Bycatch Estimator User Guide

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Introduction

The R code called 2.BycatchModels.r runs a generic model-based bycatch estimation procedure, after you first set up the data inputs and other specifications in 1.BycatchModelSpecificationsExample.r. The code can estimate both total bycatch, calculated by expanding a sample, such as an observer database, to total effort from logbooks or landings records, and an annual index of abundance, calculated only from the observer data.

The code runs best in R studio. Before running the code for the first time, install the latest versions of R (R Core Team (2020)) and RStudio (RStudio Team (2020)), as well as the following libraries: tidyverse, ggplot2, MASS, lme4, cplm, tweedie, DHARMa, tidyselect, MuMIn, gridExtra, pdftools, foreach, doParallel, reshape2, glmmTMB and quantreg (Wickham et al. (2019); Wickham (2016); Venables and Ripley (2002); Bates et al. (2015); Zhang (2013); Dunn and Smyth (2005); Hartig (2020); Henry and Wickham (2020); Barton (2020); Auguie (2017); Wickham and Pedersen (2019); Iannone, Cheng, and Schloerke (2020); Ooms (2020);Microsoft and Weston (2020);Corporation and Weston (2020); Wickham (2007); Brooks et al. (2017); Koenker (2021)). The output figures and tables are printed to a pdf file using R Markdown and the knitr library (Xie (2015)), which outputs a LaTex file; therefore, you must have a LaTex program installed, such as TinyTex (Xie (2019), Xie (2021)).

The R code estimates total bycatch as follows. First, mean catch per unit effort (CPUE) of observed sample units (trips in this example, but it could be sets) is estimated from a linear model with predictor variables. The observation error models used are delta-lognormal, delta-gamma, negative binomial (from either glm.nb in the MASS library or glmmTMB, nbinom1 and nbinom2) and Tweedie (from cpglm or glmmTMB). For comparison, simple normal and lognormal models are also available, although these methods are not expected to perform well with many zero bycatch observations. Within each observation error model group, potential predictor variables are chosen based on the user's choice of information criteria (AICc, AIC or BIC) (Barton (2020)). The user specifies a most complex and simplest model, and all intermediate models are considered. The user-specified simplest model will usually include year, and can also include, for example, stratification variables that are used in the observer program sampling design. The model with the lowest value of the information criterion is chosen as best within each observation error group.

The best candidate models in each observation error group are then compared using 10-fold cross-validation, if desired, to see which observation error model best predicts CPUE. The best model according to cross validation is the one with the lowest root mean square error (RMSE) in the predicted CPUE and the mean error closest to zero, excluding from consideration models that do not fit well according to criteria described below. Note that this model selection using information criteria and cross-validation is only intended as a guide. The user should also look at the information criteria across multiple models, as well as residuals and other diagnostics, and may want to choose a different model for bycatch estimation or abundance index calculation based on other criteria, such as the design of the observer sampling program.

For the best model in each observation error model group (according to the selected information criterion), the total bycatch is estimated by predicting the catch in all logbook trips (i.e., the whole fishery) from the

fitted model and summing across trips. There is an option to only predict bycatch from unobserved effort (i.e. trips or sets not sampled by observers) and calculate total bycatch as the observed bycatch plus the predicted bycatch in unobserved effort. This only works if it is possible to match the observed trips to the logbook trips, and the amount of observed effort in a trip is always less than or equal to the amount of total effort. For fisheries with high observer coverage (e.g. 20% or more), predicting bycatch from only unobserved effort would be preferred, because treating the whole fishery as unobserved might overestimate the variance.

The catch in each trip is predicted directly by the negative binomial models. Tweedie and normal models predict CPUE, which is then multiplied by effort. Delta-lognormal and delta-gamma models have separate components for the probability of a positive CPUE and the CPUE, which must be multiplied together (with appropriate bias corrections) and multiplied by effort to get the total catch. Catch in each trip is summed across trips to get the total catch in each year. The variance of the prediction in each trip is calculated as the variance of the prediction interval, which is the variance of the estimated mean prediction plus the residual variance. Because the predicted catches in each logbook trip are dependent on linear model coefficients, which are the same across multiple trips, the trips are not independent; thus, the variances cannot be added without accounting for the covariance. The variance of the total catch in each year is thus calculated either using Monte Carlo simulation, or using a delta method. Users may also chose not to estimate variances for large logbook datasets where these methods will not work. In the case where only the unobserved bycatch is estimated, the observed bycatch is added to the predictions as a known constant with no variance.

For the Monte Carlo variance estimation method, we first drew random values of the linear model coefficients from a multivariate normal distribution with the mean and variance/covariance matrix estimated from the model. The predictions for each trip were then drawn for each draw of the parameters using the appropriate probability density function (e.g. tweedie, negative binomial) with additional parameters (e.g. residual variance, negative binomial dispersion, tweedie power and phi) estimated by the model. Trips were then summed for each year (adding the observed catch if necessary) within each draw, and the mean, standard error, and quantiles (e.g. 2.5% and 97.5% for a 95% confidence interval) were then calculated across the Monte Carlo draws. An approximation of the total variance of the predicted bycatch can also be made using a delta method. The delta method approximates the variance of a function of a variable as the derivative of the functions squared times the variance of a the original variable. Thus, the variance of the prediction intervals in the original data scale is calculated by pre and post multiplying the derivative if the inverse link function to the variance covariance matrix of the predicted values.

$$\Sigma_p = J\Sigma_l J'$$

were Σ_l is the variance covariance matrix for the predicted trips in the stratum on the scale of the log link, and J is the matrix of derivatives. See the function MakePredictionsDeltaVar for the details for each model type.

If the logbook data is aggregated across multiple trips (e.g. by strata) the effort is allocated equally to all the trips in a row of the logbook data table for the purpose of simulating catches or estimating variances using the delta method. This allocation procedure is not needed to estimate the mean total bycatch, but it is necessary to estimate the variances correctly. When using aggregated effort, it is not yet possible to include the observed catches as known.

The model can estimate bycatch and abundance indices for multiple species or dispositions (e.g. dead discard, live release) from the same fishery simultaneously if they are all being estimated from the same data sets.

If a user requests an annual abundance index, this is calculated from the same models as were selected for bycatch estimation.

Data specification and model set up

The user must specify the names of the databases, the predictor variables to include (via the simplest and most complex model), and several other specifications in the file called 1.BycatchModelSpecificationExample.r. Everything else works automatically.

The observer data should be aggregated to the appropriate sample unit, either trips or sets. Effort must be in the same units in both data sets (e.g. sets or hook-hours). The logbook data may be aggregated to sample units, or it may be aggregated further, as long as it includes data on all stratification or predictor variables. For example, the data can be aggregated by year, region and season if those are the stratification variables, or it can be aggregated by trip. If any environmental variables, such as depth, are included, the logbook data probably has to be entered at the set level. The observer data should have columns for year and the other predictor variables, the observed effort and the observed bycatch or catch per trip of each species to be estimated. The logbook data must also have year and the other predictor variables, and the total effort in the same units (e.g. sets or hook-hours) as the observer data. There should also be a column that reports how many sample units (i.e. trips) are included in each row in the logbook data if the data are aggregated. This is needed to predict catches by trip for the variance calculations. If there are any NA values in any of the variables, those rows will be deleted from the data set. To include the observed catches as known in the totals, it is necessary to include a column for unsampled effort in the logbook data (which can be zero in completely sampled trips) and a column in both the logbook and observer data that can be used to match observed trips to logbook records.

Throughout the data specification file, change the values on the right hand side of the assignment arrow, but do not change the variable names on the left hand side. The first section specifies the data tables to be used.

```
#Specify directory where R files are found.
baseDir<-"C:/Users/ebabcock/Box Sync/bycatch project (ebabcock@miami.edu)/Current R code"
setwd(baseDir)

#Give a name to the run, which will be used to set up a directory for the the outputs
#and a run description to describe the run in the output files
runName<-"SimulatedExample"
runDescription<-"Example with simulated data"

# What would you like to estimate?
# You may calculate either an annual abundance index, or total bycatch, or both
# If you want total bycatch, you must have logbook data or some other source of total effort
EstimateIndex<-TRUE
EstimateBycatch<-TRUE

#### Read in the observer data file. This could also be an assignment to an
# R object if you have already got the data in R.
obsdat<-read.csv("ExampleObs.csv",as.is=TRUE)

#### Specify name of file with total effort data, if you are estimating total bycatch.
# It can be aggregated or may include one line per sample unit (trip).
# If estimateByatch is FALSE, this variable is not needed.
logdat<-read.csv("ExampleLog.csv",as.is=TRUE)
```

Next, give the names of the variables in the observer and (if estimating bycatch) logbook data files. You must also specify the common and scientific names of the species being analyzed, the units of the bycatch estimates (e.g. kg, numbers), and the type of catch (e.g. retained catch, dead discards, live releases). If analyzing more than one species or disposition type, some of these inputs must be vectors with the same length as the number of species and/or disposition types. If calculating catch as the sum of observed catch and predicted catch from unobserved effort (includeObsCatch=TRUE) then you must have columns for both total effort and unsampled effort in the logbook data, and a column to match observed trips to the logbook trips.

Give the formulas for the most complex and simplest model to be considered. If the simplest model requires stratification variables other than year, summaries of the predicted bycatch at the level of these stratification

variables will be printed to .csv files, but will not be plotted automatically. Abundance indices will be calculated including all the variables requested in indexVars, to allow for different indices for different stratification variables if desired (e.g. different spatial areas). You may also specify which predictor variables should be interpreted as factor (categorical). The named variables will be converted to factor before analysis. Note that year may be either a number or a factor. If year is a number, then a model such as $y \sim Year$ will estimate a linear trend across years. Polynomial regression may be a useful way to estimate more complex trends across years in data sets where not all years have enough data to estimate Year as a categorical fixed effect. This can be specified as, for example $y \sim Year + I(Year\hat{}2) + I(Year\hat{}3)$.

```
### What is the sample unit in this data set? e.g. sets or trips.
sampleUnit<-"trips" #Usually trips or sets

#Specify the name of the effort variable in the observer data and logbook data. These must be
#in the same units. (e.g. 1000 hook hours). Also specify a column for effort
#that is not sampled, in trips with observers. This can be zero in all cases if observers
#sample 100% of effort in sampled trips.
obsEffort<-"sampled.sets"
logEffort<-"sets" #This variable is only needed if estimating bycatch
logUnsampledEffort<-NULL  #This variable is only needed includeObsCatch is true

# Give the name of the column in the logbook data that gives the number of sample units (trips or sets)
# that each row includes. If the logbook data is not aggregated (i.e. each row is a #sample unit) just
logNum<-NA

# Make includeObsCatch TRUE if (1) the observed sample units can be matched to the logbook
# sample units and (2) you want to calculate total bycatch as the observed bycatch plus the
# predicted unobserved bycatch. This doesn't work with aggregated logbook effort.
includeObsCatch<-FALSE
# if includeObsCatch is true, give the name of the column that matches sample
# units between the observer and logbook data. Otherwise, this can be NA
matchColumn<-NA


#Give common and scientific names. Can be a vector of names to do multiple species at the same time
#in which case each species must have its own column in obsdat.
#This example takes the columns from a data frame to run multiple species at once.
common<-"Simulated species"
sp<-"Genus species"

#Give the name of the columns associated with the species. If it is a vector,
# it must match the common and scientific names given above
obsCatch<-"Catch"

# Give units and type of catch to go in plot labels. Must be a vector of the same length as sp
catchUnit<-rep("number",length(sp))
catchType<-rep("dead discard", length(sp))
#Specify the name of the variable defining the Years in both databases
yearVar<-"Year"

# Specify the most complex and simplest model to be considered. The code will find compare all
# intermediate models using information criteria. Use indexModel to specify which strata to
# keep separate in calculating abundance indices.
complexModel<-formula(y~(Year+season)^2)
simpleModel<-formula(y~Year)
```

```
indexModel<-formula(y~Year)

## The variables must have identical names and factor levels in the observer and logbook data sets
#Specify which of these variables should be interpreted as categorical to make sure they are in factor
#Variables not in this list will retain their original format
factorNames=c("Year","season")
```

Next, specify which models to try and which information criterion to use in narrowing down the predictor variables to use in each observation error model group. Model selection is done with dredge function in the MuMIn library(Barton (2020)). Note that the tweedie outputs should be the same whether using TMB (TweedieTMB) or the cpglm function (Tweedie). The negative binomial 2 in TMB is the same as the negative binomial in glm.nb. To get faster results, use TMB only for these distributions. They are both included for comparison.

Also, specify whether to do cross-validation to choose between observation error models, and whether to use the dredge function to use information criteria to choose the best set of predictor variables for each fold in cross validation. If DredgeCrossValidation is FALSE, the same predictor variables will be used for each fold, as selected for the full data set. This saves time with large data sets. The variable ResidualsTest allows excluding from cross-validation any model where the residuals have a P<0.01 for a Kolmogorov Smirnov test of whether the residuals are distributed as expected under the likelihood (testUniformity in DHARMa). This is useful for excluding poorly performing models. However, it may be too restrictive if none of the models perform well. Specify the confidence levels desired for the total bycatch calculations.

Also, specify whether to save the R workspace after the models run. If the variable useParallel is true and your computer has multiple cores, the dredge function will be run in parallel. This greatly speeds up the calculations. If you have trouble getting this to work, set useParallel to FALSE.

```
#Specify which observation error models to try. Options are: "Binomial", "Normal","Lognormal",
#"Delta-Lognormal", #"Delta-Gamma", "NegBin" for Negative binomial" using glm.mb in the MASS library,
#"Tweedie" for Tweedie GLM from the cpglm library, and "TMBnbinom1", "TMBnbinom2", and "TMBtweedie" for
# negative binomial 1, negative binomial 2 and Tweedie from the GLMMTMB library. Binomial is run
#automatically as part of the delta models if either of them are selected.

modelTry<-c("Binomial","Delta-Lognormal","TMBnbinom2","TMBtweedie")

#Specify preferred information criteria for model selection
# Choices are AICc, AIC and BIC.
selectCriteria<-"BIC"

#Specify whether to run a 10 fold cross-validation (TRUE or FALSE). This may not work with a small
#or unbalanced data set. DredgeCrossValidation specifies whether to use information criteria
#to find the best model in cross validation, using the dredge function, or just keep the same model for
#Do not use dredge for very large data sets, as the run will be slow.
DoCrossValidation<-TRUE
DredgeCrossValidation<-FALSE

#Specify whether to exclude models that fail the DHARMa residuals test.
ResidualTest<-FALSE

#Specify confidence interval for total bycatch estimates
CIval<-0.05 #Should be the alpha level, e.g. 0.05 for 95%

# Variance calculation method. Neither variance method will work with a very large number of sample uni
# in the logbook data. The delta method for variance calculation is not implemented
```

```
# for the delta-lognormal or delta-gamma methods.
VarCalc<-c("Simulate","DeltaMethod","None")[2]

# Specify whether to save R workspace. This should be true unless you
# don't have space on your disk. Also specify whether to use parallel processing to
# speed up calculations.
saveR<-TRUE
useParallel<-TRUE
```

Finally, if you have information on total bycatch in each year to validate your estimates, for example in a simulation study, fill out the following. Otherwise, set plotValidation to FALSE.

```
## Validation. If you have true values of the total bycatch (for example in a simulation study)  Make P
plotValidation<-FALSE
trueVals<-NULL
trueCols<-NULL
```

Running the model

Once the specification file is set up, open the file 2.ByCatchModels.r. The first section allows you to input the name of the data specification file, loads the specifications and then loads a file called "4.PreliminarySetup.r" to load all the libraries, set up the data files, and print a preliminary data summary.

The data summaries are output to directories named "output" followed by the specified run name. A pdf file with summaries for all species (DataSummary.pdf) is placed in the main output folder, and a csv file for each species is placed in an output file named for the species. Note that records with NA in the catch or effort variable are excluded from the analysis and not included in the estimated sample size. If there are any years with no data, or no positive observations, you may want to exclude those years from the analysis. The summary table also counts the number of outliers (defined as data points more than 8 standard deviations from the mean) because outliers cause problems with fitting in some models. For data-checking, this output file also includes columns with estimated bycatch and its variance using a simple unstratified ratio estimator by year (See 3.BycatchFunctions.r for all the functions). You will get an error message if if any of the variables in the specified models are not found in the data frame.

```
# Effort must be in the same units in both data sets (e.g. hook hours), but it does not matter
# how the logbook effort data is aggregated, as long has it includes data on all stratification or
# predictor variables. For example, the data can be aggregated by year, East-West and season if those
# are the stratification variables, or it can be aggregated by trip.
# The user must specify the names of the databases and the variables to include in the
# The .r file named on line 10. Everything else should work automatically.
# Contact Beth Babcock ebabcock@rsmas.miami.edu for assistance.

############### Step 1. Enter the data specification in the file named here ##########################
specFile<-"C:/Users/ebabcock/Box Sync/bycatch project (ebabcock@miami.edu)/Current R code/1.BycatchModel
# Either set the working directory or put the full patch in the filename.
# Complete the information in the file before continuing. You may run through specFile line by line, bu
# will also be sourced again later. The file will be saved, with the addition of the date, to the outpu

#############################################################################################
### From here on no changes should be needed.
#############################################################################
#Read in data specification
#source(specFile) #Commented out for user guide.
```

```
#Make data summary outputs
source(paste0(baseDir,"/4.preliminarySetup.r"))
# Stop here and check data summaries to make sure each species has reasonable number
# of observations in each year for analysis.
#The file called  "Data summary all species.pdf" has all the tables.
#There is also a .csv for each species.
```

Main analysis loop

The next section runs the loop (across the specified species, disposition types, etc.) to run the CPUE models, estimate total bycatch and/or abundance indices, and do cross-validation if requested. You can ignore the warnings and information about the models as long as the loop keeps running. Most of these are information about which variables are being tried and which models have converged, which will be summarized in the output files.

The model may be slow if you have a large data set or are doing cross-validation. The outputs all go into the directories labeled with the species names, and include a pdf will all results, and separate csv files for all the tables. Note, for this demo, we set run=1 to do one step at a time. When running the R code, this all runs in a loop. When the models are fit, the code keeps track of whether the model converged correctly, or if not, where it went wrong. An output table called modelFail.csv summarizes the results, with a "-" for models that converged successfully, "data" for models that could not be fit due to insufficient data (no positive observations in some year prevents fitting the delta models), "fit" for models that failed to converge, "cv" for models that produced results with unreasonably high CVs (>10) in the annual catch predictions, and "resid" for models that failed the Kolmogorov Smirnoff test for having the correct distribution in the DHARMa library (Hartig (2020)), if residualTest is TRUE. Models that fail in any of these ways are discarded and not used in cross-validation. If you get one of these errors for a model you want to use, you should check the data for missing combinations of predictor variables, extreme outliers, or years with too few positive observations.

The first section of the loop includes two nested loops that go through all the models in modelTry and find the best model using the specified information criterion. The first loop runs all the models that are applied to all data together (i.e. not delta models). The delta models are run separately in the second loop because they require a different data setup. There is a function called findBestModelFunc, which applies the dredge function from the MuMin library to find the best combination of the predictor variables according to the specified information criteria (Barton (2020)). The dredge function produces a table which includes all the information criteria for each model that was considered, as well as model weights calculated for the information criterion the user specified, which sum to one and indicate the degree of support for the model in the data. The best model will have the highest weight. But, in some cases other models with also have strong support, and should perhaps be considered, particularly if they are simpler. The current version of the code does not use MuMIn's model averaging function, but this may be worth considering if several models have similar weights.

A binomial model will be tried if it was requested, or if either a delta-lognormal or delta-gamma model were requested, since delta models have a binomial component. The binomial models are fitted using the glm function with a logit link. The negative binomial is run using the glm.nb function from the MASS library (Venables and Ripley (2002)) or nbinom1 nbinom2 from the glmmTMB library(Brooks et al. (2017)). The glm.nb function is very similar to the nbinom2 method in glmTMB, but both are included for comparison. Both define the variance of the negative binomial as:

$$\sigma^2 = \mu + \mu^2/\theta$$

, where θ is an estimated parameter. For nbinom1, the variance is defined as:

$$\sigma^2 = \mu(1 + \alpha)$$

, where α is an estimated parameter. This version of the negative binomial model, which is equivalent to a quasi-Poisson model, gives somewhat different results from the other negative binomial models.

The negative binomial predicts integer counts, so it is appropriate for predicting bycatch in numbers per trip for all the trips in the logbook data. To allow this model to also be used with catch or bycatch measured in weights, the code rounds the catches to integers before running this model. Check that this is appropriate for the units you are using. To predict CPUE it is necessary to include an offset in the model. We use a log link for all three binomial models, so that the model predicts:

$$log(C_i) = b_0 + b_1 x_1 + offset(log(E_i))$$

were C_i is the catch in trip i in the observer data, $b_0 + b_1 x_1$ is an example linear predictor with an intercept and a slope, and the offset is the log of the effort E_i in each trip. This is algebraically equivalent to modeling CPUE as a function of the same linear predictor (without the offset).

The Tweedie distribution is available using the cpglm function in the cplm library (Zhang (2013)) or the tweedie family in glmmTMB (Brooks et al. (2017)) by including "Tweedie" or TMBtweedie in modelTry. The Tweedie is a generalized function that estimates a distribution similar to a gamma distribution, except that it allows extra probability mass at zero. It is thus appropriate for continuous data with extra zeros. It uses a log link, and, in addition to the linear predictor for the log(mean) it estimates an index parameter p and dispersion parameter ϕ which together determine the shape of the distribution.

If all years have at least one positive observation, the loop next runs the lognormal and gamma models if requested. For the delta lognormal model, the CPUE is log transformed, and the mean CPUE for positive observations is modeled with the lm function for positive data only. For the delta-gamma method, the log link is used to model the positive CPUE values, using the glm function. The lognormal and gamma method are similar, except that they are run on all the CPUE data, including zeros, after adding a constant of 0.1.

```
############## This is the main analysis loop ##########################
StartTime<-Sys.time()
#for(run in 1:numSp) { #Loop commented out for user guide
run<-1
 datval<-dat[[run]]
 outVal<-dirname[[run]]
 varExclude<-NULL
 #Fit all models except delta
 for(mod in which(!modelTry %in% c("Delta-Lognormal","Delta-Gamma"))){
   modfit1<-findBestModelFunc(datval,modelTry[mod],printOutput=TRUE)
   modelSelectTable[[run]][[modelTry[mod]]]<-modfit1[[2]]
   modFits[[run]][[modelTry[mod]]]<-modfit1[[1]]
 }
#Fit delta models
 if("Delta-Lognormal" %in% modelTry | "Delta-Gamma" %in% modelTry) {  #Delta models if requested
   posdat<-filter(dat[[run]],pres==1)
   y<-unlist(lapply(posdat[,factorNames],function(x) length(setdiff(levels(x),x)))) #See if all levels
   varExclude<-names(y)[y>0]
   if(length(varExclude>0)) print(paste(common[run], "excluding variable",varExclude,"from delta models
   if((min(summary(posdat$Year))>0 |  is.numeric(datval$Year)) &!is.null(modFits[[run]][["Binomial"]]))
     for(mod in which(modelTry %in% c("Delta-Lognormal","Delta-Gamma")))  {
       modfit1<-findBestModelFunc(posdat,modelTry[mod],printOutput=TRUE)
       modelSelectTable[[run]][[modelTry[mod]]]<-modfit1[[2]]
       modFits[[run]][[modelTry[mod]]]<-modfit1[[1]]
     }
   } else {
     print("Not all years have positive observations, skipping delta models")
     modelFail[run,c("Delta-Lognormal","Delta-Gamma")]<-"data"
```

```
    modPredVals[[run]][[modelTry[mod]]]<-NULL
    modIndexVals[[run]][[modelTry[mod]]]<-NULL
  }
 }
```

The next section loops through all the models again, and calculates the model residuals, residual diagnostics from the DHARMa library (Hartig (2020)), and, if requested, calculations of the total bycatch and an index of abundance.

For the best model (according to the information criterion) in each model group, both ordinary residuals and DHARMa scaled residuals are plotted, and the DHARMa diagnostics are calculated. The DHARMa library uses simulation to generate scaled residuals based on the specified observation error model so that the results are more clearly interpretable than ordinary residuals for non-normal models. DHARMA draws random predicted values from the fitted model to generate an empirical predictive density for each data point and then calculates the fraction of the empirical density that is greater than the true data point. Values of 0.5 are expected, and values near 0 or 1 indicate a mismatch between the data and the model. Particularly for the binomial and negative binomial models, in which the ordinary residuals are not normally distributed, the DHARMa residuals are a better representation of whether the data are consistent with the assumed distribution. Both the regular residuals and the DHARMa residuals are appropriate for lognormal and gamma models, since they model continuous data which is expected to be approximately normal when transformed by the link function. The DHARMA residuals should be uniformly distributed, as indicted by the QQUniform plot and the Kolmogorov-Smirnov test of uniformity. If the DHARMA residuals show significant over-dispersion then the model is not appropriate. A summary of the the DHARMa residual diagnostics is added to a table called residualTab, and models that fail the Kolmogorov-Smirnov test for uniformity of the DHARMa scaled residuals are excluded from cross-validation if residualTest is TRUE. Because the cpglm functions do not produce estimates of standard error, simulation is used to generate the DHARMa residuals if "Tweedie" is the model selected, using the rtweedie distribution from the tweedie library (Dunn and Smyth (2005)). See the functions in 3.BycatchFunctions.r for details.

For each model group the best model, as selected by the information criteria, is used to predict the mean and variance of the total bycatch in each year with the exception of the binomial, for which the model predicts to the total number of positive trips. For the binomial model, the best model is used to predict probability of a positive observation in each logbook trip and these are summed to get the total number of positive trips in each year (and in each stratum if further stratification was requested). The number of positive trips is calculated because, for a very rare species that is never caught more than once in a trip, the number of positive trips would be a good estimate of total bycatch and many of the other models would fail to converge. For more common species, the estimates of total catch are more appropriate, so the results of the binomial model alone are not included in the cross-validation for model comparison.An abundance index based on the binomial distribution is also calculated, if requested.

For all the other model types, the makePredictionSimVar function calculates the total bycatch in each year, by first predicting the total catch in each trip in the logbook data and then summing over all trips in each stratum. For all the negative binomial models, the log(effort) from the logbook trips is used as an offset in the predictions, along with the values of all the predictor variables, so that the model can predict bycatch in each trip directly. For the Tweedie, normal, and gamma models the CPUE is predicted for each trip in the logbook data and must be multiplied by effort and summed across trips to get the annual summaries. For delta-gamma models, the predicted bycatch in each trip is the predicted probability of a positive observation from the binomial, time the predicted CPUE from the gamma model, times effor in the trip. For delta-lognormal models, the variance of the predicted CPUE is needed to bias-correct when converting the mean predicted log(CPUE) to mean predicted CPUE. The variance of the prediction interval for each trip is calculated as the variance of the estimated mean plus the residual variance, and this value is used in the bias correction. The total predicted CPUE is the predicted probability of a positive observation from the binomial times the predicted positive CPUE, and predicted catch is the predicted CPUE times effort. For all models, the predicted total catches summed across trips to get the totals in each stratum. For all models the variance are calculated using the Monte Carlo simulation method described above or using a delta method.

The delta method variance is not available for the delta-lognormal or delta-gamma models.

If a user requests an annual abundance index, this is also calculated from the best model in each model group. The annual abundance index is calculated by setting all variables other than year, and any variables required to be included in the index (e.g. region or fleet) to a reference level, which is the mean for numerical variables or the most common value for categorical variables. The index is calculated by predicting the mean CPUE in each year, and its standard error is calculated as the standard error of the mean prediction. For delta-lognormal and delta-gamma models the standard error of the prediciton is calculated from the means and standard errors of the binomial and positive catch models using the method of Lo, Jacobson, and Squire (1992).

Finally, this section combines all the bycatch estimates and index estimates into data frames, and prints out CSV files with the DHARMa residual diagnostics. These are P values for a Kolmogorov-Smirnoff test of whether the DHARMa residuals are uniformly distributed as expected, a test of over-dispersion, a test of zero-inflation (which is meaningless for the delta models, but helpful to see if the negative binomial model and tweedie models adequately model the zeros) and a test of whether there are more outliers than expected.

```
#Make predictions, residuals, etc. for all models
 for(mod in 1:length(modelTry)) {
   if(!is.null(modFits[[run]][[modelTry[mod]]])) {
     if(modelTry[mod] %in% c("Delta-Lognormal","Delta-Gamma")) {
        modfit1<-modFits[[run]][["Binomial"]]
        modfit2<-modFits[[run]][[modelTry[mod]]]
     } else {
        modfit1<-modFits[[run]][[modelTry[mod]]]
        modfit2<-NULL
     }
     if(EstimateBycatch) {
      if(VarCalc=="Simulate" |(VarCalc=="DeltaMethod" & modelTry[mod] %in% c("Delta-Lognormal","Delta-Ga
         if(BigData)
           modPredVals[[run]][[modelTry[mod]]]<-
            makePredictionsSimVarBig(modfit1=modfit1,modfit2=modfit2,
            modtype=modelTry[mod],newdat=logdat) else
           modPredVals[[run]][[modelTry[mod]]]<-
            makePredictionsSimVar(modfit1=modfit1,modfit2=modfit2,
            modtype=modelTry[mod],newdat=logdat)
      if(VarCalc=="DeltaMethod" & !modelTry[mod] %in% c("Delta-Lognormal","Delta-Gamma"))
           modPredVals[[run]][[modelTry[mod]]]<-
            makePredictionsDeltaVar(modfit1=modfit1,
            modtype=modelTry[mod],newdat=logdat)
      if(VarCalc=="None") {
         modPredVals[[run]][[modelTry[mod]]]<-
            makePredictionsNoVar(modfit1=modfit1,modfit2=modfit2,
            modtype=modelTry[mod],newdat=logdat)
      }
     }
     if(EstimateIndex) {
      modIndexVals[[run]][[modelTry[mod]]]<-makeIndexVar(modfit1=modfit1,modfit2=modfit2,modType=modelTr
     }
     modelTable[[run]]$formula[mod]<-
       paste(formula(modFits[[run]][[modelTry[mod]]]))[[3]]
     temp<-ResidualsFunc(modFits[[run]][[modelTry[mod]]],modelTry[mod],paste0(outVal,"Residuals",modelTr
     if(!is.null(temp)) {
       residualTab[[run]][,modelTry[mod]]<-temp
       if(residualTab[[run]]["KS.p",modelTry[mod]]<0.01 & ResidualTest) modelFail[run,modelTry[mod]]<-"
```

```
    }
    if(is.null(modPredVals[[run]][[modelTry[mod]]])) modelFail[run,modelTry[mod]]<-"cv"
  } else {
    if(modelFail[run,modelTry[mod]]=="-") modelFail[run,modelTry[mod]]<-"fit"
  }
}
#Combine all predictions, except Binomial
 if(EstimateBycatch) {
  yearsumgraph<-yearSum[[run]] %>% dplyr::select(Year=Year,Total=Cat,Total.se=Cse) %>%
    mutate(TotalVar=Total.se^2,Total.cv=Total.se/Total,
       Total.mean=NA,TotalLCI=Total-1.96*Total.se,TotalUCI=Total+1.96*Total.se)
  if(is.factor(modPredVals[[run]][[1]]$Year)) yearsumgraph$Year<-factor(yearsumgraph$Year)
  allmods[[run]]<-bind_rows(c(modPredVals[[run]],list(Ratio=yearsumgraph)),.id="Source") %>%
    filter(!Source=="Binomial")
  allmods[[run]]$Valid<-ifelse(modelFail[run,match(allmods[[run]]$Source,dimnames(modelFail)[[2]])]=="
 }
 if(EstimateIndex) {
  allindex[[run]]<-bind_rows(modIndexVals[[run]],.id="Source") %>%
    filter(!Source=="Binomial")
  allindex[[run]]$Valid<-ifelse(modelFail[run,match(allindex[[run]]$Source,dimnames(modelFail)[[2]])]=
 }
#Print the diagnostic tables
 write.csv(residualTab[[run]],paste0(outVal,"residualDiagnostics.csv"))
 write.csv(modelFail,paste0(outDir,"/modelFail.csv"))
```

The next part runs the cross validation if requested. Only observation error models that converged and produced reasonable results with the complete data set are used in cross-validation. For example, if there were not enough positive observations in all years to estimate delta-lognormal and delta-gamma models, then they will not be included in the cross-validation.

For cross-validation, the observer data are randomly divided into 10 folds. Each fold is left out one at a time and the models are fit to the other 9 folds. The same procedure described above is used to find the best model within each observation error group using information criteria and the MuMIn library if DredgeCrossValidation is TRUE, otherwise, the same variables will be used in each fold as for the full data set to save time. The fitted model is used to predict the CPUE for the left out fold, and the root mean square error is calculated as:

$$RMSE = \frac{1}{n}\sum_{i=1}^{n}(\hat{y}_i - y_i)^2$$

where n is the number of observed trips and y is the CPUE data in the left-out tenth of the observer data, and $\hat{y}$ is the CPUE predicted from the model fitted to the other 9/10th of the observer data. The model with the lowest mean RMSE across the 10 folds is selected as the best model. Mean error is also calculated as an indicator of whether the model has any systematic bias.

$$ME = \frac{1}{n}\sum_{i=1}^{n}\hat{y}_i - y_i$$

The last section of the main loop saves all the results to a file, and uses markdown to make output files that print all the graphics and tables using the file 6.PrintResults.rmd.

```
 rmsetab[[run]]<-matrix(NA,10,length(modelTry),dimnames=list(1:10,modelTry))
 rmsetab[[run]]<-rmsetab[[run]][,colnames(rmsetab[[run]])!="Binomial"]
 metab[[run]]<-rmsetab[[run]]
 if(DoCrossValidation & length(which(modelFail[run,colnames(modelFail)!="Binomial"]=="-"))>0) {  #Don't
  if(NumCores>3 & useParallel)  {
    cl<-makeCluster(NumCores-2)
    registerDoParallel(cl)
  }
  datval$cvsample<-sample(rep(1:10,length=dim(datval)[1]),replace=FALSE)
  table(datval$cvsample,datval$Year)
  foreach(i=1:10 ) %do% {
   datin<-datval[datval$cvsample!=i,]
   datout<-datval[datval$cvsample==i,]
   datout$SampleUnits<-rep(1,dim(datout)[1])
   for(mod in which(!modelTry %in% c("Delta-Lognormal","Delta-Gamma"))) {
     if(modelFail[run,modelTry[mod]]=="-") {
       if(DredgeCrossValidation) modfit1<-findBestModelFunc(datin,modelTry[mod])[[1]] else
        modfit1<-FitModelFuncCV(formula(paste0("y~",modelTable[[run]]$formula[mod])),
           modType=modelTry[mod],obsdatval=datin)
       if(modelTry[mod]!="Binomial") {
        predcpue<-makePredictions(modfit1,modType=modelTry[mod], newdat = datout)
        rmsetab[[run]][i,modelTry[mod]]<-getRMSE(predcpue$est.cpue,datout$cpue)
        metab[[run]][i,modelTry[mod]]<-getME(predcpue$est.cpue,datout$cpue)
       } else {
        bin1<-modfit1
       }
     }
   }
   if("Delta-Lognormal" %in% modelTry | "Delta-Gamma" %in% modelTry) {
     posdat<-filter(datin,pres==1)
     for(mod in which(modelTry %in% c("Delta-Lognormal","Delta-Gamma"))) {
       if(modelFail[run,modelTry[mod]]=="-" & !(!is.numeric(posdat$Year) & min(table(posdat$Year))==0))
         if(DredgeCrossValidation) modfit1<-findBestModelFunc(posdat,modelTry[mod])[[1]] else
          modfit1<-FitModelFuncCV(formula(paste0("y~",modelTable[[run]]$formula[mod])),modType=modelTry
         predcpue<-makePredictions(bin1,modfit1,modelTry[mod],datout)
         rmsetab[[run]][i,modelTry[mod]]<-getRMSE(predcpue$est.cpue,datout$cpue)
         metab[[run]][i,modelTry[mod]]<-getME(predcpue$est.cpue,datout$cpue)
       }
     }
   }
  }
 if(NumCores>3) stopCluster(cl)
# Calculate RMSE and ME
 modelTable[[run]]$RMSE[modelTable[[run]]$model!="Binomial"]<-apply(rmsetab[[run]],2,mean,na.rm=TRUE)
 modelTable[[run]]$ME[modelTable[[run]]$model!="Binomial"]<-apply(metab[[run]],2,mean,na.rm=TRUE)
 write.csv(residualTab[[run]],paste0(outVal,"modelSummary.csv"))
 write.csv(rmsetab[[run]],paste0(outVal,"rmse.csv"))
 write.csv(metab[[run]],paste0(outVal,"me.csv"))
 #Select best model based on cross validation
   best<-which(!is.na( modelTable[[run]]$RMSE) &
     modelTable[[run]]$RMSE==min(modelTable[[run]]$RMSE,na.rm=TRUE))
  if(length(best) >0 ) {
   bestmod[run]<-modelTry[best]
```

```
   predbestmod[[run]]<-modPredVals[[run]][[modelTry[best]]]
   indexbestmod[[run]]<-modIndexVals[[run]][[modelTry[best]]]
 } else {
   bestmod[run]<-"None"
 }
}
#Rest commented out for User Guide
# save(list=c("numSp","yearSum","runName", "common", "sp","bestmod",
#   "predbestmod","indexbestmod","allmods","allindex","modelTable",
#  "modelSelectTable","modFits","modPredVals","VarCalc"
#  ,"modIndexVals","modelFail","rmsetab","metab",
#  "residualTab" ,"run","modelTry","EstimateIndex","EstimateBycatch",
#   "DoCrossValidation","indexVarNames","selectCriteria","sampleUnit",
#    "modelTry","catchType","catchUnit","residualTab",
#    "plotValidation","trueVals","trueCols","startYear"),
#   file=paste0(outVal,"/","resultsR"))
# rmarkdown::render("6.PrintResults.rmd",
#    params=list(outVal=outVal))
# file.rename(paste0(getwd(),"/6.PrintResults.pdf"),paste0(outVal,"/",common[run],catchType[run],"resul
# print(paste(run, common[run],"complete, ",Sys.time()))
# }
###################### End of analysis loop ######################

#Save R workspace
#if(saveR) save.image(file=paste0(outDir,"/R.workspace.rData"))
Sys.time()
```

```
## [1] "2021-10-20 09:52:22 EDT"
```

```
Sys.time()-StartTime
```

```
## Time difference of 42.70611 secs
```

Final results markdown

The R markdown file prints a .pdf file with the figures and tables to the output directory for each species labeled with the species and disposition code (e.g. SimulatedSpeciesDeadDiscardResults.pdf). These results may be all that is needed. However, if you want to look more closely at a specific model result, whether or not it was selected by the information criteria and cross-validation, all the outputs are printed to .csv files in the folders listed for each species. The total bycatch figures for each individual model show both the analytical estimateo of the total bycatch, and the mean across the Monte Carlo draws. These should be very similar, but may be different in years with small sample sizes due to sampling error.

```
#load(paste0(outVal,"/","resultsR"))
theme_set(theme_bw())
fignum<-1
tablenum<-1
```

Summary of results for SimulatedExample for Simulated species (Genus species)

2021-10-20

```
#Print data summary
cat("Table ", tablenum,". Input data summary.", sep="")
```

Table 1. Input data summary.

```
tablenum<-tablenum+1
yearSum[[run]] %>%
  mutate_if(is.numeric,   ~ ifelse(abs(.x) > 1, round(.x), round(.x, 2))) %>%
  remove_rownames() %>%
  kbl(format="latex") %>%
  kable_styling(
     latex_options = c("hold_position","scale_down","basic")) %>%
  print()
```

Year	OCat	OEff	OUnit	CPUE	CPse	Out	Pos	PFrac	Eff	Units	EFrac	UFrac	Cat	Cse
2009	6	814	33	0.01	0.01	0	3	0.09	17749	778	0.05	0.04	131	84
2010	6	1374	53	0.00	0.00	0	5	0.09	13906	541	0.10	0.10	61	47
2011	133	2516	81	0.09	0.03	0	22	0.27	20128	872	0.12	0.09	1064	42
2012	33	568	19	0.08	0.04	0	6	0.32	17564	1034	0.03	0.02	1021	84
2013	215	2327	82	0.09	0.02	0	31	0.38	20844	810	0.11	0.10	1926	53
2014	6	870	27	0.01	0.00	0	5	0.19	23539	799	0.04	0.03	162	83
2015	2	774	26	0.01	0.00	0	2	0.08	26741	729	0.03	0.04	69	108
2016	31	1957	55	0.02	0.00	0	13	0.24	28397	805	0.07	0.07	450	59
2017	2	527	14	0.00	0.00	0	1	0.07	27410	740	0.02	0.02	104	107
2018	3	159	4	0.01	0.01	0	1	0.25	24204	686	0.01	0.01	455	162

```
#Print modelTable including ModelFail
cat("Table ",tablenum,". Formula of ",selectCriteria," best model, along whether models were fit succes
```

Table 2. Formula of BIC best model, along whether models were fit successfully. A dash (-) means the model converged. Failure to converge may be from data (not all years had a positive observation for delta models), fit (models did not converge) or CV (bycatch estimates had very large CVs). If cross-validation was done, mean RMSE and mean ME across folds is shown (near zero is better)

```
tablenum<-tablenum+1
df1<-modelTable[[run]] %>%
  mutate(Failure=modelFail[run,]) %>%
   mutate_if(is.numeric,round,2)
if(!DoCrossValidation) df1<-dplyr::select(df1,-c("RMSE","ME"))
kbl(df1,format="latex") %>%
   kable_styling(
     latex_options = c("hold_position","basic")) %>%
    print()
```

model	formula	RMSE	ME	Failure
Binomial	1 + Year	NA	NA	-
Delta-Lognormal	1 + Year	0.17	0	-
TMBnbinom2	1 + Year + offset(log(Effort))	0.15	0	-
TMBtweedie	1 + Year	0.15	0	-

```
#Table residual summary
cat("Table ",tablenum,". DHARMa residual tests. Significant P values may indicate poor model specificati
```

Table 3. DHARMa residual tests. Significant P values may indicate poor model specification.

```
tablenum<-tablenum+1
data.frame(residualTab[[run]]) %>%
 kbl(format="latex",digits = 2) %>%
   kable_styling(
     latex_options = c("hold_position","scale_down","basic")) %>%
    print()
```

	Binomial	Delta.Lognormal	TMBnbinom2	TMBtweedie
KS.D	0.03	0.09	0.03	0.05
KS.p	0.78	0.46	0.76	0.24
Dispersion.ratio	1.01	0.90	0.40	1.61
Dispersion.p	0.89	0.47	0.18	0.10
ZeroInf.ratio	1.00	NA	1.00	1.00
ZeroInf.p	0.97	NA	0.90	1.00
Outlier	0.00	0.00	2.00	4.00
Outlier.p	1.00	1.00	1.00	0.56

```
# Figures of All models together
if(EstimateBycatch ) {
 if(plotValidation)  plotSumsValidate(filter(allmods[[run]],Valid==1),trueVals,NULL,trueCols[run]) else
    plotSums(filter(allmods[[run]],Valid==1),"All",NULL)
  cat("\n Figure ",fignum,". Total bycatch estimates for all valid models, including a simple unstratifi
  fignum<-fignum+1
}
```

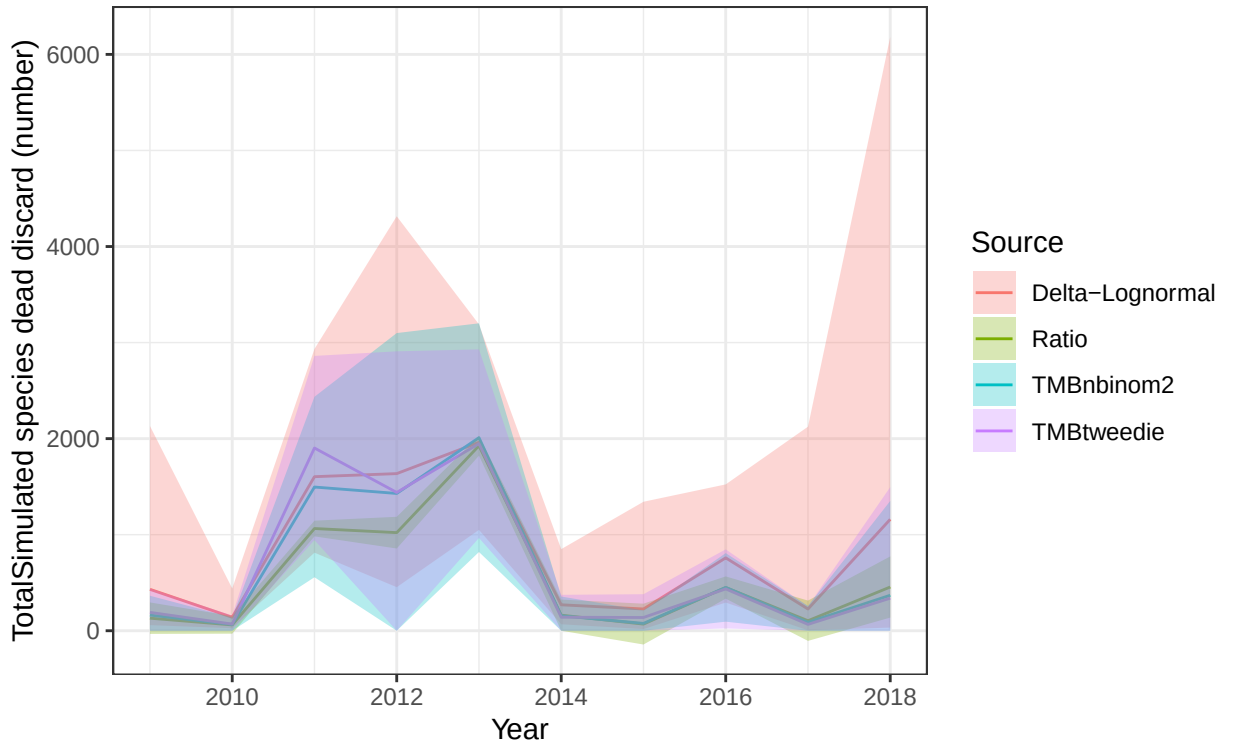

Figure 1. Total bycatch estimates for all valid models, including a simple unstratified ratio estimator, for Simulated species, with 95 % confidence interval.

```
if(EstimateIndex & any(allindex[[run]]$Valid==1)) {
 plotIndex(filter(allindex[[run]],Valid==1),"All",NULL)
 cat("\n Figure ",fignum,". Abundance indices from all valid models for ",common[run],". \n",sep="")
 fignum<-fignum+1
}
```

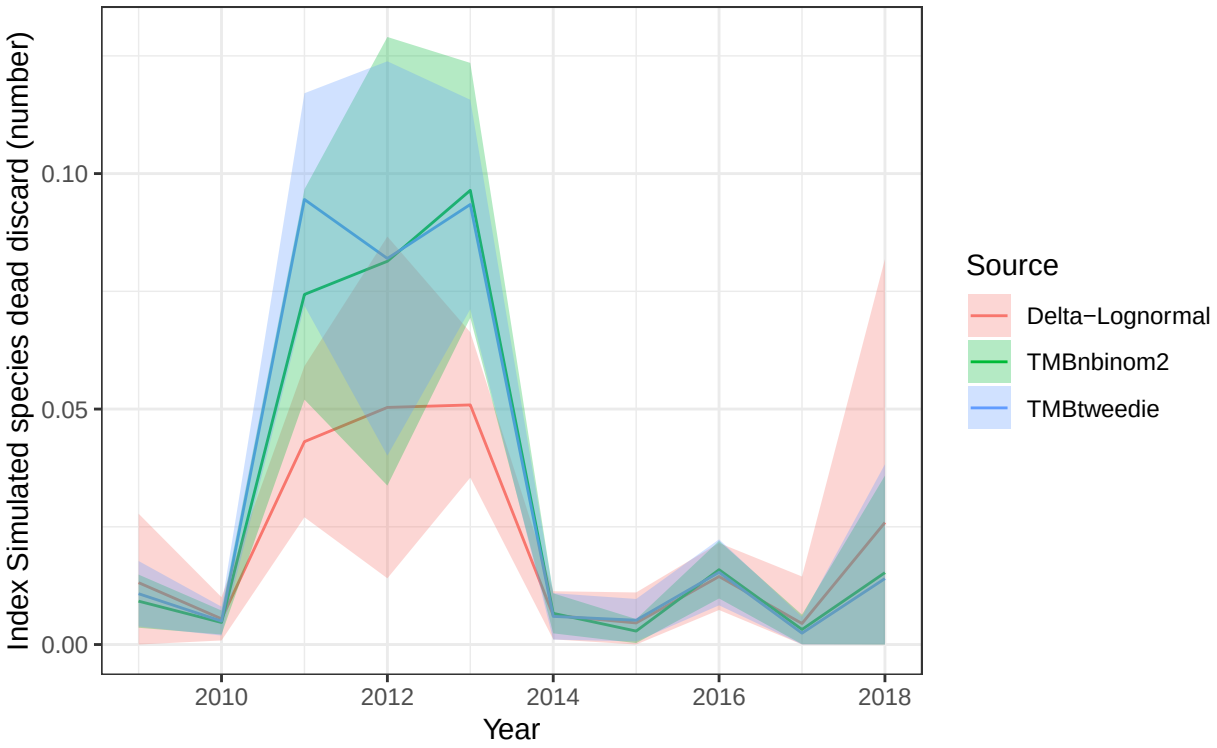

Figure 2. Abundance indices from all valid models for Simulated species.

```
#Show cross validation figures
if(DoCrossValidation &!all(is.na(modelTable[[run]]$RMSE))) {
 plotCrossVal(rmsetab[[run]],metab[[run]],NULL)
 cat("\n Figure ",fignum,". Cross validation results for ",common[run],". Lowest RMSE model is ",bestmo
 fignum<-fignum+1
}
```

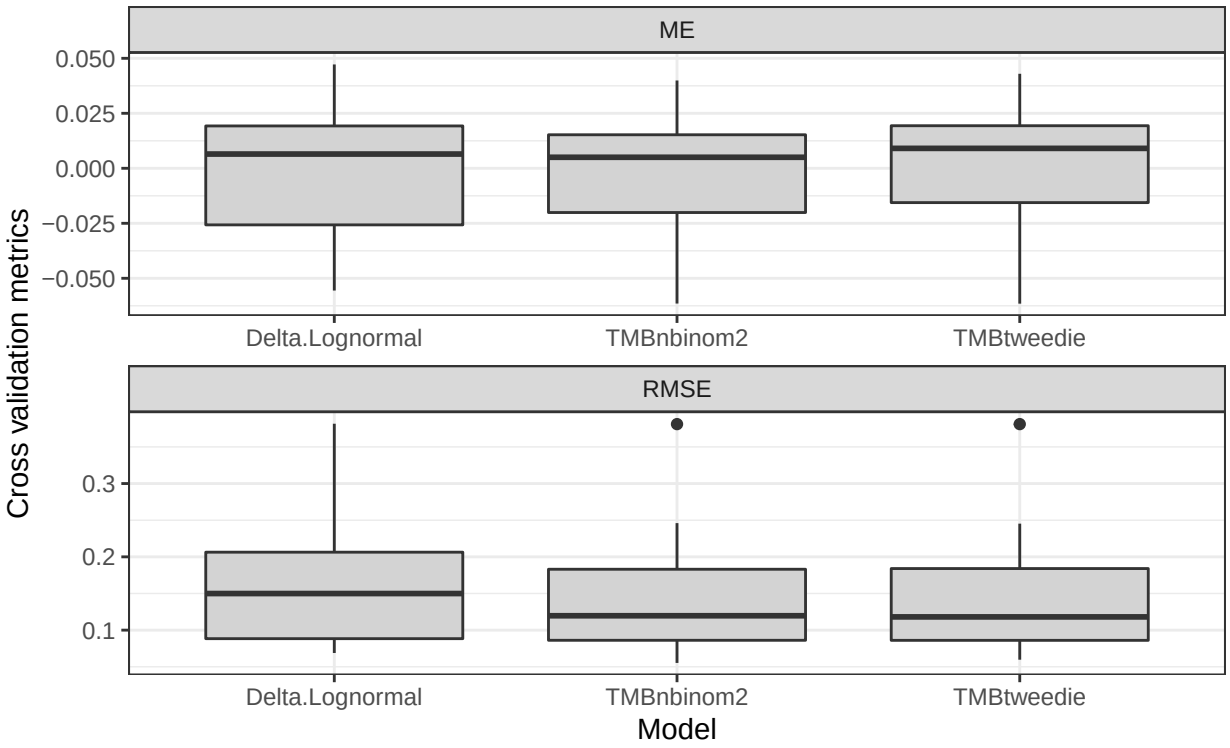

Figure 3. Cross validation results for Simulated species. Lowest RMSE model is TMBnbinom2.

```
#Print for each model type
for(mod in 1:length(modelTry)) {
if(modelFail[run,mod]=="-") {
  cat("\n Table ",tablenum,". Model selection table for ",modelTry[mod],". Weights are calculated based
  tablenum<-tablenum+1
  data.frame(modelSelectTable[[run]][[modelTry[mod]]]) %>%
   mutate_if(is.numeric,~ ifelse(abs(.x) > 1, round(.x,1), round(.x, 2))) %>%
   kbl(format="latex") %>%
   kable_styling(
     latex_options = c("hold_position","scale_down","basic")) %>%
    print()
   temp<-ResidualsFunc(modFits[[run]][[modelTry[mod]]],modelTry[mod],fileName=NULL)
   cat("\n Figure ",fignum,". Residuals for the ",selectCriteria, " best model for ",        modelTry[mo
   fignum<-fignum+1
  lineText=ifelse(VarCalc=="Simulate","Solid line is the best estimate and dashed line is the mean acros
  if(EstimateBycatch) {
   if(plotValidation & modelTry[mod]!="Binomial")  plotSumsValidate(filter(allmods[[run]],Source==modelT
   plotSums(modPredVals[[run]][[modelTry[mod]]],modelTry[mod],fileName=NULL)
  if(modelTry[mod]=="Binomial")  cat("\n Figure ",fignum,". Estimated total number of positive ",sampleU
   cat("\n Figure ",fignum,". Estimated total bycatch from ",modelTry[mod]," with ",(1-CIval)*100,"% co
   fignum<-fignum+1
 }
 if(EstimateIndex) {
   plotIndex(modIndexVals[[run]][[modelTry[mod]]],modelTry[mod],fileName=NULL)
   cat("\n Figure ",fignum,". Estimated relative index from ",modelTry[mod],". \n",sep="")
   fignum<-fignum+1
 }
```

```
}
}
```

Table 4. Model selection table for Binomial. Weights are calculated based on BIC.

	X.Intercept.	season	Year	season.Year	AICc	AIC	BIC	df	logLik	selectCriteria	delta	weight
0	-2.3	NA	+	NA	412.8	412.3	452	10	-196.1	452	0.0	0.95
1	-2.3	+	+	NA	414.9	414.2	458	11	-196.1	458	5.9	0.05
3	-2.3	+	+	+	420.7	418.4	498	20	-189.2	498	46.0	0.00

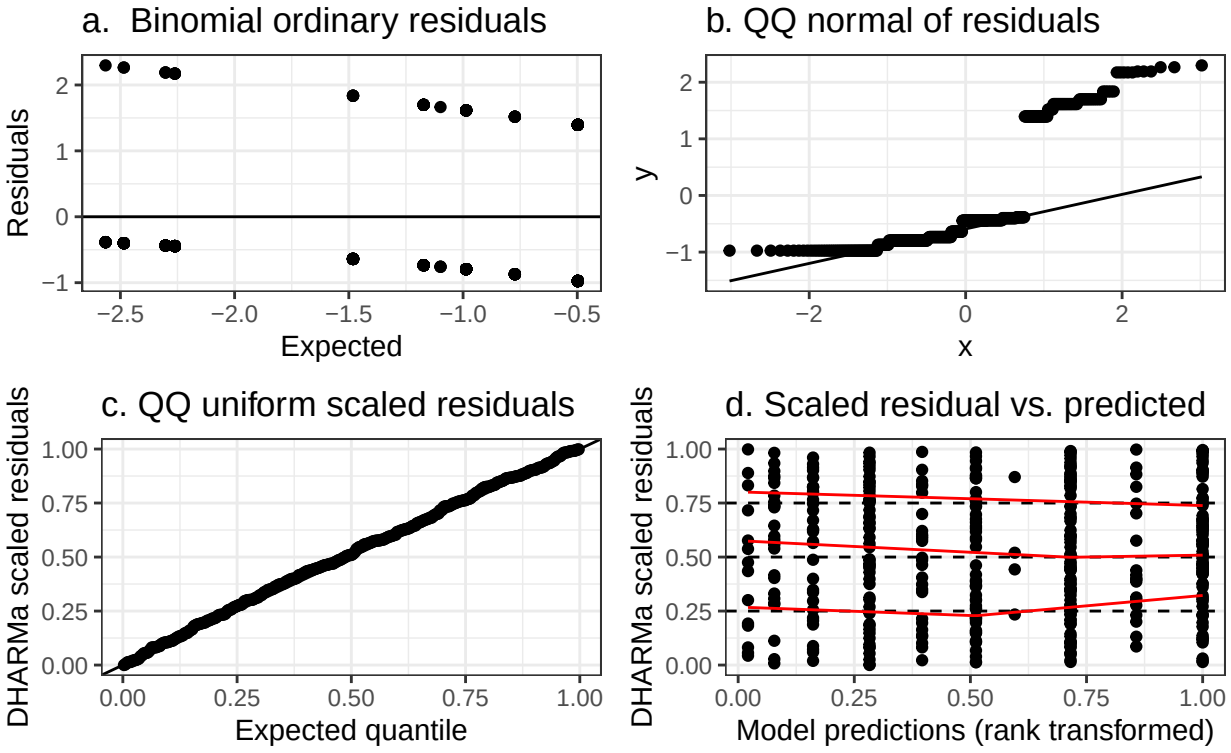

Figure 4. Residuals for the BIC best model for Binomial.

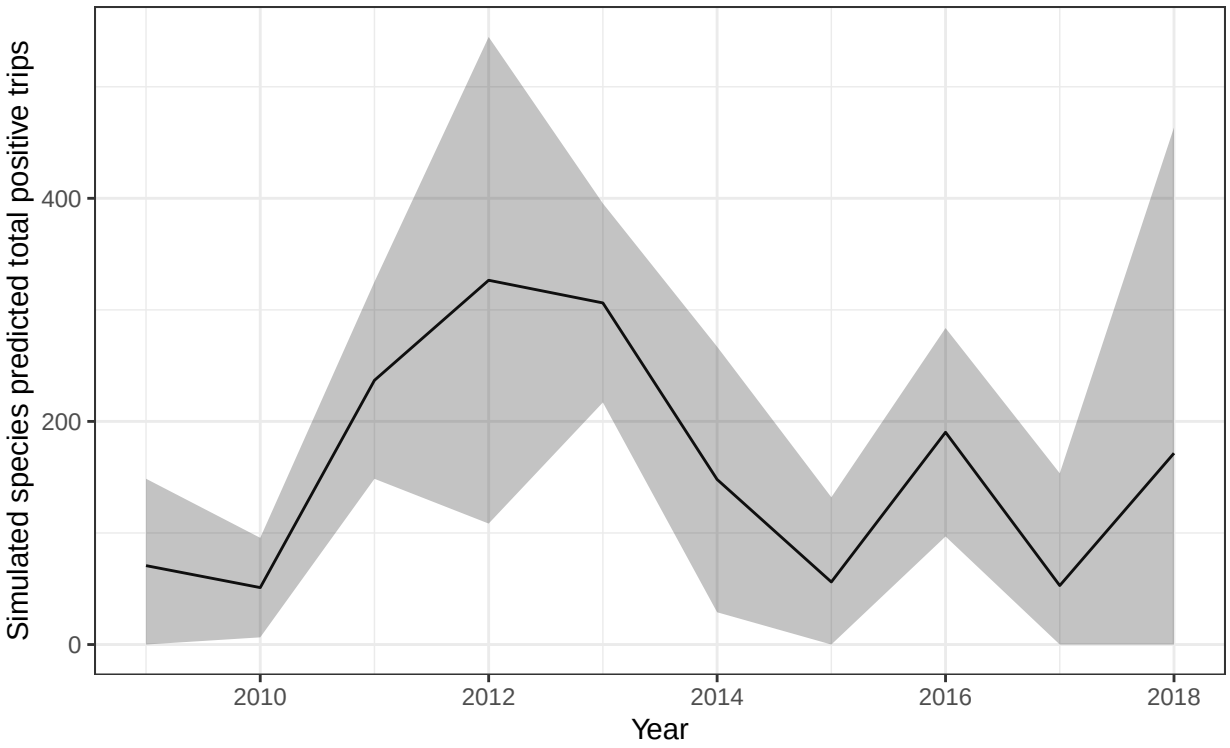

Figure 5. Estimated total number of positive trips from Binomial with 95% confidence interval.

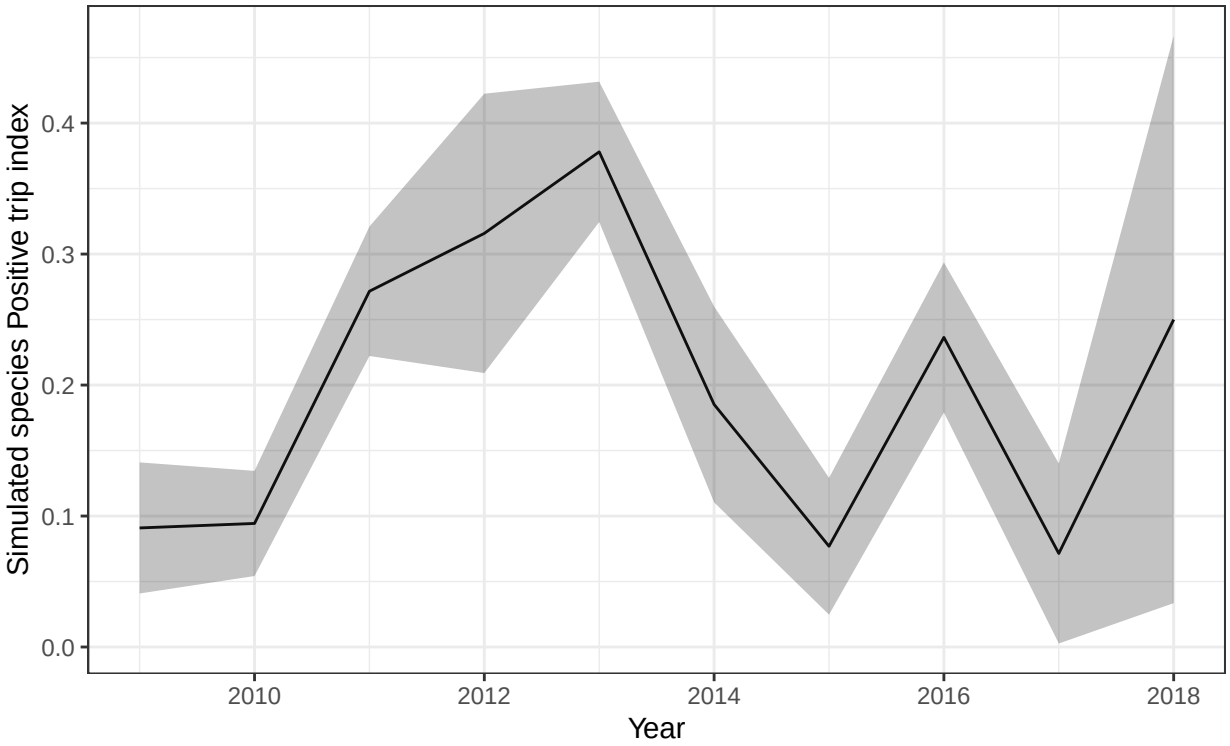

Figure 6. Estimated relative index from Binomial.

Table 5. Model selection table for Delta-Lognormal. Weights are calculated based on BIC.

	X.Intercept.	season	Year	AICc	AIC	BIC	df	logLik	selectCriteria	delta	weight
0	-2.1	NA	+	285.8	282.4	309.8	11	-130.2	309.8	0.0	0.69
1	-2.1	+	+	285.6	281.5	311.4	12	-128.8	311.4	1.6	0.31

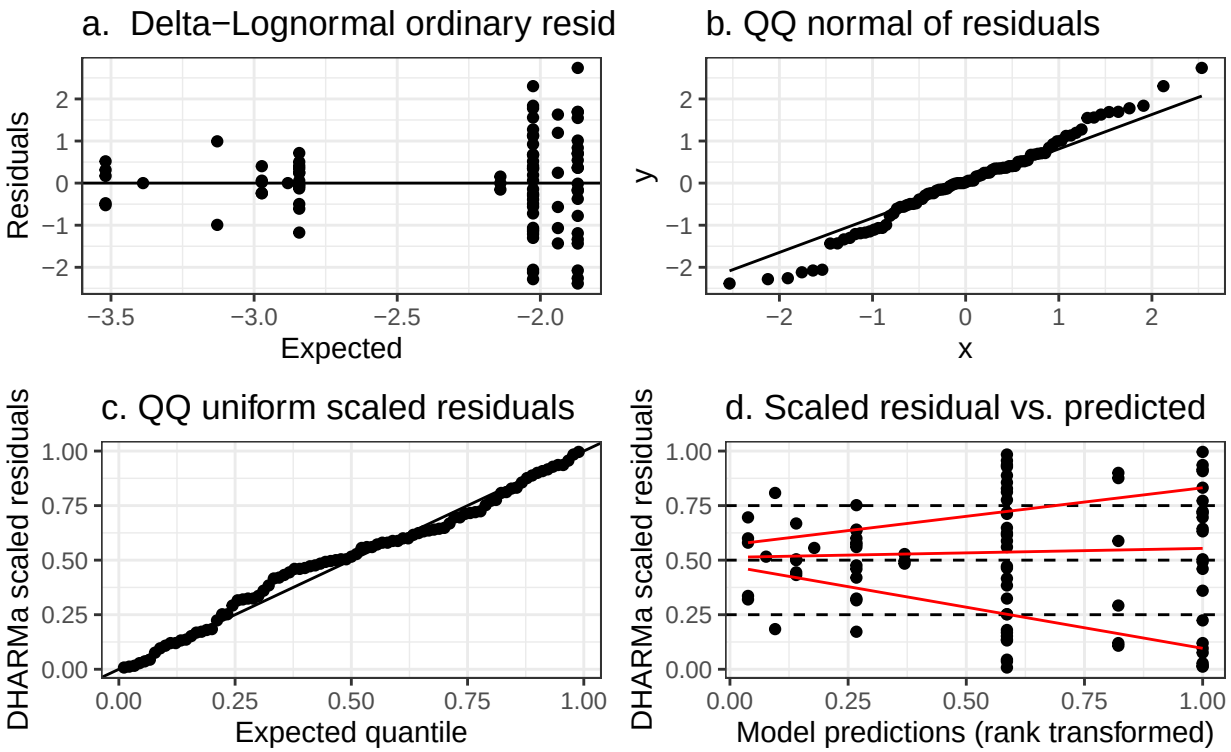

Figure 7. Residuals for the BIC best model for Delta-Lognormal.

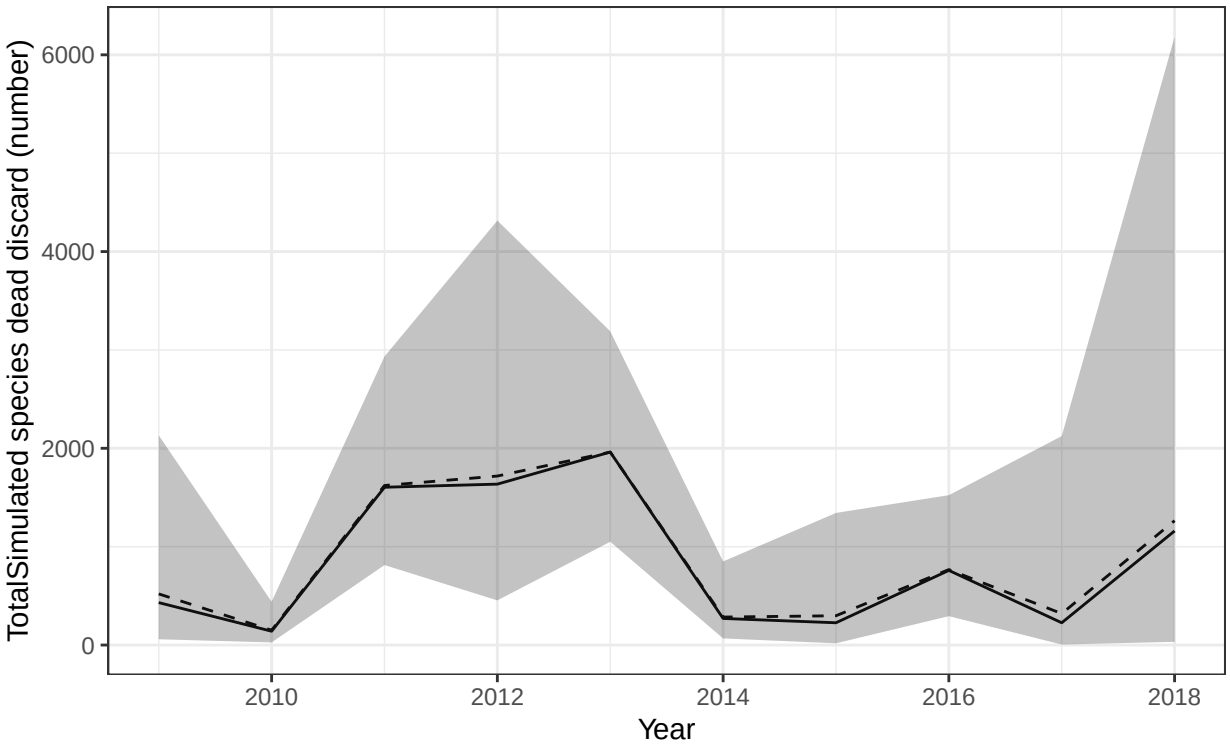

Figure 8. Estimated total bycatch from Delta-Lognormal with 95% confidence interval.

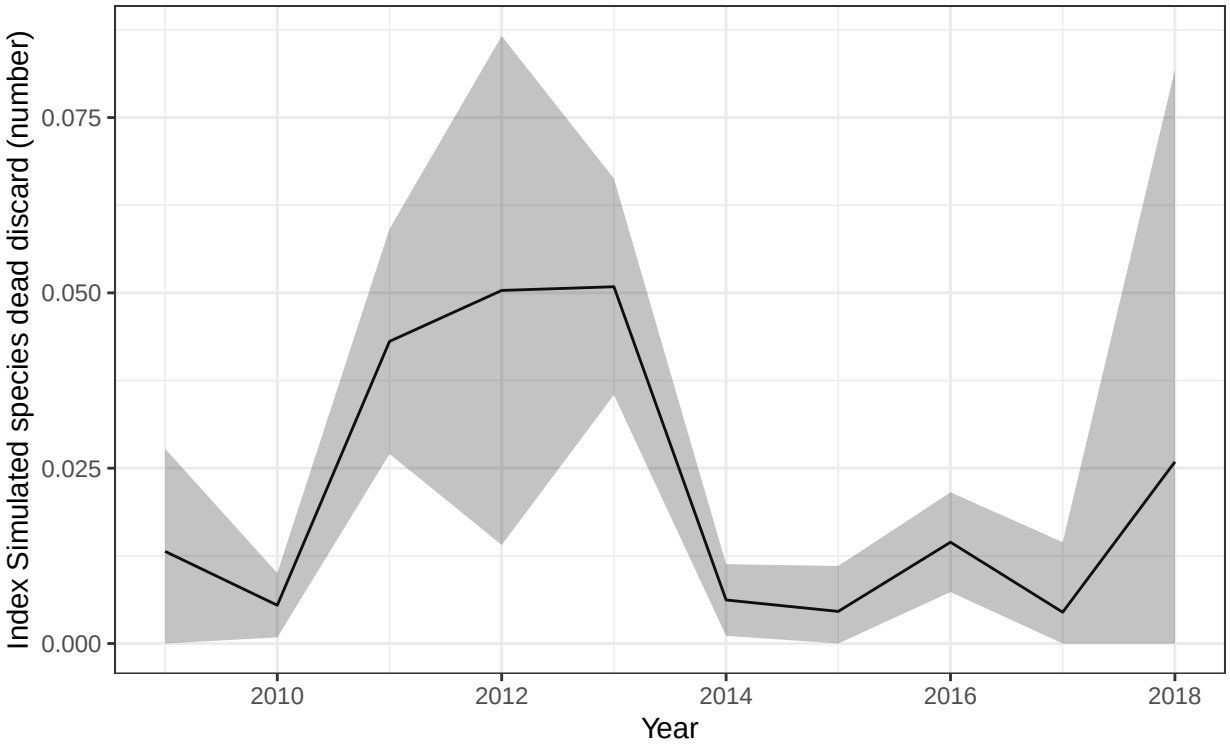

Figure 9. Estimated relative index from Delta-Lognormal.

Table 6. Model selection table for TMBnbinom2. Weights are calculated based on BIC.

	cond..Int..	disp..Int..	cond.season.	cond.Year.	cond.season.Year.	cond.offset.log.Effort...	AICc	AIC	BIC	df	logLik	selectCriteria	delta	weight
0	-4.7	+	NA	+	NA	+	815.6	814.9	858.6	11	-396.4	858.6	NA	NA
1	-4.7	+	+	+	NA	+	816.2	815.4	863.1	12	-395.7	863.1	NA	NA
3	-4.6	+	+	+	+	+	NA	NA	NA	21	NA	NA	NA	NA

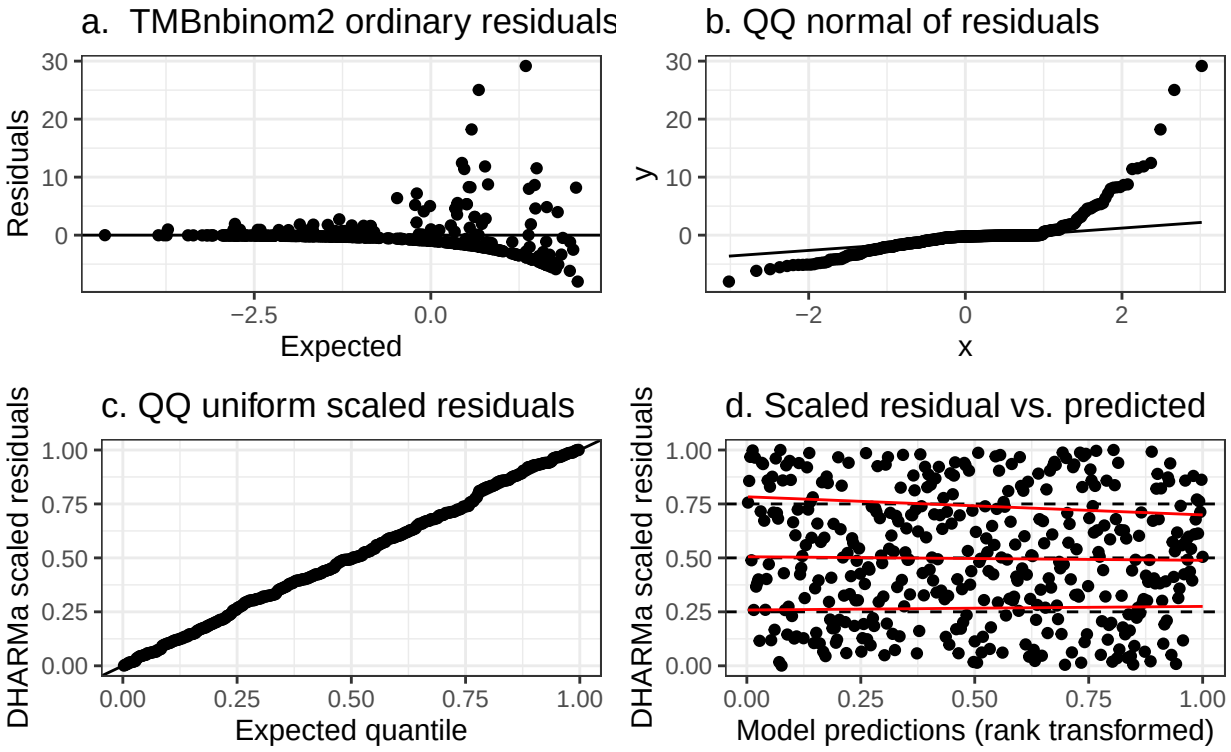

Figure 10. Residuals for the BIC best model for TMBnbinom2.

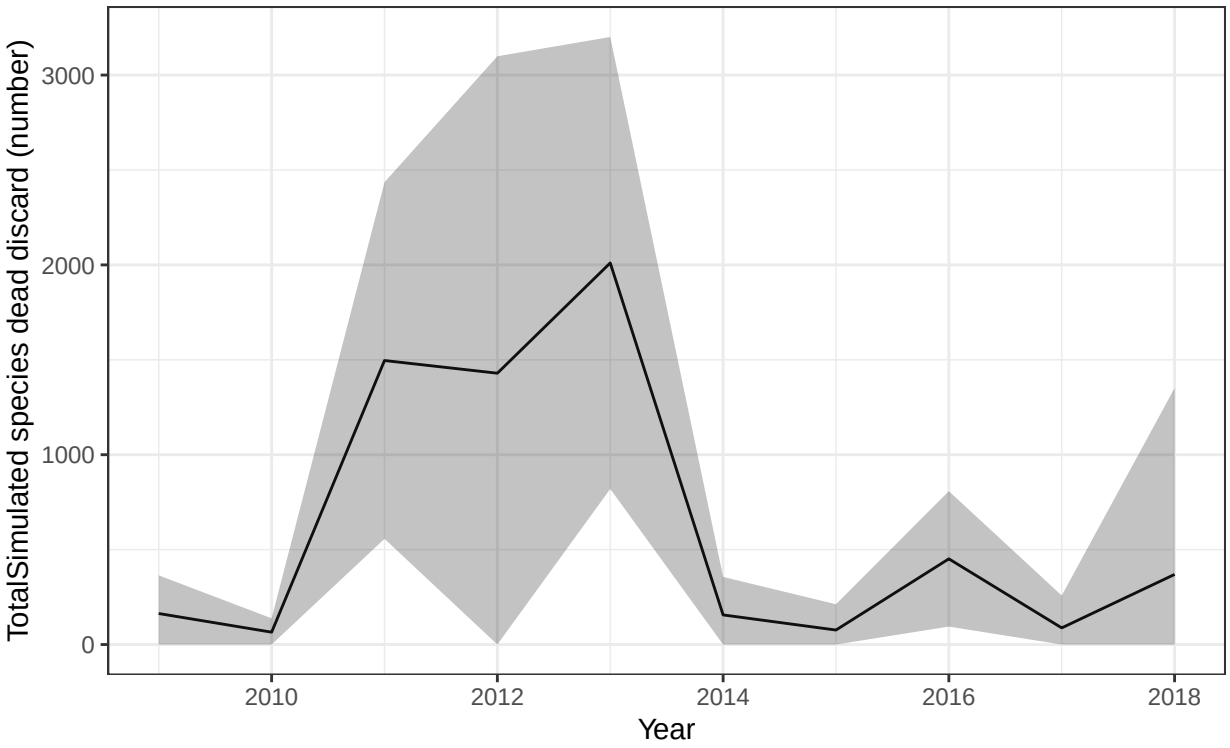

Figure 11. Estimated total bycatch from TMBnbinom2 with 95% confidence interval.

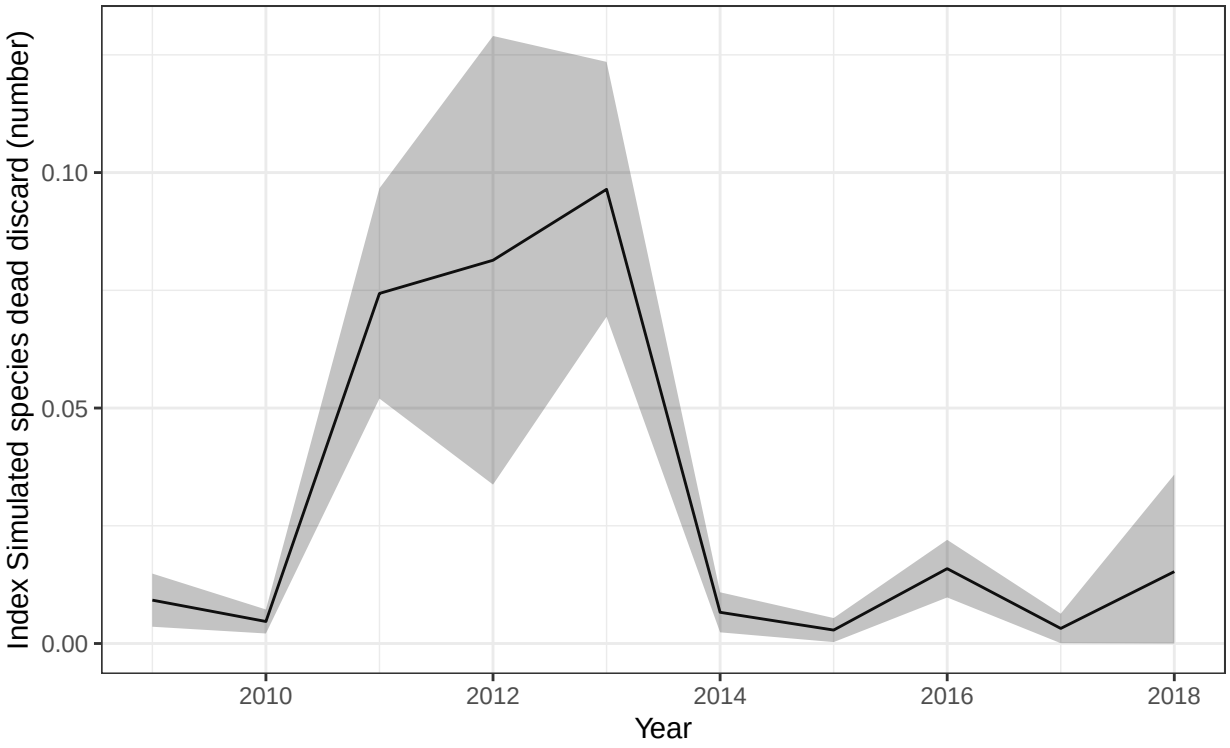

Figure 12. Estimated relative index from TMBnbinom2.

Table 7. Model selection table for TMBtweedie. Weights are calculated based on BIC.

	cond..Int..	disp..Int..	cond.season.	cond.Year.	cond.season.Year.	AICc	AIC	BIC	df	logLik	selectCriteria	delta	weight
0	-4.5	+	NA	+	NA	288.7	287.9	335.6	12	-131.9	335.6	NA	NA
1	-4.5	+	+	+	NA	286.3	285.4	337.1	13	-129.7	337.1	NA	NA
3	-4.5	+	+	+	+	NA	NA	NA	22	NA	NA	NA	NA

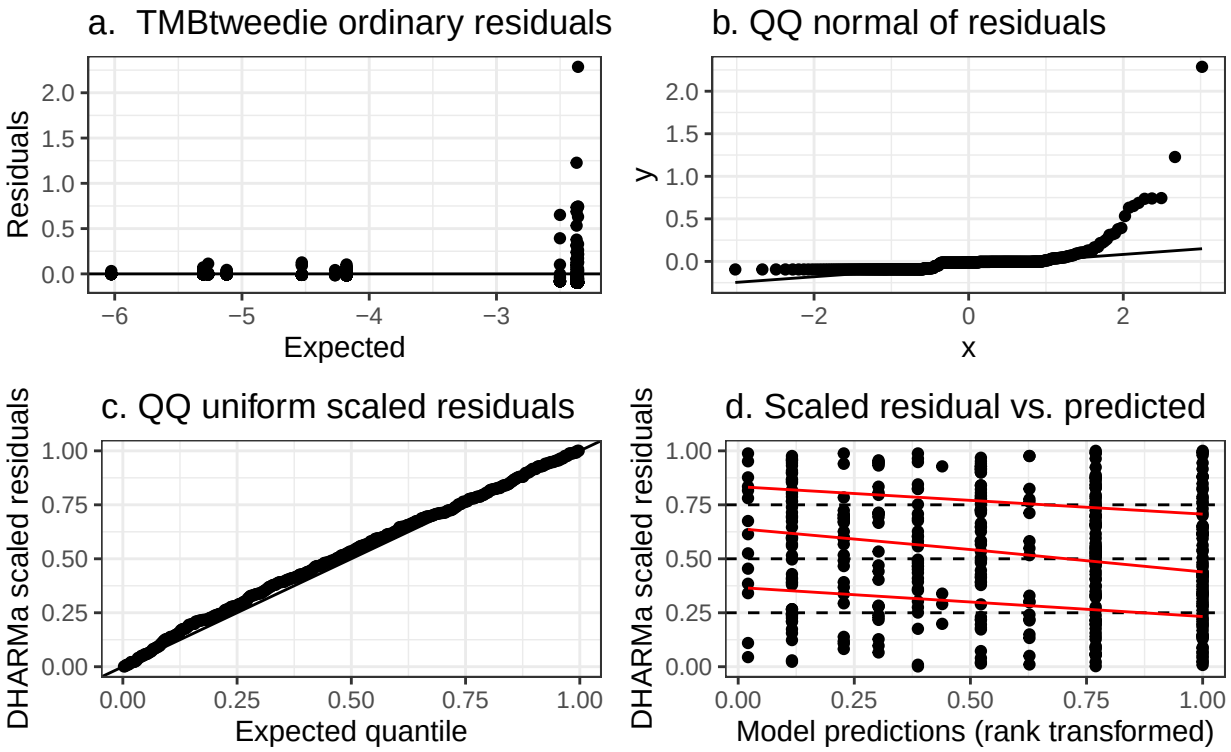

Figure 13. Residuals for the BIC best model for TMBtweedie.

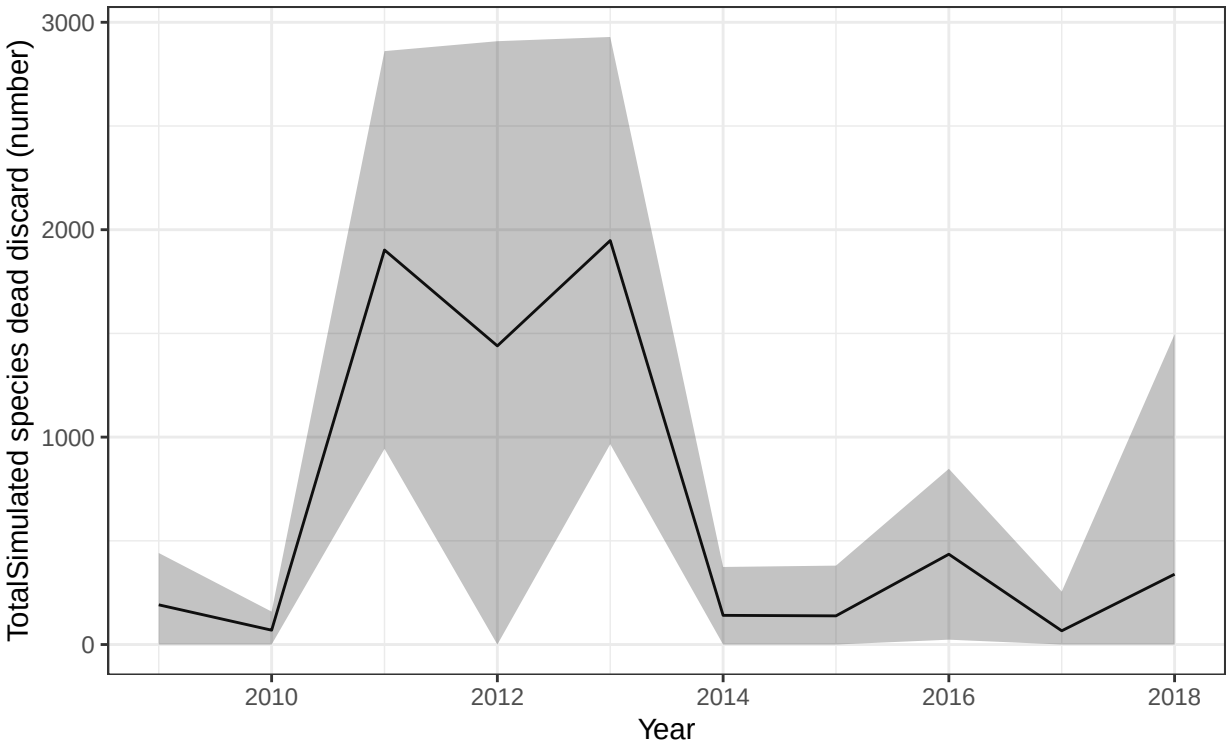

Figure 14. Estimated total bycatch from TMBtweedie with 95% confidence interval.

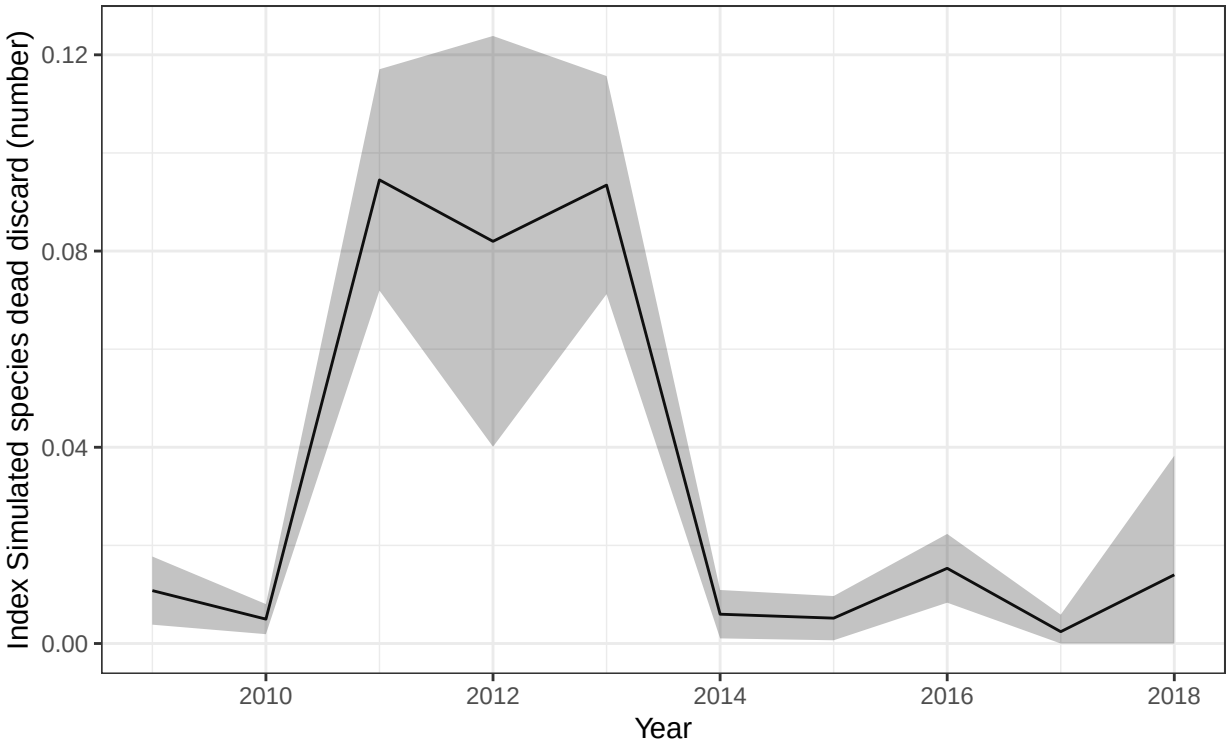

Figure 15. Estimated relative index from TMBtweedie.

Conclusions

Although this code automates the whole process of model selection, it is not recommended that the final model be used without looking closely at the outputs. The selected model must have good fits and should be reasonably consistent with data according to the DHARMa residuals. The results should appear reasonable and be around the same scale as the ratio estimator results. The model should not be overly complex. Also, look at the model selection table to see if other models are also supported by the data.

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