mean : 293224 Mean : 217907   
 3rd Qu.: 342060 3rd Qu.: 167487   
 Max. :1699296 Max. :1206057   
 NA's :82 NA's :132

# Print the first few lines of the data   
dat %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("species\_code", "worms", "itis"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **species\_code** | **scientific\_name** | **common\_name** | **id\_rank** | **worms** | **itis** |
| --- | --- | --- | --- | --- | --- |
| 1 |  | fish egg unid. |  |  |  |
| 2 |  | fish larvae unid. |  |  |  |
| 3 |  | fish unid. |  |  |  |

# save outputs for later comparison  
dat\_species\_api <- dat

## 14.2 Ex. Create zero-filled data using data loaded in last example

It is important to create and have access to zero-fill (presence and absence) so you can do simple analyses and plot data.

First prepare a table with all combinations of what species should be listed for what hauls/surveys. For zero-filled data, all species caught in a survey need to have zero or non-zero row entries for a haul

comb <- dplyr::full\_join(  
 # find all species that have been caught, by survey  
 x = dplyr::left\_join(dat\_catch\_api, dat\_haul\_api, by = "hauljoin") %>%  
 dplyr::select(survey\_definition\_id, species\_code) %>%  
 dplyr::distinct(),  
 # find all haul events (hauljoins), by survey  
 y = dat\_haul\_api %>%  
 dplyr::select(survey\_definition\_id, hauljoin) %>%  
 dplyr::distinct(),  
 relationship = "many-to-many",  
 by = "survey\_definition\_id"  
) %>%   
 dplyr::select(-survey\_definition\_id) # now, redundant

Explore the data contents:

print(paste0("rows: ", nrow(comb), "; cols: ", ncol(comb)))

[1] "rows: 21733474; cols: 2"

comb %>% head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("species\_code", "hauljoin"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **species\_code** | **hauljoin** |
| --- | --- |
| 20510 | 1225491 |
| 20510 | 1225492 |
| 20510 | 1225493 |

Now, using that table of combinations (here, called comb), join data to make a full zero-filled CPUE dataset. When all of the data have been full joined together, there should be the maximum number of rows in comb.

dat <- comb %>%  
 # add species data  
 dplyr::left\_join(dat\_species\_api) %>% # , "species\_code"  
 # add haul data  
 dplyr::left\_join(dat\_haul\_api) %>% # , c("hauljoin")  
 # add catch data  
 dplyr::left\_join(dat\_catch\_api) %>% # , c("species\_code", "hauljoin")  
 # modify/clean up zero-filled rows  
 dplyr::mutate(  
 cpue\_kgkm2 = ifelse(is.na(cpue\_kgkm2), 0, cpue\_kgkm2),  
 cpue\_nokm2 = ifelse(is.na(cpue\_nokm2), 0, cpue\_nokm2),  
 count = ifelse(is.na(count), 0, count),  
 weight\_kg = ifelse(is.na(weight\_kg), 0, weight\_kg))

TRUE Joining with `by = join\_by(species\_code)`  
TRUE Joining with `by = join\_by(hauljoin)`  
TRUE Joining with `by = join\_by(species\_code, hauljoin)`

Explore the data contents:

# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 21733474; cols: 38"

# learn about the structure of the data  
summary(dat)

species\_code hauljoin scientific\_name common\_name   
 Min. : 1 Min. : -23911 Length:21733474 Length:21733474   
 1st Qu.:21810 1st Qu.: -14004 Class :character Class :character   
 Median :66839 Median : -4364 Mode :character Mode :character   
 Mean :50538 Mean : 298229   
 3rd Qu.:74986 3rd Qu.: 821816   
 Max. :99999 Max. :1225635   
   
 id\_rank worms itis year   
 Length:21733474 Min. : 51 Min. : 46861 Min. :1982   
 Class :character 1st Qu.: 126824 1st Qu.: 97160 1st Qu.:1997   
 Mode :character Median : 254510 Median : 160846 Median :2006   
 Mean : 269709 Mean : 203649 Mean :2006   
 3rd Qu.: 292719 3rd Qu.: 167456 3rd Qu.:2015   
 Max. :1699296 Max. :1206057 Max. :2024   
 NA's :1584968 NA's :2475974   
 srvy survey survey\_name survey\_definition\_id  
 Length:21733474 Length:21733474 Length:21733474 Min. : 47.00   
 Class :character Class :character Class :character 1st Qu.: 47.00   
 Mode :character Mode :character Mode :character Median : 52.00   
 Mean : 68.95   
 3rd Qu.: 98.00   
 Max. :143.00   
   
 cruise cruisejoin haul stratum   
 Min. :198201 Min. : -770 Min. : 1.0 Min. : 10.0   
 1st Qu.:199701 1st Qu.: -697 1st Qu.: 59.0 1st Qu.: 31.0   
 Median :200601 Median : -616 Median :117.0 Median : 61.0   
 Mean :200556 Mean : 303023 Mean :122.7 Mean :142.1   
 3rd Qu.:201501 3rd Qu.: 837800 3rd Qu.:177.0 3rd Qu.:212.0   
 Max. :202401 Max. :1225395 Max. :355.0 Max. :794.0   
   
 station vessel\_id vessel\_name date\_time   
 Length:21733474 Min. : 1 Length:21733474 Length:21733474   
 Class :character 1st Qu.: 88 Class :character Class :character   
 Mode :character Median : 94 Mode :character Mode :character   
 Mean :110   
 3rd Qu.:147   
 Max. :178   
   
 latitude\_dd\_start longitude\_dd\_start latitude\_dd\_end longitude\_dd\_end  
 Min. :51.19 Min. :-180.0 Min. :51.19 Min. :-180.0   
 1st Qu.:54.68 1st Qu.:-169.9 1st Qu.:54.68 1st Qu.:-169.9   
 Median :56.98 Median :-163.4 Median :56.98 Median :-163.4   
 Mean :56.61 Mean :-136.6 Mean :56.61 Mean :-136.6   
 3rd Qu.:58.67 3rd Qu.:-152.1 3rd Qu.:58.67 3rd Qu.:-152.1   
 Max. :65.34 Max. : 180.0 Max. :65.35 Max. : 180.0   
 NA's :2268 NA's :2268   
 bottom\_temperature\_c surface\_temperature\_c depth\_m distance\_fished\_km  
 Min. :-2.1 Min. :-1.1 Min. : 9 Min. :0.135   
 1st Qu.: 3.1 1st Qu.: 5.9 1st Qu.: 71 1st Qu.:1.481   
 Median : 4.3 Median : 7.6 Median : 109 Median :1.677   
 Mean : 4.1 Mean : 8.0 Mean : 142 Mean :2.096   
 3rd Qu.: 5.4 3rd Qu.: 9.7 3rd Qu.: 167 3rd Qu.:2.800   
 Max. :15.3 Max. :18.1 Max. :1200 Max. :4.334   
 NA's :1106136 NA's :598744   
 duration\_hr net\_width\_m net\_height\_m area\_swept\_km2   
 Min. :0.0250 Min. : 7.51 Min. : 0.0 Min. :0.002314   
 1st Qu.:0.2690 1st Qu.:15.54 1st Qu.: 2.6 1st Qu.:0.023802   
 Median :0.3050 Median :16.32 Median : 6.2 Median :0.027834   
 Mean :0.3798 Mean :16.36 Mean : 5.2 Mean :0.034427   
 3rd Qu.:0.5000 3rd Qu.:17.12 3rd Qu.: 6.9 3rd Qu.:0.046295   
 Max. :0.9800 Max. :23.82 Max. :11.0 Max. :0.077795   
 NA's :1736222   
 performance cpue\_kgkm2 cpue\_nokm2 count   
 Min. :0.0000 Min. : 0 Min. : 0 Min. : 0.0   
 1st Qu.:0.0000 1st Qu.: 0 1st Qu.: 0 1st Qu.: 0.0   
 Median :0.0000 Median : 0 Median : 0 Median : 0.0   
 Mean :0.2925 Mean : 51 Mean : 170 Mean : 6.7   
 3rd Qu.:0.0000 3rd Qu.: 0 3rd Qu.: 0 3rd Qu.: 0.0   
 Max. :7.0000 Max. :3226235 Max. :21780780 Max. :867119.0   
   
 weight\_kg taxon\_confidence   
 Min. : 0.000 Length:21733474   
 1st Qu.: 0.000 Class :character   
 Median : 0.000 Mode :character   
 Mean : 1.711   
 3rd Qu.: 0.000   
 Max. :18187.700

# Print the first few lines of the data   
dat %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("species\_code", "worms", "itis", "hauljoin", "year", "cruise", "cruisejoin"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **species\_code** | **hauljoin** | **scientific\_name** | **common\_name** | **id\_rank** | **worms** | **itis** | **year** | **srvy** | **survey** | **survey\_name** | **survey\_definition\_id** | **cruise** | **cruisejoin** | **haul** | **stratum** | **station** | **vessel\_id** | **vessel\_name** | **date\_time** | **latitude\_dd\_start** | **longitude\_dd\_start** | **latitude\_dd\_end** | **longitude\_dd\_end** | **bottom\_temperature\_c** | **surface\_temperature\_c** | **depth\_m** | **distance\_fished\_km** | **duration\_hr** | **net\_width\_m** | **net\_height\_m** | **area\_swept\_km2** | **performance** | **cpue\_kgkm2** | **cpue\_nokm2** | **count** | **weight\_kg** | **taxon\_confidence** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 20510 | 1225491 | Anoplopoma fimbria | sablefish | species | 159463 | 167123 | 2004 | BSS | Bering Sea Slope | Eastern Bering Sea Slope Bottom Trawl Survey | 78 | 200401 | 1225395 | 225 | 12 | 76 | 134 | NORTHWEST EXPLORER | 2004-08-05T18:18:27Z | 54.57648 | -166.5989 | 54.57169 | -166.6362 | 3.9 | 9.3 | 413 | 2.470 | 0.53 | 15.576 | 6.953 | 0.038473 | 0 | 520.3687 | 233.93199 | 9 | 20.02 | High |
| 20510 | 1225492 | Anoplopoma fimbria | sablefish | species | 159463 | 167123 | 2004 | BSS | Bering Sea Slope | Eastern Bering Sea Slope Bottom Trawl Survey | 78 | 200401 | 1225395 | 192 | 12 | 89 | 134 | NORTHWEST EXPLORER | 2004-07-29T18:02:55Z | 55.12762 | -167.8108 | 55.10951 | -167.7877 | 3.8 | 9.7 | 430 | 2.494 | 0.52 | 15.778 | 6.768 | 0.039350 | 0 | 199.7442 | 101.65099 | 4 | 7.86 | High |
| 20510 | 1225493 | Anoplopoma fimbria | sablefish | species | 159463 | 167123 | 2004 | BSS | Bering Sea Slope | Eastern Bering Sea Slope Bottom Trawl Survey | 78 | 200401 | 1225395 | 193 | 15 | 149 | 134 | NORTHWEST EXPLORER | 2004-07-30T08:04:59Z | 54.94091 | -167.7837 | 54.92692 | -167.7685 | 2.8 | 8.6 | 1,016 | 1.827 | 0.38 | 16.519 | 6.204 | 0.030180 | 0 | 440.6861 | 99.40288 | 3 | 13.30 | High |

# save outputs for later comparison  
dat\_zerofill\_api <- dat

## 14.3 Ex. Visualize zero-filled data for 2023 eastern Bering Sea walleye pollock in CPUE data in distribution map

Using the zero-filled data from the previous example, we can make a few plots!

Here is some example data of 2023 through 2019 (year %in% 2019:2023) eastern and northern Bering Sea (srvy %in% c("EBS", "NBS)) walleye pollock (species\_code == 21740).

dat <- dat\_zerofill\_api %>%   
 dplyr::filter(year %in% 2019:2023 &   
 srvy %in% c("EBS", "NBS") &   
 species\_code == 21740) %>%   
 dplyr::select(year, common\_name, longitude\_dd\_start, latitude\_dd\_start, cpue\_kgkm2)  
  
# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 2052; cols: 5"

# # learn about the structure of the data  
# summary(dat)  
  
# Print the first few lines of the data   
dat %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("year"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **year** | **common\_name** | **longitude\_dd\_start** | **latitude\_dd\_start** | **cpue\_kgkm2** |
| --- | --- | --- | --- | --- |
| 2023 | walleye pollock | -168.2743 | 63.69779 | 2,970.544 |
| 2023 | walleye pollock | -168.2171 | 63.02298 | 1,291.441 |
| 2023 | walleye pollock | -168.8329 | 62.88096 | 4,573.617 |

### 14.3.1 Plot locations on map

library(ggplot2)  
  
ggplot2::ggplot(data = dat %>% dplyr::filter(cpue\_kgkm2 != 0),   
 mapping = aes(x = longitude\_dd\_start,   
 y = latitude\_dd\_start,   
 size = cpue\_kgkm2)) +   
 ggplot2::geom\_point(alpha = .75) +  
 ggplot2::geom\_point(data = dat %>% dplyr::filter(cpue\_kgkm2 == 0),   
 color = "red",   
 shape = 17,  
 alpha = .75,  
 size = 3) +  
 ggplot2::xlab("Longitude \*W") +  
 ggplot2::ylab("Latitude \*N") +  
 ggplot2::ggtitle(label = "CPUE (kg/km^2) of walleye pollock (Weight CPUE; kg/km2)",   
 subtitle = "Eastern Bering Sea bottom trawl survey") +  
 ggplot2::scale\_size\_continuous(name = "Weight (kg)") +   
 ggplot2::facet\_wrap(facets = vars(year)) +   
 ggplot2::theme\_bw()



### 14.3.2 Plot inverse-distance weighted plot of CPUE

This map is constructed using [akgfmaps](https://github.com/afsc-gap-products/akgfmaps). To make IDW plots, you must have data from all stations surveyed, even if no fish of interest were found there.

These plots are similar to those published in the [annual Bering Sea data reports](https://www.fisheries.noaa.gov/alaska/science-data/groundfish-assessment-program-bottom-trawl-surveys#communications).

# devtools::install\_github("afsc-gap-products/akgfmaps", build\_vignettes = TRUE)  
library(akgfmaps)  
idw <- akgfmaps::make\_idw\_stack(  
 x = dat %>%   
 dplyr::select(COMMON\_NAME = common\_name,   
 CPUE\_KGHA = cpue\_kgkm2,   
 LATITUDE = latitude\_dd\_start,   
 LONGITUDE = longitude\_dd\_start,   
 year),   
 grouping.vars = "year",   
 region = "bs.all", # Predefined EBS area  
 set.breaks = "jenks", # Gets Jenks breaks from classint::classIntervals()  
 in.crs = "+proj=longlat", # Set input coordinate reference system  
 out.crs = "EPSG:3338", # Set output coordinate reference system  
 extrapolation.grid.type = "sf")

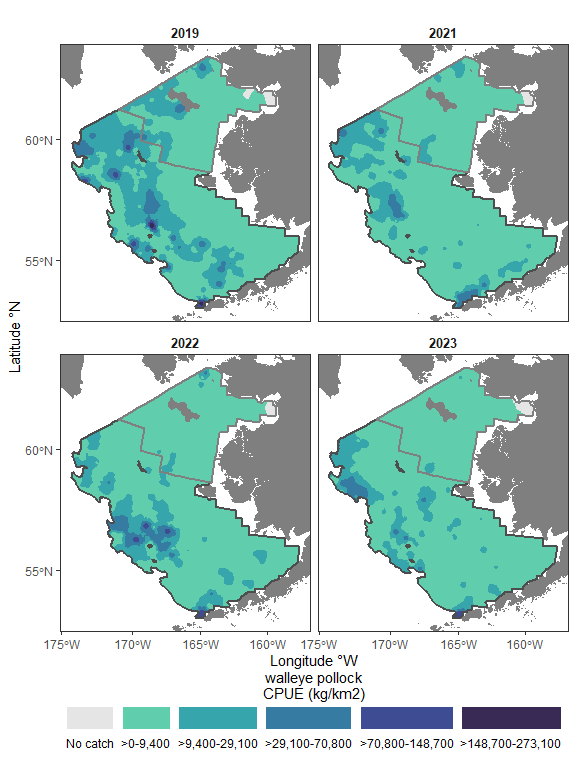
[inverse distance weighted interpolation]  
[inverse distance weighted interpolation]

[inverse distance weighted interpolation]  
[inverse distance weighted interpolation]

[inverse distance weighted interpolation]  
[inverse distance weighted interpolation]

[inverse distance weighted interpolation]  
[inverse distance weighted interpolation]

shps <- akgfmaps::get\_base\_layers(  
 select.region = "bs.all",   
 include.corners = TRUE,   
 set.crs = "EPSG:3338")  
  
# set.breaks <- akgfmaps::eval\_plot\_breaks(CPUE = dat$cpue\_kgkm2, n.breaks = 5)  
# set.breaks <- as.vector(unlist(set.breaks[set.breaks$style == "pretty", -1]))  
set.breaks <- c(0, 50000, 100000, 150000, 200000, 250000)  
  
figure\_print <- ggplot() +  
 # add map of alaska  
 ggplot2::geom\_sf(data = shps$akland,  
 color = NA,  
 fill = "grey50") +  
 # add IDW plots  
 geom\_sf(data = idw$extrapolation.stack,  
 mapping = aes(fill = var1.pred),  
 na.rm = FALSE,  
 show.legend = TRUE,   
 color = NA) +  
 ggplot2::scale\_fill\_manual(  
 name = "walleye pollock\nCPUE (kg/km2)",  
 values = c("gray90",  
 viridis::viridis(  
 option = "mako",  
 direction = -1,  
 n = length(set.breaks)-1,  
 begin = 0.20,  
 end = 0.80)),  
 na.translate = FALSE, # Don't use NA  
 drop = FALSE) +   
 # seperate plots by year  
 ggplot2::facet\_wrap(facets = vars(year), nrow = 2) +   
 # add survey area  
 ggplot2::geom\_sf(  
 data = shps$survey.area,   
 mapping = aes(color = SURVEY,   
 geometry = geometry),   
 fill = "transparent",   
 linewidth = 1,   
 show.legend = FALSE) +  
 ggplot2::scale\_color\_manual(  
 name = " ",   
 values = c("grey30", "grey50"),  
 breaks = shps$survey.area$SURVEY,  
 labels = shps$survey.area$SRVY) +   
 # lat/lon axis and map bounds  
 ggplot2::scale\_x\_continuous(name = "Longitude °W",  
 breaks = seq(-180, -150, 5)) +  
 ggplot2::scale\_y\_continuous(name = "Latitude °N",  
 breaks = seq(50, 65, 5)) + # seq(52, 62, 2)  
 ggplot2::coord\_sf(xlim = sf::st\_bbox(shps$survey.area)[c(1,3)],  
 ylim = sf::st\_bbox(shps$survey.area)[c(2,4)]) +  
 # add theme aesthetics  
 ggplot2::guides(  
 fill = guide\_legend(  
 order = 1,  
 title.position = "top",  
 label.position = "bottom",  
 title.hjust = 0.5,  
 override.aes = list(color = NA),  
 nrow = 1),  
 color = "none") +  
 ggplot2::theme(   
 panel.background = element\_rect(fill = "white", colour = NA),   
 panel.border = element\_rect(fill = NA, colour = "grey20"),   
 strip.background = element\_blank(),   
 strip.text = element\_text(size = 10, face = "bold"),   
 legend.text = element\_text(size = 9),  
 legend.background = element\_rect(colour = "transparent",   
 fill = "transparent"),  
 legend.key = element\_rect(colour = "transparent",   
 fill = "transparent"),  
 legend.position = "bottom",   
 legend.box = "horizontal",  
 legend.box.spacing = unit(0, "pt"), # reduce space between legend & plot  
 legend.margin=margin(0, 0, 0, 0) )  
  
figure\_print



## 14.4 Ex. Show catch data for 2023 eastern Bering Sea Walleye Pollock (one species in one survey region in one year)

Data downloads and joins for just one species, survey, and year are much faster and easier to do.

First, because year is identified in the haul table, we need to identify all of the hauls (or more specifically, hauljoin codes) that were completed in the eastern Bering Sea ("srvy":"EBS") in 2023 ("year":2023).

Note: Check how many rows and columns are in the data pull. The eastern Bering Sea survey (before 2024) has 376 stations in it, and pollock are often found in throughout the region so this should have a similar number of rows.

## query the API link  
res <- httr::GET(url = paste0(api\_link\_haul, '?limit=10000&q={"year":2023,"srvy":"EBS"}'))  
  
## convert from JSON format  
data <- jsonlite::fromJSON(base::rawToChar(res$content))   
dat <- data$items %>%  
 dplyr::select(-links) # necessary for API accounting, but not part of the dataset  
  
## show summary of data to make sure it is subset correctly  
summary(dat %>% dplyr::mutate(srvy = as.factor(srvy)))

year srvy survey survey\_name   
 Min. :2023 EBS:376 Length:376 Length:376   
 1st Qu.:2023 Class :character Class :character   
 Median :2023 Mode :character Mode :character   
 Mean :2023   
 3rd Qu.:2023   
 Max. :2023   
 survey\_definition\_id cruise cruisejoin hauljoin   
 Min. :98 Min. :202301 Min. :-760.0 Min. :-23019   
 1st Qu.:98 1st Qu.:202301 1st Qu.:-760.0 1st Qu.:-22776   
 Median :98 Median :202301 Median :-759.0 Median :-22539   
 Mean :98 Mean :202301 Mean :-759.5 Mean :-22552   
 3rd Qu.:98 3rd Qu.:202301 3rd Qu.:-759.0 3rd Qu.:-22333   
 Max. :98 Max. :202301 Max. :-759.0 Max. :-22110   
 haul stratum station vessel\_id   
 Min. : 7.00 Min. :10.00 Length:376 Min. :134.0   
 1st Qu.: 65.75 1st Qu.:31.00 Class :character 1st Qu.:134.0   
 Median :114.00 Median :41.00 Mode :character Median :162.0   
 Mean :114.16 Mean :39.22 Mean :148.3   
 3rd Qu.:161.25 3rd Qu.:50.00 3rd Qu.:162.0   
 Max. :224.00 Max. :90.00 Max. :162.0   
 vessel\_name date\_time latitude\_dd\_start longitude\_dd\_start  
 Length:376 Length:376 Min. :54.66 Min. :-178.2   
 Class :character Class :character 1st Qu.:57.00 1st Qu.:-172.7   
 Mode :character Mode :character Median :58.02 Median :-168.9   
 Mean :58.26 Mean :-168.8   
 3rd Qu.:59.50 3rd Qu.:-165.2   
 Max. :62.01 Max. :-158.3   
 latitude\_dd\_end longitude\_dd\_end bottom\_temperature\_c surface\_temperature\_c  
 Min. :54.68 Min. :-178.2 Min. :-1.600 Min. : 1.700   
 1st Qu.:57.01 1st Qu.:-172.7 1st Qu.: 1.200 1st Qu.: 4.200   
 Median :58.02 Median :-168.9 Median : 2.700 Median : 6.550   
 Mean :58.26 Mean :-168.8 Mean : 2.249 Mean : 6.386   
 3rd Qu.:59.50 3rd Qu.:-165.2 3rd Qu.: 3.500 3rd Qu.: 8.525   
 Max. :62.01 Max. :-158.3 Max. : 5.400 Max. :11.000   
 depth\_m distance\_fished\_km duration\_hr net\_width\_m   
 Min. : 20.00 Min. :1.065 Min. :0.1890 Min. :12.90   
 1st Qu.: 54.75 1st Qu.:2.805 1st Qu.:0.5100 1st Qu.:16.66   
 Median : 74.00 Median :2.889 Median :0.5180 Median :17.27   
 Mean : 80.75 Mean :2.854 Mean :0.5129 Mean :17.15   
 3rd Qu.:105.00 3rd Qu.:2.945 3rd Qu.:0.5260 3rd Qu.:17.83   
 Max. :171.00 Max. :3.849 Max. :0.6560 Max. :20.29   
 net\_height\_m area\_swept\_km2 performance   
 Min. :1.300 Min. :0.02017 Min. :0.0000   
 1st Qu.:1.875 1st Qu.:0.04725 1st Qu.:0.0000   
 Median :2.064 Median :0.04944 Median :0.0000   
 Mean :2.107 Mean :0.04892 Mean :0.1075   
 3rd Qu.:2.343 3rd Qu.:0.05134 3rd Qu.:0.0000   
 Max. :3.196 Max. :0.06369 Max. :6.2200

## Find how many rows and columns are in the data pull.   
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 376; cols: 27"

# save outputs for later comparison  
dat\_haul\_ex <- dat

# Print the first few lines of the data   
dat\_haul\_ex %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("year", "hauljoin", "cruise"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **year** | **srvy** | **survey** | **survey\_name** | **survey\_definition\_id** | **cruise** | **cruisejoin** | **hauljoin** | **haul** | **stratum** | **station** | **vessel\_id** | **vessel\_name** | **date\_time** | **latitude\_dd\_start** | **longitude\_dd\_start** | **latitude\_dd\_end** | **longitude\_dd\_end** | **bottom\_temperature\_c** | **surface\_temperature\_c** | **depth\_m** | **distance\_fished\_km** | **duration\_hr** | **net\_width\_m** | **net\_height\_m** | **area\_swept\_km2** | **performance** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 2023 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 202301 | -760 | -22472 | 94 | 50 | C-01 | 134 | NORTHWEST EXPLORER | 2023-06-21T15:22:41Z | 55.66353 | -167.5917 | 55.68996 | -167.5982 | 4.4 | 7.8 | 135 | 2.966 | 0.512 | 18.647 | 1.587 | 0.055307 | 0 |
| 2023 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 202301 | -760 | -22510 | 95 | 50 | C-18 | 134 | NORTHWEST EXPLORER | 2023-06-22T07:11:43Z | 55.66357 | -168.2098 | 55.68946 | -168.2130 | 4.4 | 8.0 | 136 | 2.884 | 0.519 | 17.259 | 1.931 | 0.049775 | 0 |
| 2023 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 202301 | -760 | -22511 | 96 | 50 | D-18 | 134 | NORTHWEST EXPLORER | 2023-06-22T10:18:09Z | 55.99245 | -168.2189 | 56.01884 | -168.2278 | 4.3 | 7.6 | 151 | 2.986 | 0.528 | 17.520 | 2.042 | 0.052315 | 0 |

### 14.4.1 Identify species\_code for walleye pollock

In the catch data, we itemize species catches by species\_code. To find out which species\_code to use, you can check variations on the following code. Note that here the word pollock is case sensitive. All species common\_name entries are lower case except for proper nouns (e.g., “Pacific”). The notation for finding a string is to use % around the phrase. Since % is a reserved character in a URL, you have to replace % with %25. Similarly, %20 needs to be used in place of a space (e.g., between “walleye” and “pollock”: "walleye%20pollock"}').

## query the API link. Use:   
res <- httr::GET(url = paste0(api\_link\_species, '?q={%22common\_name%22:%22walleye%20pollock%22}'))  
# OR  
res <- httr::GET(url = paste0(api\_link\_species, '?q={"common\_name":{"$like":"%25pollock%25"}}'))  
# OR  
res <- httr::GET(url = paste0(api\_link\_species, '?q={"common\_name":"walleye%20pollock"}'))  
  
## convert from JSON format  
data <- jsonlite::fromJSON(base::rawToChar(res$content))   
  
# save outputs for later comparison  
dat\_species\_ex <- data$items %>% dplyr::select(-links) # necessary for API accounting, but not part of the dataset

# Print the first few lines of the data  
dat\_species\_ex %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("species\_code"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **species\_code** | **scientific\_name** | **common\_name** | **id\_rank** | **worms** | **itis** |
| --- | --- | --- | --- | --- | --- |
| 21740 | Gadus chalcogrammus | walleye pollock | species | 300,735 | 934,083 |

### 14.4.2 Then, apply the hauljoins and species\_code to catch query

We’ll use the data from the haul and species table we collected before to select 2023 eastern Bering Sea walleye pollock catch data.

## query the API link  
# data for all walleye pollock caught in all 2023 eastern Bering Sea survey hauls  
dat <- data.frame()  
# there must be a better way to select multiple values for one parameter,   
# but saving that, we will loop through each hauljoin and collect the data of interest  
for (i in 1:nrow(dat\_haul\_ex)) {  
 res <- httr::GET(url = paste0(  
 api\_link\_catch,   
 '?q={"species\_code":21740,"hauljoin":', dat\_haul\_ex$hauljoin[i],'}'))  
 ## convert from JSON format  
 data <- jsonlite::fromJSON(base::rawToChar(res$content))   
 if (length(data$items) != 0) {  
 dat <- dplyr::bind\_rows(  
 dat,  
 data$items %>%   
 dplyr::select(-links)) # necessary for API accounting, but not part of the dataset  
 }  
}

Explore data:

# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 374; cols: 7"

# learn about the structure of the data  
summary(dat)

hauljoin species\_code cpue\_kgkm2 cpue\_nokm2   
 Min. :-23019 Min. :21740 Min. : 10.34 Min. : 18.26   
 1st Qu.:-22777 1st Qu.:21740 1st Qu.: 1454.44 1st Qu.: 2281.20   
 Median :-22540 Median :21740 Median : 3286.76 Median : 5863.07   
 Mean :-22553 Mean :21740 Mean : 6364.85 Mean : 11540.65   
 3rd Qu.:-22324 3rd Qu.:21740 3rd Qu.: 6956.25 3rd Qu.: 12456.99   
 Max. :-22110 Max. :21740 Max. :148679.68 Max. :202321.08   
 count weight\_kg taxon\_confidence   
 Min. : 1.0 Min. : 0.492 Length:374   
 1st Qu.: 113.2 1st Qu.: 71.560 Class :character   
 Median : 284.0 Median : 162.310 Mode :character   
 Mean : 572.8 Mean : 315.419   
 3rd Qu.: 616.5 3rd Qu.: 350.399   
 Max. :9997.0 Max. :7346.495

# Print the first few lines of the data   
dat %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("hauljoin", "species\_code"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **hauljoin** | **species\_code** | **cpue\_kgkm2** | **cpue\_nokm2** | **count** | **weight\_kg** | **taxon\_confidence** |
| --- | --- | --- | --- | --- | --- | --- |
| -22472 | 21740 | 52.6154 | 72.32357 | 4 | 2.91 | High |
| -22510 | 21740 | 351.5824 | 361.62764 | 18 | 17.50 | High |
| -22511 | 21740 | 3,110.7879 | 3,784.78562 | 198 | 162.74 | High |

# save outputs for later comparison  
dat\_catch\_ex <- dat

For reference and to help break down the above query, see these other query examples:

# data for haul -22775 (i.e., one specific haul)?  
res <- httr::GET(url = paste0(api\_link\_catch,   
 '?offset=',i,'&limit=10000&q={"hauljoin":-22775}'))  
  
# data for all walleye pollock (i.e., one species) caught in all years and surveys  
res <- httr::GET(url = paste0(api\_link\_catch,   
 '?offset=',i,'&limit=10000&q={"species\_code":21740}'))

### 14.4.3 Create zero-filled data for 2023 eastern Bering Sea walleye pollock and plot

It is important to create and have access to zero-fill (presence and absence) so you can do simple analyses and plot data.

dat <- dplyr::full\_join(  
 dat\_haul\_ex,  
 dat\_catch\_ex) %>%   
 dplyr::full\_join(  
 dat\_species\_ex) %>%   
 # modify zero-filled rows  
 dplyr::mutate(  
 cpue\_kgkm2 = ifelse(is.na(cpue\_kgkm2), 0, cpue\_kgkm2),  
 cpue\_nokm2 = ifelse(is.na(cpue\_nokm2), 0, cpue\_nokm2),  
 count = ifelse(is.na(count), 0, count),  
 weight\_kg = ifelse(is.na(weight\_kg), 0, weight\_kg))

Explore data

# Find how many rows and columns are in the data pull  
print(paste0("rows: ", nrow(dat), "; cols: ", ncol(dat)))

[1] "rows: 376; cols: 38"

# learn about the structure of the data  
summary(dat)

year srvy survey survey\_name   
 Min. :2023 Length:376 Length:376 Length:376   
 1st Qu.:2023 Class :character Class :character Class :character   
 Median :2023 Mode :character Mode :character Mode :character   
 Mean :2023   
 3rd Qu.:2023   
 Max. :2023   
   
 survey\_definition\_id cruise cruisejoin hauljoin   
 Min. :98 Min. :202301 Min. :-760.0 Min. :-23019   
 1st Qu.:98 1st Qu.:202301 1st Qu.:-760.0 1st Qu.:-22776   
 Median :98 Median :202301 Median :-759.0 Median :-22539   
 Mean :98 Mean :202301 Mean :-759.5 Mean :-22552   
 3rd Qu.:98 3rd Qu.:202301 3rd Qu.:-759.0 3rd Qu.:-22333   
 Max. :98 Max. :202301 Max. :-759.0 Max. :-22110   
   
 haul stratum station vessel\_id   
 Min. : 7.00 Min. :10.00 Length:376 Min. :134.0   
 1st Qu.: 65.75 1st Qu.:31.00 Class :character 1st Qu.:134.0   
 Median :114.00 Median :41.00 Mode :character Median :162.0   
 Mean :114.16 Mean :39.22 Mean :148.3   
 3rd Qu.:161.25 3rd Qu.:50.00 3rd Qu.:162.0   
 Max. :224.00 Max. :90.00 Max. :162.0   
   
 vessel\_name date\_time latitude\_dd\_start longitude\_dd\_start  
 Length:376 Length:376 Min. :54.66 Min. :-178.2   
 Class :character Class :character 1st Qu.:57.00 1st Qu.:-172.7   
 Mode :character Mode :character Median :58.02 Median :-168.9   
 Mean :58.26 Mean :-168.8   
 3rd Qu.:59.50 3rd Qu.:-165.2   
 Max. :62.01 Max. :-158.3   
   
 latitude\_dd\_end longitude\_dd\_end bottom\_temperature\_c surface\_temperature\_c  
 Min. :54.68 Min. :-178.2 Min. :-1.600 Min. : 1.700   
 1st Qu.:57.01 1st Qu.:-172.7 1st Qu.: 1.200 1st Qu.: 4.200   
 Median :58.02 Median :-168.9 Median : 2.700 Median : 6.550   
 Mean :58.26 Mean :-168.8 Mean : 2.249 Mean : 6.386   
 3rd Qu.:59.50 3rd Qu.:-165.2 3rd Qu.: 3.500 3rd Qu.: 8.525   
 Max. :62.01 Max. :-158.3 Max. : 5.400 Max. :11.000   
   
 depth\_m distance\_fished\_km duration\_hr net\_width\_m   
 Min. : 20.00 Min. :1.065 Min. :0.1890 Min. :12.90   
 1st Qu.: 54.75 1st Qu.:2.805 1st Qu.:0.5100 1st Qu.:16.66   
 Median : 74.00 Median :2.889 Median :0.5180 Median :17.27   
 Mean : 80.75 Mean :2.854 Mean :0.5129 Mean :17.15   
 3rd Qu.:105.00 3rd Qu.:2.945 3rd Qu.:0.5260 3rd Qu.:17.83   
 Max. :171.00 Max. :3.849 Max. :0.6560 Max. :20.29   
   
 net\_height\_m area\_swept\_km2 performance species\_code   
 Min. :1.300 Min. :0.02017 Min. :0.0000 Min. :21740   
 1st Qu.:1.875 1st Qu.:0.04725 1st Qu.:0.0000 1st Qu.:21740   
 Median :2.064 Median :0.04944 Median :0.0000 Median :21740   
 Mean :2.107 Mean :0.04892 Mean :0.1075 Mean :21740   
 3rd Qu.:2.343 3rd Qu.:0.05134 3rd Qu.:0.0000 3rd Qu.:21740   
 Max. :3.196 Max. :0.06369 Max. :6.2200 Max. :21740   
 NA's :2   
 cpue\_kgkm2 cpue\_nokm2 count weight\_kg   
 Min. : 0 Min. : 0 Min. : 0.0 Min. : 0.00   
 1st Qu.: 1431 1st Qu.: 2268 1st Qu.: 112.0 1st Qu.: 70.64   
 Median : 3273 Median : 5842 Median : 280.0 Median : 161.44   
 Mean : 6331 Mean : 11479 Mean : 569.8 Mean : 313.74   
 3rd Qu.: 6946 3rd Qu.: 12345 3rd Qu.: 611.5 3rd Qu.: 349.81   
 Max. :148680 Max. :202321 Max. :9997.0 Max. :7346.49   
   
 taxon\_confidence scientific\_name common\_name id\_rank   
 Length:376 Length:376 Length:376 Length:376   
 Class :character Class :character Class :character Class :character   
 Mode :character Mode :character Mode :character Mode :character   
   
   
   
   
 worms itis   
 Min. :300735 Min. :934083   
 1st Qu.:300735 1st Qu.:934083   
 Median :300735 Median :934083   
 Mean :300735 Mean :934083   
 3rd Qu.:300735 3rd Qu.:934083   
 Max. :300735 Max. :934083   
 NA's :2 NA's :2

# Print the first few lines of the data   
dat %>%   
 head(3) %>%   
 flextable::flextable() %>%  
 flextable::colformat\_num(  
 x = .,   
 j = c("year", "cruise", "cruisejoin", "species\_code"),   
 big.mark = "") %>%   
 flextable::theme\_zebra()

| **year** | **srvy** | **survey** | **survey\_name** | **survey\_definition\_id** | **cruise** | **cruisejoin** | **hauljoin** | **haul** | **stratum** | **station** | **vessel\_id** | **vessel\_name** | **date\_time** | **latitude\_dd\_start** | **longitude\_dd\_start** | **latitude\_dd\_end** | **longitude\_dd\_end** | **bottom\_temperature\_c** | **surface\_temperature\_c** | **depth\_m** | **distance\_fished\_km** | **duration\_hr** | **net\_width\_m** | **net\_height\_m** | **area\_swept\_km2** | **performance** | **species\_code** | **cpue\_kgkm2** | **cpue\_nokm2** | **count** | **weight\_kg** | **taxon\_confidence** | **scientific\_name** | **common\_name** | **id\_rank** | **worms** | **itis** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 2023 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 202301 | -760 | -22,472 | 94 | 50 | C-01 | 134 | NORTHWEST EXPLORER | 2023-06-21T15:22:41Z | 55.66353 | -167.5917 | 55.68996 | -167.5982 | 4.4 | 7.8 | 135 | 2.966 | 0.512 | 18.647 | 1.587 | 0.055307 | 0 | 21740 | 52.6154 | 72.32357 | 4 | 2.91 | High | Gadus chalcogrammus | walleye pollock | species | 300,735 | 934,083 |
| 2023 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 202301 | -760 | -22,510 | 95 | 50 | C-18 | 134 | NORTHWEST EXPLORER | 2023-06-22T07:11:43Z | 55.66357 | -168.2098 | 55.68946 | -168.2130 | 4.4 | 8.0 | 136 | 2.884 | 0.519 | 17.259 | 1.931 | 0.049775 | 0 | 21740 | 351.5824 | 361.62764 | 18 | 17.50 | High | Gadus chalcogrammus | walleye pollock | species | 300,735 | 934,083 |
| 2023 | EBS | eastern Bering Sea | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 98 | 202301 | -760 | -22,511 | 96 | 50 | D-18 | 134 | NORTHWEST EXPLORER | 2023-06-22T10:18:09Z | 55.99245 | -168.2189 | 56.01884 | -168.2278 | 4.3 | 7.6 | 151 | 2.986 | 0.528 | 17.520 | 2.042 | 0.052315 | 0 | 21740 | 3,110.7879 | 3,784.78562 | 198 | 162.74 | High | Gadus chalcogrammus | walleye pollock | species | 300,735 | 934,083 |

### 14.4.4 Visualize CPUE data in distribution map

Using the zero-filled data from the previous example, we can make a few plots!

## 14.5 Plot locations

library(ggplot2)  
  
ggplot2::ggplot(data = dat %>% dplyr::filter(cpue\_kgkm2 != 0),   
 mapping = aes(x = longitude\_dd\_start,   
 y = latitude\_dd\_start,   
 size = cpue\_kgkm2)) +   
 ggplot2::geom\_point(alpha = .75) +  
 ggplot2::geom\_point(data = dat %>% dplyr::filter(cpue\_kgkm2 == 0),   
 color = "red",   
 shape = 17,  
 alpha = .75,  
 size = 3) +  
 ggplot2::xlab("Longitude \*W") +  
 ggplot2::ylab("Latitude \*N") +  
 ggplot2::ggtitle(label = "Catches of walleye pollock (Weight CPUE; kg/km2)",   
 subtitle = "2023 eastern Bering Sea bottom trawl survey") +  
 ggplot2::scale\_size\_continuous(name = "Weight (kg)") +   
 ggplot2::theme\_bw()



### 14.5.1 Plot inverse-distance weighted modeled product of locations

This map is constructed using [akgfmaps](https://github.com/afsc-gap-products/akgfmaps)

# devtools::install\_github("afsc-gap-products/akgfmaps", build\_vignettes = TRUE)  
library(akgfmaps)  
  
figure0 <- akgfmaps::make\_idw\_map(  
 CPUE\_KGHA = dat$cpue\_kgkm2, # calculates the same, regardless of units.   
 LATITUDE = dat$latitude\_dd\_start,   
 LONGITUDE = dat$longitude\_dd\_start,   
 region = "bs.south", # Predefined EBS area  
 set.breaks = "jenks", # Gets Jenks breaks from classint::classIntervals()  
 in.crs = "+proj=longlat", # Set input coordinate reference system  
 out.crs = "EPSG:3338", # Set output coordinate reference system  
 extrapolation.grid.type = "sf")

[inverse distance weighted interpolation]  
[inverse distance weighted interpolation]

figure0$plot + # 20x20km grid  
 ggplot2::guides(fill=guide\_legend(title = "walleye pollock\nCPUE (kg/km2)"))



## 14.6 Other query examples

### 14.6.1 Ex. Combination of year, srvy, stratum

Show haul data where year is less than 1989, srvy = “EBS”, and stratum is not equal to 81.

res <- httr::GET(  
 url = paste0(api\_link\_haul,   
 '?&limit=10000&q={"year":{"$lt":1989},"stratum":{"$ne":"81"},"srvy":"EBS"}}'))  
data <- jsonlite::fromJSON(base::rawToChar(res$content))  
dat <- data$items %>%   
 dplyr::select(-links) # necessary for API accounting, but not part of the dataset)

Explore data:

# 15. Access via API and Python

### 15.0.1 {afscgap} Library Installation

author: Sam Pottinger (sam.pottinger@berkeley.edu; GitHub::sampottinger) date: May 13, 2023

The third-party afscgap Python package interfaces with FOSS to access AFSC GAP data. It can be installed via pip:

#The reticulate package provides a comprehensive set of tools for interoperability between Python and R.   
library(reticulate)

pip install afscgap  
pip install git+https://github.com/SchmidtDSE/afscgap.git@main

For more information on installation and deployment, see the [library documentation](https://pyafscgap.org).

### 15.0.2 Basic query

This first example queries for Pacific glass shrimp (*Pasiphaea pacifica*) in the Gulf of Alaska in 2021. The library will automatically generate HTTP queries, converting from Python types to [ORDS](https://www.oracle.com/database/technologies/appdev/rest.html) query syntax.

import afscgap  
  
query = afscgap.Query()  
query.filter\_year(eq=2021)  
query.filter\_srvy(eq='GOA')  
query.filter\_scientific\_name(eq='Pasiphaea pacifica')  
  
results = query.execute()

The results variable in this example is an iterator that will automatically perform pagination behind the scenes.

### 15.0.3 Iterating with a for loop

The easiest way to interact with results is a simple for loop. This next example determines the frequency of different catch per unit effort where Pacific glass shrimp were reported:

import afscgap  
  
# Mapping from CPUE to count  
count\_by\_cpue = {}  
  
# Build query  
query = afscgap.Query()  
query.filter\_year(eq=2021)  
query.filter\_srvy(eq='GOA')  
query.filter\_scientific\_name(eq='Pasiphaea pacifica')  
results = query.execute()  
  
# Iterate through results and count  
for record in results:  
 cpue = record.get\_cpue\_weight(units='kg/ha')  
 cpue\_rounded = round(cpue)  
 count = count\_by\_cpue.get(cpue\_rounded, 0) + 1  
 count\_by\_cpue[cpue\_rounded] = count  
  
# Print the result  
print(count\_by\_cpue)

Note that, in this example, only records with Pacific glass shrimp are included (“presence-only” data). See zero catch inference below. In other words, it reports on CPUE only for hauls in which Pacific glass shrimp were recorded, excluding some hauls like those in which Pacific glass shrimp were not found at all.

### 15.0.4 Iterating with functional programming

A for loop is not the only option for iterating through results. List comprehensions and other functional programming methods can be used as well.

import statistics  
  
import afscgap  
  
# Build query  
query = afscgap.Query()  
query.filter\_year(eq=2021)  
query.filter\_srvy(eq='GOA')  
query.filter\_scientific\_name(eq='Pasiphaea pacifica')  
results = query.execute()  
  
# Get temperatures in Celsius  
temperatures = [record.get\_bottom\_temperature(units='c') for record in results]  
  
# Take the median  
print(statistics.median(temperatures))

This example reports the median temperature in Celcius for when Pacific glass shrimp was reported.

### 15.0.5 Load into Pandas

The results from the afscgap package are serializable and can be loaded into other tools like [Pandas](https://pandas.pydata.org/). This example loads Pacific glass shrimp from 2021 Gulf of Alaska into a data frame.

import pandas  
  
import afscgap  
  
query = afscgap.Query()  
query.filter\_year(eq=2021)  
query.filter\_srvy(eq='GOA')  
query.filter\_scientific\_name(eq='Pasiphaea pacifica')  
results = query.execute()  
  
pandas.DataFrame(results.to\_dicts())

Specifically, to\_dicts provides an iterator over a dictionary form of the data that can be read into tools like Pandas.

### 15.0.6 Advanced filtering

Queries so far have focused on filters requiring equality but range queries can be built as well.

import afscgap  
  
# Build query  
query = afscgap.Query()  
query.filter\_year(min\_val=2015, max\_val=2019) # Note min/max\_val  
query.filter\_srvy(eq='GOA')  
query.filter\_scientific\_name(eq='Pasiphaea pacifica')  
results = query.execute()  
  
# Sum weight  
weights = map(lambda x: x.get\_weight(units='kg'), results)  
total\_weight = sum(weights)  
print(total\_weight)

This example queries for Pacific glass shrimp data between 2015 and 2019, summing the total weight caught. Note that most users will likely take advantage of built-in Python to [ORDS](https://www.oracle.com/database/technologies/appdev/rest.html) query generation which dictates how the library communicates with the API service. However, users can provide raw ORDS queries as well using [manual filtering](https://pyafscgap.org/devdocs/afscgap.html#manual-filtering).

### 15.0.7 Zero-catch inference

Until this point, these examples use presence-only data. However, the afscgap package can infer negative or “zero catch” records as well.

import afscgap  
  
# Mapping from CPUE to count  
count\_by\_cpue = {}  
  
# Build query  
query = afscgap.Query()  
query.filter\_year(eq=2021)  
query.filter\_srvy(eq='GOA')  
query.filter\_scientific\_name(eq='Pasiphaea pacifica')  
query.set\_presence\_only(False) # Added to earlier example  
results = query.execute()  
  
# Iterate through results and count  
for record in results:  
 cpue = record.get\_cpue\_weight(units='kg/ha')  
 cpue\_rounded = round(cpue)  
 count = count\_by\_cpue.get(cpue\_rounded, 0) + 1  
 count\_by\_cpue[cpue\_rounded] = count  
  
# Print the result  
print(count\_by\_cpue)

This example revisits the earlier snippet for CPUE counts but set\_presence\_only(False) directs the library to look at additional data on hauls, determining which hauls did not have Pacific glass shrimp. This lets the library return records for hauls in which Pacific glass shrimp were not found. This can be seen in differences in counts reported:

| Rounded CPUE | Count with set\_presence\_only(True) | Count with set\_presence\_only(False) |
| --- | --- | --- |
| 0 kg/ha | 44 | 521 |
| 1 kg/ha | 7 | 7 |
| 2 kg/ha | 1 | 1 |

Put simply, while the earlier example showed CPUE counts for hauls in which Pacific glass shrimp were seen, this revised example reports for all hauls in the Gulf of Alaska in 2021.

### 15.0.8 More information

Please see the [API documentation](https://pyafscgap.org/devdocs/afscgap.html) for the Python library for additional details.

# 16. Access via Oracle and R (AFSC Staff only)

If the user has access to the AFSC Oracle database, the user can use SQL developer to view and pull the FOSS public data directly from the GAP\_PRODUCTS Oracle schema.

### 16.0.1 Connect to Oracle from R

Many users will want to access the data from Oracle using R. The user will need to install the RODBC R package and ask OFIS (IT) connect R to Oracle. Then, use the following code in R to establish a connection from R to Oracle:

Here, the user can write in their username and password directly into the RODBC connect function. Never save usernames or passwords in scripts that may be intentionally or unintentionally shared with others. If no username and password is entered in the function, pop-ups will appear on the screen asking for the username and password.

library(gapindex)  
channel <- gapindex::get\_connected()

### 16.0.2 Ex. Wholesale download data and join data in R

locations <- c(  
 "GAP\_PRODUCTS.FOSS\_CATCH",  
 "GAP\_PRODUCTS.FOSS\_HAUL",  
 "GAP\_PRODUCTS.FOSS\_SPECIES"  
)  
  
print(Sys.Date())  
  
error\_loading <- c() # log if any tables are unable to download   
for (i in 1:length(locations)){  
 print(locations[i])  
 a <- RODBC::sqlQuery(channel, paste0("SELECT \* FROM ", locations[i], "; "))  
 if (is.null(nrow(a))) { # if an error in downloading has occurred  
 error\_loading <- c(error\_loading, locations[i])  
 } else { # if no error in downloading has occurred  
 write.csv(x = a,   
 # change file name to be more computer file storage friendly  
 here::here(paste0(tolower(gsub(  
 pattern = '.',   
 replacement = "\_",   
 x = locations[i],   
 fixed = TRUE)),  
 ".csv")))  
 }  
}  
error\_loading

Join downloaded files into presence-only table

# Load data  
library(dplyr)  
library(here)  
library(readr)  
catch <- readr::read\_csv(file = here::here("data/gap\_products\_foss\_catch.csv"))[,-1] # remove "row number" column  
haul <- readr::read\_csv(file = here::here("data/gap\_products\_foss\_haul.csv"))[,-1] # remove "row number" column  
species <- readr::read\_csv(file = here::here("data/gap\_products\_foss\_species.csv"))[,-1] # remove "row number" column  
  
dat <-   
 # join haul and catch data to unique species by survey table  
 dplyr::left\_join(haul, catch) %>%   
 # join species data to unique species by survey table  
 dplyr::left\_join(species) %>%   
 # modify zero-filled rows  
 dplyr::mutate(  
 CPUE\_KGKM2 = ifelse(is.null(CPUE\_KGKM2), 0, CPUE\_KGKM2), # just in case  
 CPUE\_KGHA = CPUE\_KGKM2/100, # Hectares  
 CPUE\_NOKM2 = ifelse(is.null(CPUE\_NOKM2), 0, CPUE\_NOKM2), # just in case  
 CPUE\_NOHA = CPUE\_NOKM2/100, # Hectares  
 COUNT = ifelse(is.null(COUNT), 0, COUNT),  
 WEIGHT\_KG = ifelse(is.null(WEIGHT\_KG), 0, WEIGHT\_KG) )

Join downloaded files into zero-filled table

# Load data  
library(dplyr)  
library(here)  
library(readr)  
catch <- readr::read\_csv(file = here::here("data/gap\_products\_foss\_catch.csv"))[,-1] # remove "row number" column  
haul <- readr::read\_csv(file = here::here("data/gap\_products\_foss\_haul.csv"))[,-1] # remove "row number" column  
species <- readr::read\_csv(file = here::here("data/gap\_products\_foss\_species.csv"))[,-1] # remove "row number" column  
  
# come up with full combination of what species should be listed for what hauls/surveys  
# for zero-filled data, all species caught in a survey need to have zero or non-zero row entries for a haul  
comb <- dplyr::full\_join(  
 x = dplyr::left\_join(catch, haul, by = "HAULJOIN") %>%  
 dplyr::select(SURVEY\_DEFINITION\_ID, SPECIES\_CODE) %>%  
 dplyr::distinct(),  
 y = haul %>%  
 dplyr::select(SURVEY\_DEFINITION\_ID, HAULJOIN) %>%  
 dplyr::distinct(),   
 by = "SURVEY\_DEFINITION\_ID",   
 relationship = "many-to-many"  
)  
  
# Join data to make a full zero-filled CPUE dataset  
dat <- comb %>%   
 # add species data to unique species by survey table  
 dplyr::left\_join(species, "SPECIES\_CODE") %>%   
 # add catch data  
 dplyr::full\_join(catch, c("SPECIES\_CODE", "HAULJOIN")) %>%   
 # add haul data  
 dplyr::full\_join(haul) %>% # , c("SURVEY\_DEFINITION\_ID", "HAULJOIN")  
 # modify zero-filled rows  
 dplyr::mutate(  
 CPUE\_KGKM2 = ifelse(is.null(CPUE\_KGKM2), 0, CPUE\_KGKM2),  
 CPUE\_KGHA = CPUE\_KGKM2/100, # Hectares  
 CPUE\_NOKM2 = ifelse(is.null(CPUE\_NOKM2), 0, CPUE\_NOKM2),  
 CPUE\_NOHA = CPUE\_NOKM2/100, # Hectares  
 COUNT = ifelse(is.null(COUNT), 0, COUNT),  
 WEIGHT\_KG = ifelse(is.null(WEIGHT\_KG), 0, WEIGHT\_KG) )

### 16.0.3 Ex. Join data using Oracle

To join these tables in Oracle, you may use a variant of the following code:

SELECT   
hh.YEAR,  
hh.SRVY,   
hh.SURVEY,  
hh.SURVEY\_DEFINITION\_ID,  
hh.SURVEY\_NAME,  
hh.CRUISE,  
hh.CRUISEJOIN,   
hh.HAUL,  
hh.HAULJOIN,  
hh.STRATUM,  
hh.STATION,  
hh.VESSEL\_ID,  
hh.VESSEL\_NAME,   
hh.DATE\_TIME,  
hh.LATITUDE\_DD\_START,   
hh.LONGITUDE\_DD\_START,   
hh.LATITUDE\_DD\_END,  
hh.LONGITUDE\_DD\_END,   
hh.BOTTOM\_TEMPERATURE\_C,  
hh.SURFACE\_TEMPERATURE\_C,  
hh.DEPTH\_M,  
cc.SPECIES\_CODE,  
ss.ITIS,  
ss.WORMS,  
ss.COMMON\_NAME,   
ss.SCIENTIFIC\_NAME,  
ss.ID\_RANK,  
CASE WHEN cc.CPUE\_KGKM2 IS NULL THEN 0 ELSE cc.CPUE\_KGKM2 END AS CPUE\_KGKM2,  
CASE WHEN cc.CPUE\_NOKM2 IS NULL THEN 0 ELSE cc.CPUE\_NOKM2 END AS CPUE\_NOKM2,  
CASE WHEN cc.COUNT IS NULL THEN 0 ELSE cc.COUNT END AS COUNT,  
CASE WHEN cc.WEIGHT\_KG IS NULL THEN 0 ELSE cc.WEIGHT\_KG END AS WEIGHT\_KG,  
CASE WHEN cc.TAXON\_CONFIDENCE IS NULL THEN NULL ELSE cc.TAXON\_CONFIDENCE END AS TAXON\_CONFIDENCE,  
hh.AREA\_SWEPT\_KM2,   
hh.DISTANCE\_FISHED\_KM,  
hh.DURATION\_HR,   
hh.NET\_WIDTH\_M,  
hh.NET\_HEIGHT\_M,  
hh.PERFORMANCE   
FROM GAP\_PRODUCTS.FOSS\_SURVEY\_SPECIES sv  
FULL OUTER JOIN GAP\_PRODUCTS.FOSS\_SPECIES ss  
ON sv.SPECIES\_CODE = ss.SPECIES\_CODE  
FULL OUTER JOIN GAP\_PRODUCTS.FOSS\_HAUL hh  
ON sv.SURVEY\_DEFINITION\_ID = hh.SURVEY\_DEFINITION\_ID  
FULL OUTER JOIN GAP\_PRODUCTS.FOSS\_CATCH cc  
ON sv.SPECIES\_CODE = cc.SPECIES\_CODE  
AND hh.HAULJOIN = cc.HAULJOIN

### 16.0.4 Ex. Subset data

Here, we are pulling EBS Pacific cod from 2010 - 2021:

# Pull data  
data <- RODBC::sqlQuery(  
channel = channel,   
query =   
"SELECT \* FROM GAP\_PRODUCTS.FOSS\_CATCH cc  
JOIN GAP\_PRODUCTS.FOSS\_HAUL hh  
ON cc.HAULJOIN = hh.HAULJOIN  
WHERE SRVY = 'EBS'   
AND SPECIES\_CODE = 21720 -- 'Pacific cod'   
AND YEAR >= 2010   
AND YEAR < 2021")  
  
flextable::flextable(data[1:3,]) %>%   
 flextable::theme\_zebra()

| **HAULJOIN** | **SPECIES\_CODE** | **CPUE\_KGKM2** | **CPUE\_NOKM2** | **COUNT** | **WEIGHT\_KG** | **TAXON\_CONFIDENCE** | **YEAR** | **SRVY** | **SURVEY** | **SURVEY\_DEFINITION\_ID** | **SURVEY\_NAME** | **CRUISE** | **CRUISEJOIN** | **HAULJOIN.1** | **HAUL** | **STRATUM** | **STATION** | **VESSEL\_ID** | **VESSEL\_NAME** | **DATE\_TIME** | **LATITUDE\_DD\_START** | **LONGITUDE\_DD\_START** | **LATITUDE\_DD\_END** | **LONGITUDE\_DD\_END** | **BOTTOM\_TEMPERATURE\_C** | **SURFACE\_TEMPERATURE\_C** | **DEPTH\_M** | **DISTANCE\_FISHED\_KM** | **DURATION\_HR** | **NET\_WIDTH\_M** | **NET\_HEIGHT\_M** | **AREA\_SWEPT\_KM2** | **PERFORMANCE** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| -19,461 | 21,720 | 646.8800 | 200.3345 | 10 | 32.29 | High | 2,019 | EBS | eastern Bering Sea | 98 | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 201,901 | -726 | -19,461 | 197 | 41 | R-27 | 94 | VESTERAALEN | 2019-07-26 13:05:25 | 60.65452 | -174.8251 | 60.68077 | -174.8282 | 2.4 | 10.3 | 97 | 2.922 | 0.533 | 17.083 | 2.424 | 0.04991653 | 0 |
| -19,446 | 21,720 | 1,212.7733 | 164.7230 | 8 | 58.90 | High | 2,019 | EBS | eastern Bering Sea | 98 | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 201,901 | -727 | -19,446 | 168 | 61 | Q-28 | 162 | ALASKA KNIGHT | 2019-07-20 07:45:12 | 60.34982 | -175.3932 | 60.32608 | -175.3835 | 2.6 | 10.1 | 111 | 2.692 | 0.506 | 18.041 | 2.460 | 0.04856637 | 0 |
| -19,422 | 21,720 | 313.8482 | 108.5980 | 6 | 17.34 | High | 2,019 | EBS | eastern Bering Sea | 98 | Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey | 201,901 | -726 | -19,422 | 180 | 61 | L-29 | 94 | VESTERAALEN | 2019-07-22 17:45:32 | 58.67524 | -175.5278 | 58.67691 | -175.5795 | 3.7 | 10.3 | 135 | 3.014 | 0.541 | 18.331 | 1.751 | 0.05524963 | 0 |

### 16.0.5 Ex. Find all species found in the eastern Bering Sea (EBS) survey in 2023

# Pull data  
data <- RODBC::sqlQuery(  
channel = channel,   
query =   
"SELECT DISTINCT   
ss.COMMON\_NAME,  
ss.SCIENTIFIC\_NAME,   
ss.ID\_RANK,   
ss.WORMS  
FROM GAP\_PRODUCTS.FOSS\_CATCH cc -- get species codes  
LEFT JOIN GAP\_PRODUCTS.FOSS\_SPECIES ss -- get species info  
ON cc.SPECIES\_CODE = ss.SPECIES\_CODE  
LEFT JOIN GAP\_PRODUCTS.FOSS\_HAUL hh -- filter by year and survey  
ON cc.HAULJOIN = hh.HAULJOIN  
WHERE hh.YEAR = 2023  
AND hh.SURVEY\_DEFINITION\_ID = 98 -- EBS survey  
ORDER BY COMMON\_NAME")  
  
flextable::flextable(data[1:3,]) %>%   
 # flextable::fit\_to\_width(max\_width = 6) %>%   
 flextable::theme\_zebra()

| **COMMON\_NAME** | **SCIENTIFIC\_NAME** | **ID\_RANK** | **WORMS** |
| --- | --- | --- | --- |
| Alaska great-tellin | Megangulus luteus | species | 423,511 |
| Alaska plaice | Pleuronectes quadrituberculatus | species | 254,564 |
| Alaska skate | Arctoraja parmifera | species | 1,577,324 |

# 17. Open source code

## 17.1 R Packages

### 17.1.1 [akgfmaps R package](https://github.com/afsc-gap-products/akgfmaps)

Bttom trawl survey maps layers and plotting examples. **POC:** Sean Rohan

### 17.1.2 [coldpool R package](https://github.com/afsc-gap-products/coldpool)

Cold pool area and temperature data products for the Bering Sea. **POC:** Sean Rohan

### 17.1.3 [akfishcondition R package](https://github.com/afsc-gap-products/akfishcondition)

Groundfish morphometric condition indicators for fish in the Bering Sea, Aleutian Islands, and Gulf of Alaska. **POC:** Sean Rohan

### 17.1.4 [gapindex R package](https://github.com/afsc-gap-products/gapindex)

Calculation of Design-Based Indices of Abundance and Composition for AFSC GAP Bottom Trawl Surveys. **POC:** Zack Oyafuso and Margaret Siple

# 18. Production run notes

Report run date: Tuesday, January 14, 2025

# 19. R Version Metadata

R version 4.4.2 (2024-10-31 ucrt)  
Platform: x86\_64-w64-mingw32/x64  
Running under: Windows 10 x64 (build 19045)  
  
Matrix products: default  
  
  
locale:  
[1] LC\_COLLATE=English\_United States.utf8   
[2] LC\_CTYPE=English\_United States.utf8   
[3] LC\_MONETARY=English\_United States.utf8  
[4] LC\_NUMERIC=C   
[5] LC\_TIME=English\_United States.utf8   
  
time zone: America/Los\_Angeles  
tzcode source: internal  
  
attached base packages:  
[1] stats graphics grDevices utils datasets methods base   
  
loaded via a namespace (and not attached):  
 [1] compiler\_4.4.2 fastmap\_1.2.0 cli\_3.6.3 tools\_4.4.2   
 [5] htmltools\_0.5.8.1 rstudioapi\_0.17.1 yaml\_2.3.10 rmarkdown\_2.29   
 [9] knitr\_1.49 jsonlite\_1.8.9 xfun\_0.49 digest\_0.6.37   
[13] rlang\_1.1.4 evaluate\_1.0.1

### 19.0.1 NOAA README

This repository is a scientific product and is not official communication of the National Oceanic and Atmospheric Administration, or the United States Department of Commerce. All NOAA GitHub project code is provided on an ‘as is’ basis and the user assumes responsibility for its use. Any claims against the Department of Commerce or Department of Commerce bureaus stemming from the use of this GitHub project will be governed by all applicable Federal law. Any reference to specific commercial products, processes, or services by service mark, trademark, manufacturer, or otherwise, does not constitute or imply their endorsement, recommendation or favoring by the Department of Commerce. The Department of Commerce seal and logo, or the seal and logo of a DOC bureau, shall not be used in any manner to imply endorsement of any commercial product or activity by DOC or the United States Government.

### 19.0.2 NOAA License

Software code created by U.S. Government employees is not subject to copyright in the United States (17 U.S.C. §105). The United States/Department of Commerce reserve all rights to seek and obtain copyright protection in countries other than the United States for Software authored in its entirety by the Department of Commerce. To this end, the Department of Commerce hereby grants to Recipient a royalty-free, nonexclusive license to use, copy, and create derivative works of the Software outside of the United States.

# 20. Acknowledgments

# 21. Community Acknowledgments

We would like to thank the many communities of Alaska and their members who have helped contribute to this body of work. The knowledge, experiences, and insights have been instrumental in expanding the scope of our science and knowledge to encompass the many issues that face this important ecosystem. We appreciate feedback from those residing in the region that are willing to share their insights and participation in an open dialog about how we can improve our collective knowledge of the ecosystem and the region.

# 22. Land Acknowledgements

We would like to thank the many communities of the Bering Strait region and their members who have helped contribute to this document. The knowledge, experiences, and insights of the people of the Bering Strait region have been instrumental in expanding the scope of our science and knowledge to encompass the many issues that face this important ecosystem. We appreciate feedback from those residing in the region that are willing to share their insights, including the local names used for the species covered by this document, identifying species of interest or concern that should be included in this document, and participation in an open dialog about how we can improve our collective knowledge of the ecosystem and the region.

NOAA Fisheries Alaska Fisheries Science Center’s work is conducted in the waters and along the coastlines of Alaska, which include the traditional home lands and waters of the Inupiat, Yupiit, Siberian Yupiit, Unangax, Alutiiq/Sugpiaq, Eyak, Dena’ina Athabascan, Tlingit, Haida, and Tsimshian who have stewarded their lands and waters since time immemorial. We are indebted to these peoples for their wisdom and knowledge of their lands and waters.

This document was prepared in the greater Seattle area, which are the traditional lands of the Coast Salish people, including the Duwamish people, past and present. We are grateful for their continued sharing of vision, wisdom, values, and leadership.

# 23. Technical Acknowledgments

This quarto book is based off the [NOAA-quarto-book](https://github.com/nmfs-opensci/NOAA-quarto-book) GitHub repo designed by Eli Holmes.

This repo and GitHub Action was based on the tutorial by Openscapes [quarto-website-tutorial](https://github.com/Openscapes/quarto-website-tutorial) by Julia Lowndes and Stefanie Butland.

## 23.1 Partners

Scientists from the Alaska Fisheries Science Center conduct these bottom trawl surveys with participation from the Alaska Department of Fish & Game (ADF&G), the International Pacific Halibut Commission (IPHC), and universities. This research is conducted on chartered fishing vessels.

## 23.2 Collaborators

Our data are used in many annual publications, including but not limited to the list below:

* [Alaska Stock Assessments](https://www.fisheries.noaa.gov/alaska/population-assessments/alaska-stock-assessments)
* [North Pacific Groundfish Stock Assessment and Fishery Evaluation Reports](https://www.fisheries.noaa.gov/alaska/population-assessments/north-pacific-groundfish-stock-assessment-and-fishery-evaluation)
* [Groundfish Economic Status Reports for the Gulf of Alaska and Bering Sea and Aleutian Islands](https://www.fisheries.noaa.gov/alaska/commercial-fishing/groundfish-economic-status-reports-gulf-alaska-and-bering-sea-and-aleutian-islands)
* [Alaska Marine Ecosystem Status Report Database](https://www.fisheries.noaa.gov/resource/data/alaska-marine-ecosystem-status-report-archive)
* [Southeast Alaska Coastal Monitoring Survey Reports](https://www.fisheries.noaa.gov/alaska/commercial-fishing/southeast-alaska-coastal-monitoring-survey-reports)
* [Alaska Fisheries Life History Database](https://www.fisheries.noaa.gov/resource/data/alaska-fisheries-life-history-database)
* [Essential Fish Habitat Research Plan in Alaska](https://www.fisheries.noaa.gov/alaska/habitat-conservation/essential-fish-habitat-research-plan-alaska)

# 24. Citations and References

# 25. Access Constraints

There are no legal restrictions on access to the data. They reside in public domain and can be freely distributed.

**User Constraints:** Users must read and fully comprehend the metadata prior to use. Data should not be used beyond the limits of the source scale. Acknowledgement of AFSC Groundfish Assessment Program, as the source from which these data were obtained, in any publications and/or other representations of these data, is suggested.

# 26. References

Hoff, G. R. (2016). *Results of the 2016 eastern Bering Sea upper continental slope survey of groundfishes and invertebrate resources* (NOAA Tech. Memo. NOAA-AFSC-339). U.S. Dep. Commer. <https://doi.org/10.7289/V5/TM-AFSC-339>

Markowitz, E. H., Dawson, E. J., Wassermann, S., Anderson, C. B., Rohan, S. K., Charriere, B. K., and Stevenson, D. E. (2024). *Results of the 2023 eastern and northern Bering Sea continental shelf bottom trawl survey of groundfish and invertebrate fauna* (NOAA Tech. Memo. NMFS-AFSC-487; p. 242). U.S. Dep. Commer. <https://doi.org/10.25923/2mry-yx09>

Siple, M. C., Szalay, P. G. von, Raring, N. W., Dowlin, A. N., and Riggle, B. C. (2024). *Data report: 2023 gulf of alaska bottom trawl survey* (NOAA Tech. Memo. AFSC processed report; 2024-09). U.S. Dep. Commer. <https://doi.org/10.25923/gbb1-x748>

Von Szalay, P. G., Raring, N. W., Siple, M. C., Dowlin, A. N., Riggle, B. C., and Laman, E. A. and. (2023). *Data report: 2022 Aleutian Islands bottom trawl survey* (AFSC Processed Rep. 2023-07; p. 230). U.S. Dep. Commer. <https://doi.org/10.25923/85cy-g225>