Simple\_report

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# Overview

An extention of the Verde fish model [here](https://github.com/jdtonkin/fishmodel-verde)

Code and data associated with [Rogosch et al. 2019](https://esajournals.onlinelibrary.wiley.com/doi/full/10.1002/ecs2.2681) manuscript examining fish communities in the Verde River, AZ, USA. The model is a community-wide stochastic matrix population model that links population dynamics with river flow regimes.

## Readme start

## Required manusript libraries  
library(ggplot2)  
library(plyr)  
library(tidyverse)

## -- Attaching packages ------------------------------------------------------------------------------------ tidyverse 1.2.1 --

## v tibble 2.1.3 v purrr 0.3.2  
## v tidyr 1.0.0 v dplyr 0.8.3  
## v readr 1.3.1 v stringr 1.4.0  
## v tibble 2.1.3 v forcats 0.4.0

## -- Conflicts --------------------------------------------------------------------------------------- tidyverse\_conflicts() --  
## x dplyr::arrange() masks plyr::arrange()  
## x purrr::compact() masks plyr::compact()  
## x dplyr::count() masks plyr::count()  
## x dplyr::failwith() masks plyr::failwith()  
## x dplyr::filter() masks stats::filter()  
## x dplyr::id() masks plyr::id()  
## x dplyr::lag() masks stats::lag()  
## x dplyr::mutate() masks plyr::mutate()  
## x dplyr::rename() masks plyr::rename()  
## x dplyr::summarise() masks plyr::summarise()  
## x dplyr::summarize() masks plyr::summarize()

library(popbio)  
## Required simulation libraries  
# library(plyr)  
# library(tidyverse)  
# library(popbio)  
library(iterators)  
library(foreach)

##   
## Attaching package: 'foreach'

## The following objects are masked from 'package:purrr':  
##   
## accumulate, when

# library(doMC)  
library(doParallel)

## Loading required package: parallel

library(doSNOW)

## Loading required package: snow

##   
## Attaching package: 'snow'

## The following objects are masked from 'package:parallel':  
##   
## clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,  
## clusterExport, clusterMap, clusterSplit, makeCluster,  
## parApply, parCapply, parLapply, parRapply, parSapply,  
## splitIndices, stopCluster

## This is code to make a list of all possible future flow regimes.  
## This will then get read into the main model (fish-model-all-spp.R) as a list.   
## Make flowdata file with spring and summer floods and minimum baseflow dur  
  
## rm(list = ls()) # clearing the workspace   
  
# library(plyr)  
# library(tidyverse)  
library(waterData) # for getting USGS flow data  
  
## Verde Fish Model  
## Code used for simulations of spp combos.  
## This is to be run in combo with shell script on HPC.  
## Not part of Rogosch ms.   
  
## Required libraries  
  
## Better to install individually  
# install.packages("plyr", lib="Rpackages", repos = "http://cran.case.edu")  
# install.packages("tidyverse", lib="Rpackages", repos = "http://cran.case.edu")  
# install.packages("popbio", lib="Rpackages", repos = "http://cran.case.edu")  
# install.packages("iterators", lib="Rpackages", repos = "http://cran.case.edu")  
# install.packages("foreach", lib="Rpackages", repos = "http://cran.case.edu")  
# install.packages("doMC", lib="C://Program Files/R/R-3.6.1/library/", repos = "http://cran.case.edu")  
# install.packages("doParallel", lib="Rpackages", repos = "http://cran.case.edu")  
# install.packages("doSNOW", lib="Rpackages", repos = "http://cran.case.edu")  
  
## \* SETUP ---------------------------------------------------------------------  
  
rm(list = ls()) # clearing the workspace   
  
## Bringing in flow data  
all.scenarios.list <- readRDS('./data/all\_scenarios\_list.rds')  
## Loading functions from functions.R file--------------------------------------  
source('./R/functions.R')

#### fish-model-all-spp.R

“is the core model used to generate results in the manuscript: community-wide stage-structured stochastic matrix population model (7 spp.).”

# source("./R/fish-model-all-spp.R")  
## \* SETUP ---------------------------------------------------------------------  
  
#rm(list = ls()) # clearing the workspace   
  
## Bringing in flow data  
all.scenarios.list <- readRDS('./data/all\_scenarios\_list.rds')  
  
## When using natural flow data, just pull it out from the list here  
flowdata <- all.scenarios.list$natural.flow  
  
count <- 54 # 54 years in flow record, if count = 45 goes to 2008   
iterations <- 10 # number of replicate projections to run (mid loop)  
  
## Modifiers  
modifiers <- read.csv('data/modifiers-all-spp.csv')  
  
## adding 'Modifier' value from csv to 'Code' in csv  
for(j in 1:length(modifiers[,1])) {  
 nam <- paste(modifiers[j,4])  
 assign(nam, modifiers[j,5])   
}  
  
## Vital rates  
## Baseline maturation probability, aCACL3 (adult senescence rate)  
## Background mortality  
## Initial volume in grams in 100-m reach  
## Fecundity based on year type and GSI  
## Stage specific densities (ind./g)  
  
vitalrates <- read.csv('data/vital-rates.csv')   
  
## assigning vital rate values from column 3 to 'code' in column 2  
for(k in 1:length(vitalrates[,1])) {  
 nam <- paste(vitalrates[k,2])  
 assign(nam, vitalrates[k,3])   
}  
  
## \* Key -----------------------------------------------------------------------  
## CACL (Catostomus clarki) – desert sucker   
## GIRO (Gila robusta) – roundtail chub  
## LECY (Lepomis cyanellus) – green sunfish  
## CAIN (Catostomus insignis) – sonora sucker  
## MIDO (Micropterus dolomieu) - smallmouth bass  
## CYLU (Cyprinella lutrensis) – red shiner  
## AMNA (Ameiurus natalis) – yellow bullhead  
  
## Average total volume of water per 100 m reach in m3: 307  
## Average total fish biomass per 100 m reach in g: 4766  
## Average total biomass Bonar 2004 in g/100m2: 606  
## Max for a 100 m rech in Gibson samples (excluding GAAF): 6996  
  
## vector of species names  
sppnames <- c('CACL', 'GIRO', 'LECY', 'CAIN', 'MIDO', 'CYLU', 'AMNA')  
  
K = 47660 # mean for 1-km reach across 6 replicate reaches  
  
## Loading functions from functions.R file -------------------------------------  
source('./R/functions.R')  
  
## \* ITERATION PARAMETERS ------------------------------------------------------  
## Setting up arrays/vectors to fill with data from loops  
  
## Mid loop details ------------------------------------------------------------  
## 'iterations' - number of replicate flow sequences to run for averaging  
  
years <- flowdata$year  
stages <- as.character(c("S1", "S2", "S3"))  
  
## Total. N of stages 2 and 3 each year ----------------------------------------  
## Takes all stages 2 and 3 and sums them for each year and iteration  
# Total.N <- array(0,  
# dim = c(54, iterations),  
# dimnames = list(years, 1:iterations)  
# )

#### First break in code …

#### make-multiflow.R This is code to make a list of all possible future flow regimes. Pulls hydrograph data from USGS. This will then get read into the main model (fish-model-all-spp.R) as a list.

* functions.R: Some functions used in running the various scripts.
* fish-model-flowsims.R: Code used for simulations of spp combinations. This is to be run in combination with shell script (not included in repo) on HPC. This is not part of the Rogosch et al. manuscript.
* Raw data
* vital-rates.csv: Vital rates needed to run the model.
* modifiers-all-spp.csv: Modifiers that act on the vital rates under different hydrograph settings.
* Rel\_Abu\_Verde\_94-08.csv: Empirical fish relative abundance data from the Verde River, used to test model.

The remaining data is generated from the various scripts. But generated flow data required to run fish-model-all-spp.R is included in the repo.

[[<https://zenodo.org/badge/DOI/10.5281/zenodo.1308208.svg>][<https://zenodo.org/badge/DOI/10.5281/zenodo.1308208.svg>]]

## Simple layout