

The ATTACH model

Package Version 2.0.0

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1. Introduction

The catchfunction package (which we refer to as the ABC To TAC and Commercial Harvest, aka ATTACH, model: R package rename forthcoming) was created for the [Alaska Climate Integrated Modeling Project](#) (ACLIM) by Amanda Faig (University of Washington; School of Aquatic Fisheries and Sciences) and Alan Haynie (NOAA; NMFS). This function, in a nutshell, takes Bering Sea (BS) acceptable biological catch (ABC) as input and uses a series of regression estimates to predict total allowable catch (TAC) and from that the commercial harvest in the Bering Sea, based on ABC, TAC, and catch data from 1992 to 2017.

If you have yet to install the R package (or if you want to update your package, e.g. to see if a newer version has been released) run the following code:

```
install.packages("devtools")
library("devtools")
install_github("amandafaig/catchfunction")
library("catchfunction")
```

Otherwise, simply load the library:

```
library(catchfunction)
```

Please note that this manual is for version 2 of ATTACH. To see the manual for version 1, the version used by Reum et al. and Holsman et al. (both forthcoming), [click here](#).

Versions 1 and 2 differ in two key ways:

- Version 2 uses 1992-2018 data, while Version 1 uses data from 1992-2017.
- Version 2 uses a different ensemble. Thus section 4 of the manual, which is dedicated to describing the ensemble, is where you will find most major differences between the Version 1 and Version 2 manual.

To download version 1 of the R package, run the following code:

```
install.packages("devtools")
library("devtools")
install_github("amandafaig/catchfunction@v1.6.0")
library("catchfunction")
```

2. Predicting TAC

We created ATTACH as a two-step model. In the first step, TAC is predicted from ABC. The user passes, as inputs, the Bering Sea ABCs into the model for as many species as are defined in their biological models; up to the 22 species under the BSAI 2 million ton ecosystem cap (“the ecosystem cap”). To see the full list of species included in the cap, see the list of arguments in the help file, or in the [pdf manual](#).

?catch_function

Since the ecosystem cap is for the entire BSAI, but the ABC input is only for the Bering Sea, the ATTACH model first calculates BSAI ABCs from the BS ABC inputs. (The ABC input is only for the Bering Sea is this is the scope of the ACLIM project.) We calculate BSAI ABCs assuming that the Aleutian Island ABC rises and falls (relative to the historical mean) in proportion to how the (user defined) Bering Sea ABC compares to its historical mean. For ABCs left undefined by the user, we assume those species ABCs are at their historical means.

The entire set of BSAI ABCs is then passed into the first step of the model: estimating TAC. Each year the North Pacific Fishery Management Council (“the Council”) sets the TAC of individual stocks based on the ABC estimates for the individual stocks. The ecosystem cap mandates that the Council must ensure the sum of these TACs does not exceed 2 million metric tons. The stock assessment ABCs and the TACs set by the Council are published annually in the [Alaska Region’s groundfish harvest specifications](#). We used data from 1992 to 2017 to create the current version of the model (version 1).

TACs for each stock were estimated statistically using a log-linear model. For $j = 1, 2, \dots, n$ stocks, the general model for stock i took the form:

$$\ln(TAC_{i,t}) = \alpha_i + \beta_i \ln(ABC_{i,t}) + \sum_{j \neq i}^n \beta_j ABC_{j,t} + \sum_{k=1}^m \beta_k I_{k,t} + \varepsilon_{i,t}$$

where α_i is the stock-specific intercept for species i , β_i is the elasticity of the TAC of species i with respect to its own ABC, and β_j relates the ABC of some species $j \neq i$ to the TAC of species i . The effect (β_k) of $k = 1, 2, \dots, m$ events or policy changes (e.g., changes in management, area closures, or implementation of catch share programs) on TAC was also estimated where $I_{k,t}$ is an indicator variable for event k in year t , and $\varepsilon_{i,t}$ denotes the residual error for the prediction in year t . How the errors handled is discussed more in section 4. To see each individual equation see Haynie et al. (in prep).

ATTACH uses the predicted coefficients to predict TAC from ABCs. The events/policies are assumed to reflect the last year of the dataset. So, for example, the Amendment 80 indicator variable is set to 1 in predictions, while the Steller Sea Lion closure of 2011 to 2014 is set to 0 (and the Steller Sea Lion limited reopening is set to 1).

When the model is passed a set of historical ABCs, the predicted TACs add up to less than 2 million metric tons, since necessarily these combinations led to a net TAC at or below the ecosystem cap. (Even this is not guaranteed, however, due to prediction error.) When the set of ABCs input into ATTACH is not a historical set, it is possible the predicted TACs based on the regression estimates alone could together exceed the ecosystem cap. To ensure ATTACH does not violate the ecosystem cap, we check the sum of the TACs and, if they exceed 2 million metric tons, we decrease all TACs proportionally, except for that of BS and AI Sablefish, BSAI Shortraker rockfish, and BSAI Northern rockfish.

3. Predicting Catch

The output from the TAC prediction step is then passed to another sub-model, the catch prediction step. Catch estimates are based on TAC data (from the aforementioned groundfish harvest specifications) and catch data from the [Catch Accounting System](#). As in the first step, we use data from 1992 to 2017.

Catches for each stock were estimated statistically using a log-linear model. For $j = 1, 2, \dots, n$ stocks, the general model for stock i took the form:

$$\ln(catch_{i,t}) = \alpha_i + \beta_i \ln(TAC_{i,t}) + \sum_{j \neq i}^n \beta_j TAC_{j,t} + \sum_{k=1}^m \beta_k I_{k,t} + \varepsilon_{i,t}$$

where α_i is the stock-specific intercept for species i , β_i is the elasticity of the catch of species i with respect to its own TAC, and β_j relates the TAC of some species $j \neq i$ to the catch of species i . The effect (β_k) of $k = 1, 2, \dots, m$ events or policy changes (e.g., changes in management, area closures, or implementation of catch share programs) on TAC was also estimated where $I_{k,t}$ is an indicator variable for event k in year t , and $\varepsilon_{i,t}$ denotes the residual error for the prediction in year t . How the errors handled is discussed more in section 4. To see each individual equation see Haynie et al. (in prep).

The catch estimate for a given species can exceed it's own TAC. This is because the TAC measure we use is the TAC set at the beginning of the season, and in-season management can adjust TAC to an extent. In ATTACH we check that catch does not exceed the BSAI wide ABC and that the ecosystem cap, but otherwise allow predicted catch to exceed TAC.

4. The Ensemble

ATTACH is an ensemble of three models that include different explanatory variables that fit data better for different species. We chose the ensemble rather than any individual model because it better captures possible environmental and policy uncertainty and is therefore more likely to be robust to ABC combinations and individual ABC levels outside of historical bounds. The three models in the ensemble differ in the error structures in both the TAC and catch estimation equations. In all of the models, the errors in the TAC estimation stage are linked via Seemingly Unrelated Regressions (SUR; Zellner 1962), a common econometric modeling technique. The format of the SUR here is a set of linear regression equations that are valid independently for each species; exogenous shocks which affect one species are then assumed to affect all the included species, implying the error terms are correlated across species. This error covariance is especially strong in the TAC stage, where the 2 million ton cap ensures the errors of all species sum to zero. In the catch estimation stage, model 1 assumes that each log-linear regression is independent, model 2 has two groups of SUR-linked regressions (representing species that are typically caught concurrently), and model 3 includes a group of species that are caught concurrently.

The ensemble averages the estimated catch of the three models equally before returning the estimated Bering Sea catch to the user. Only the estimates for the species whose ABCs were specified by the user are returned.

5. Performance

As a rule, it is easier to predict TAC and catch in directed fisheries (e.g. pollock, Pacific cod, yellowfin sole) than in bycatch fisheries. In particular in the catch prediction stage, there is a large degree of randomness in some of the bycatch fisheries. Despite this, in all fisheries using the ATTACH estimate provides a better estimate of catch than the standard assumption made in biological modeling, which is to set catch equal to ABC. In some fisheries outside of the BSAI this may not be a terrible assumption but in the BSAI, for most species managed under the ecosystem cap, this would result in the chronic overestimation of harvest.

The following figure illustrates how the ATTACH predictions compare to setting catch equal to ABC in selected species, created originally for Reum et al. (in prep).

For each stock, performance of the models was evaluated using leave-one-out cross-validation (LOO-CV). We estimated the coefficients of each model using all but one year in the data-set, and then used the estimators to predict the TAC and catch of the omitted year. We followed this process for each year and saved the predicted catches of that year. We calculated the difference between the predicted and actual catch for each year (1992-2017) and used this to create a variety of metrics: a simple sum of differences; a sum of percent differences; sums of squared differences, weighted by value, ABC, TAC, or catch; and the sum of squared percent differences. We calculated these same metrics for in-sample predictions as well (that is, predictions were made for each year based on the complete sample of years).

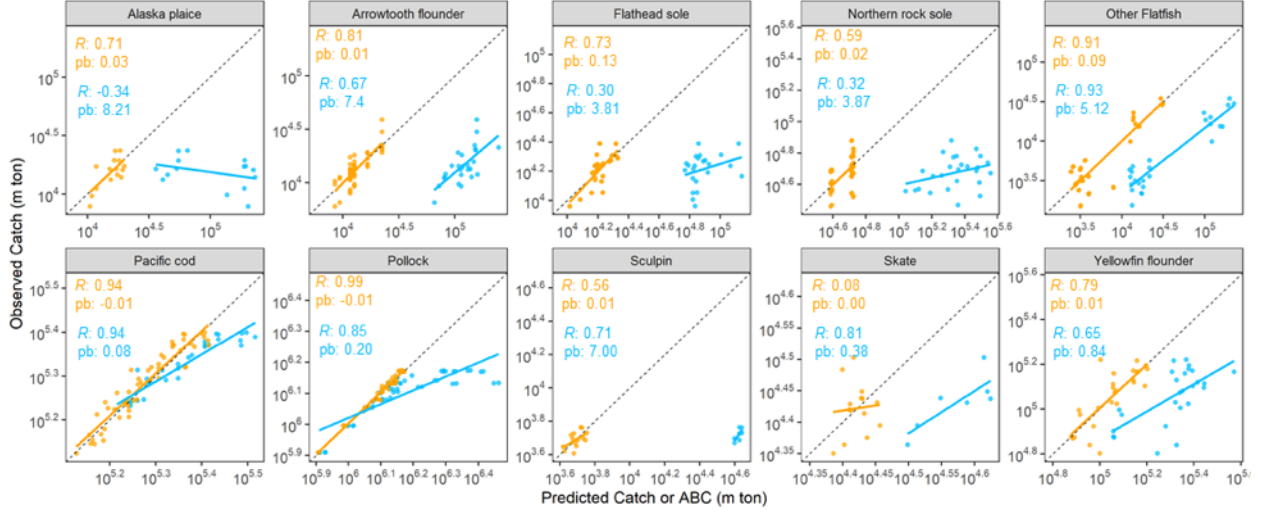


Figure 1: Comparison of observed catches in the Bering Sea-Aluetian Islands against predicted catches from the ATTACH fishery submodel (orange circles) and Allowable Biological Catch (ABC) values from stock assessments (blue symbols). ATTACH accounts for policy considerations in the setting of catch limits and provides a more accurate representation of realized catches relative to information on ABC alone. For each species, Pearson's correlation coefficient (R) and the proportional bias (pb) are provided. The dashed black line corresponds to the 1:1 relationship and linear trend lines (orange and blue) are provided for each relationship. Data and predictions span the period 1992 to 2017.

6. Scenarios

Whitefish Preference scenario (Scenario 2)

In the “whitefish preference” scenario the Council allocates an extra 10% TAC to whitefish, decreasing flatfish TAC by up to 50% in order to do so and still comply with the ecosystem cap. (Whitefish are defined as Alaska pollock and Pacific cod; flatfish are defined as yellowfin sole, northern rock sole, Kamchatka flounder, Alaska plaice, Greenland turbot, Other flatfish, flathead sole, and arrowtooth flounder.)

We model this by first estimating TAC using the base model. We then define x as minimum of: 10% whitefish TAC; 50% flatfish TAC; and the difference between whitefish ABC and TAC.

We increase pollock and Pacific cod TAC by raising both TACs equally until either the net increase in whitefish TAC is x , or one of the whitefish species' TAC is equal to its respective ABC. If the latter occurs, we then increase only the species whose TAC is less than its ABC until the net increase in whitefish TAC is equal to x .

We decrease flatfish TAC by x , spreading the decrease proportionally across the flatfish species.

We then pass these adjusted TACs to the catch portion of the model to estimate catch.

Flatfish Preference scenario (Scenario 3)

In the “flatfish preference” scenario the Council decreases whitefish TAC by up to 10%, and increases flatfish TAC by that amount. (Whitefish and flatfish defined as in scenario 2.)

We model this by first estimating TAC using the base model. We then define y as the minimum of: 10% whitefish TAC; the difference between flatfish ABC and TAC; and the difference between whitefish TAC and the ‘threshold’. (Below a threshold of approximately 1.5 million tons, we have found that the Council sets TAC equal to ABC in whitefish. For this scenario we adjust this threshold down by 10%, to 1.35 million tons.)

We increase all flatfish proportionally until either the net increase in flatfish TAC is equal to y , or one of the flatfish species' TAC is equal to its ABC. If the latter occurs, we remove that species from the set and repeat the pattern until the net increase in TAC is equal to y .

We decrease whitefish TAC proportionally so that the net decrease in whitefish TAC is y .

We then pass the adjusted TACs to the catch portion of the model to estimate catch. Unlike in scenario 2, where we assume catch behaves as usual relative to TAC, in the flatfish preference scenario we assume the fleet is better able to catch flatfish TAC. We make this assumption because currently most flatfish species' catches are rarely limited by TAC. We assume catch is up to 30% higher for each flatfish species than it would normally be for any given TAC; still respecting the rule that catch for any given species cannot exceed its respective ABC and net catch cannot exceed the ecosystem cap.

7. Examples

If you are interested in predicting what catch would be, assuming everything about the world stays as it was in 2017 (A80 and AFA alive and well, Steller Sea Lion closure partially reopened, etc...). You would simply use:

```
AP_BS_ABC = 2e6
ATF_BS_ABC = 2e5
YFS_BS_ABC = 2e5
catch_function(scenario = 1,
               Pollock = AP_BS_ABC,
               Arrowtooth = ATF_BS_ABC,
               Yellowfin = YFS_BS_ABC)
#> Arrowtooth Pollock Yellowfin
#> 1 8485.962 1347540 134489.5
```

In the above example we defined the ABCs before calling `catch_function` simply to illustrate that the numbers chosen were not significant. Scenario 1 is the status quo scenario. Scenarios 2+ are defined in the help file, and correspond to alternative scenarios like the whitefish and flatfish preference scenarios described in the previous section.

If for your purposes you only want the predicted TAC allocation for these species, you would simply use:

```
TAC_function(scenario = 1,
              Pollock = AP_BS_ABC,
              Arrowtooth = ATF_BS_ABC,
              Yellowfin = YFS_BS_ABC)
#> Arrowtooth Pollock Yellowfin
#> 1 16041.87 1330002 146890.5
```

Note, `TAC_function` is based on annual allocations and thus returns BSAI TAC for all species except Alaska Pollock, Greenland turbot, Pacific ocean perch, Sablefish and Other rockfish. This is because those are the species for which TAC is set on the BS level*.

*Pacific cod is also set on a BS level, but this is a more recent development, and so for now we still model TAC as being set on a BSAI level in Pacific cod.

8. Future Steps

- Version 2
 - New ensemble. We have chosen a different set of models to make the ensemble, looking specifically for variation in predictive ability across species.
 - More data. 2018 and 2019 data is now available.

- Flatfish flex. Now that 2018 and 2019 data is available, there are enough years with the flatfish flex policy (which began in 2015) that including it as a predictor variable in certain regression leads to significant coefficient estimates.
- BSAI wide estimation
 - Catch (and TAC) function(s) that take BSAI inputs and returns BSAI outputs